Internal migration, area effects and health: Does where you move to impact upon your health?

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Abstract

Evidence surrounding the importance of neighbourhood on health has been mostly restricted to observational data analyses. However, observational data are often the only source of information available to test this association and can fail to accurately draw out casual effects. This study employs a pseudo-experimental design to provide a novel test for the evidence of neighbourhood effects on health, using migration as a mechanism for assessing the role of neighbourhood. Coarsened exact matching was employed on the British Household Panel Survey (2006-2008) to analyse the association between migration (by area type, measured using a classification of mortality patterns) and health. Although an overall significant positive association between migration and health was observed, once the effect was disaggregated by location and destination it disappeared. Rather, evidence of health selective migration was found whereby individuals of poorer health migrated to areas that displayed poorer health and social characteristics (and *vice versa*). Migration is an important process that through the social sorting of individuals in terms of their health, contributes to the growing polarisation and inequality in health patterns. The study helps to build upon previous research through providing a new and stronger form of analysis that reduces the influence of bias on results. Incorporating this under-utilised methodology and research design in future studies could help develop public health and geographical research.

Key Words: Migration; Neighbourhood; Health; Matching; British Household Panel Survey.

Introduction

Neighbourhood has been shown to be important in influencing individual health (Pickett & Pearl, 2001; Riva, Gauvin, & Barnett, 2007). However, some researchers have questioned the importance of such findings. Part of the argument lies in methodological limitations (Riva et al., 2007). Most studies that have found associations between neighbourhood factors and health have been based on observational data. However, such data can usually only present cross-sectional associations and is constrained in its ability to draw out causal effects from the data (S. M. Iacus, King, & Porro, 2012). Nevertheless, observational data are often the only available source of information on a topic.

Randomised controlled trials are viewed as the gold standard of evidence, however they are often not viable in social science research. Nevertheless, incorporating aspects of their design can give more accurate estimates of effects not offered by traditional methods. Such an approach can be applied to test the possible role of neighbourhood on health. Although we as researchers cannot physically alter the characteristics of the environment in which an individual lives, an individual themselves can. If neighbourhood is important then, as individuals migrate to an area with different neighbourhood characteristics, we would expect to observe an effect on their health.

Research that has examined the association between internal migration and health has been usually limited to analysing whether health inequalities are the product of migration patterns (Bentham, 1988; Boyle, 2004; Anonymous, 2000; Cox, Boyle, Davey, & Morris, 2007; Popham, Boyle, O'Reilly, & Leyland, 2011; Riva, Curtis, & Norman, 2011; Tunstall, Pickett, & Johnson, 2010). There is evidence of health selective migration, whereby internal migration acts as an internal sorting process with individuals of the best health migrating to the areas that contain the healthiest individuals (and *vice versa*). The incorporation of these

studies into research about the role of neighbourhood are limited. They often ignore migration between multiple different area types (e.g. just urban versus rural or deprived versus affluent, reducing the detail of the analysis) and are conducted over long time periods (usually comparing place of birth with current residence/place of death). There are also few sources of data that combine information on health and migration (Boyle, 2004; Larson, Bell, & Young, 2004).

'Moving to Opportunity for Fair Housing Demonstration' (MtO) is one of very few studies to have demonstrated the usefulness of incorporating migration into analysing the role of neighbourhood. Families who lived in deprived neighbourhoods in five US cities were offered either a housing voucher to move to an affluent areas (through subsidised rent), traditional housing support with no restriction on where they could move to, or no additional help (as part of a randomised controlled trial) (Shroder & Orr, 2012). It has been shown that those who migrated to the affluent areas experienced a small improvement in health across multiple domains including obesity and risk of diabetes (Ludwig et al., 2011), subjective well-being (Ludwig et al., 2012) and mental health (Leventhal & Brooks-Gunn, 2003). Learning from this research design could help frame a useful empirical model of analysis.

This paper applies the design of the MtO study and randomised controlled trials to observational data through using matching methods to create a pseudo-experiment to estimate the impact of migration on health to better understand the role of neighbourhoods. Only the potential impact of migration across neighbourhood types is assessed here. The overall impact of migration is likely to be higher so this paper provides a conservative estimate. It is also important to point out that here we are considering relatively short term migration (impact after one year) and not the possible effects of where people live across their whole lifetimes from place of childhood to place of eventual demise.

Methodology

Data

Data were taken from the British Household Panel Survey (BHPS), a large longitudinal survey with roughly 10,000 individuals at each yearly wave (1991 to 2008). The survey contains data on both health and migration (as well as demographic information). Special licence access was granted by the Economic and Social Data Service that provided data on the geographical location of individuals for each wave (Lower Super Output Area).

The waves 2006 to 2008 were pooled together to improve both the stability and the power of analyses. These years were chosen as they correspond with the measure of neighbourhood. Data were recoded to identify variables for the same individual for both the year prior to (referred to as year A) and including the year where migration was taken from (year B). This allowed a stable and accurate model to be built and tested. This approach has been useful in previous migration research (Evandrou, Falkingham, & Green, 2010). There were 1789 migrations in the data (8.6%), although only 1259 individuals contained geographical data at both time points (see Supplementary Table 1 for the cross-classification of migrations between area type).

Through pooling the panel data, individuals interviewed in each wave will appear multiple times. This may be problematic as correlation exists within the cases of the data. 29.6% (529) of individuals migrated more than once. However, any issues this will create are likely to be offset by the advantages of having a greater sample size (Evandrou et al., 2010). Effectively tripling the data set gives greater power when running models, keeping the standard errors lower and providing more accurate results. We re-ran the analyses excluding these cases and the results remained similar.

The types of areas that individuals migrated between was captured using a recently developed neighbourhood classification of mortality for England and Wales, 2006-2008 (Anonymous, 2013; Anonymous, 2014). Mortality patterns across 63 causes for Middle Super Output Areas (MSOAs) (n=7194) were input into a k-means cluster analysis, with the results producing eight distinct clusters of mortality patterns. The mortality characteristics of the clusters were (including additional demographic characteristics of the areas not included in the model; see Anonymous (2013) and Anonymous (2014) for greater detail):

1. *Best Health and Most Desirable:* The cluster contain the lowest mortality rates across all causes of death included in the model. Life expectancy at birth was 81.3 for males and 85.1 for females. Lowest levels of poverty. 1562 MSOAs.

2. *Average Mortality Profiles:* The cluster contain moderate mortality rates, with standardised mortality rates fluctuating around average (i.e. 100). Life expectancy at birth was 77.9 for males and 82.5 for females. An above average poverty rate. 1149 MSOAs.

3. *Good Health Areas:* The cluster falls in-between the first two clusters, with overall low mortality rates. Life expectancy at birth was 79.4 for males and 83.5 for females. Low levels of poverty. 1309 MSOAs.

4. *The Middle:* The main characteristic is that the cluster falls in the middle of all the clusters, with above average mortality rates. Higher mortality rates for heart-, digestion- and accident-related causes. Life expectancy at birth was 75.9 for males and 80.6 for females. High levels of poverty. 854 MSOAs.

5. *Poor Health Experiences:* High mortality rates particularly for respiratory causes and those related to the digestive process (i.e. unhealthy behaviours). Life expectancy at birth was 74.5 for males and 79.7 for females. High levels of poverty. 656 MSOAs.

6. *Poorest Health and Least Desirable:* The cluster contains most of the highest

   mortality rates for causes, with particularly high rates for respiratory-, liver- and

   accident-related causes. Life expectancy at birth was 72.2 for males and 77.2 for

   females. Highest levels of poverty. 296 MSOAs.

7. *Poorest Neurodegenerative Health:* High mortality rates, especially for

   neurodegenerative diseases (e.g. Dementia, Parkinson's disease and Alzheimer's

   disease). Life expectancy at birth was 75 for males and 78.6 for females. An above

   average poverty rate. High in-migration of individuals aged over 65 and above

   average numbers of communal establishments. 322 MSOAs.

8. *Mixed Experiences:* A variety of cause specific mortality rates with both high

   (neurodegenerative diseases) and low (most cancers, digestive- and heart-related

   causes) mortality rates. Life expectancy at birth was 78.5 for males and 81.7 for

   females. Below average poverty rate for areas, with high in-migration of individuals

   aged over 65 and number of communal establishments. 1046 MSOAs.

Figure 1 displays the geographical distribution of the clusters across England and Wales. The
demographic characteristics of the individuals in the BHPS split by the cluster they resided in
is presented in Table 1. The demographic characteristics found in the BHPS are similar to
the characteristics of the clusters, with a higher proportion of individuals with good health
and higher income levels found in the clusters with better mortality profiles (Anonymous,
2013; Anonymous, 2014).
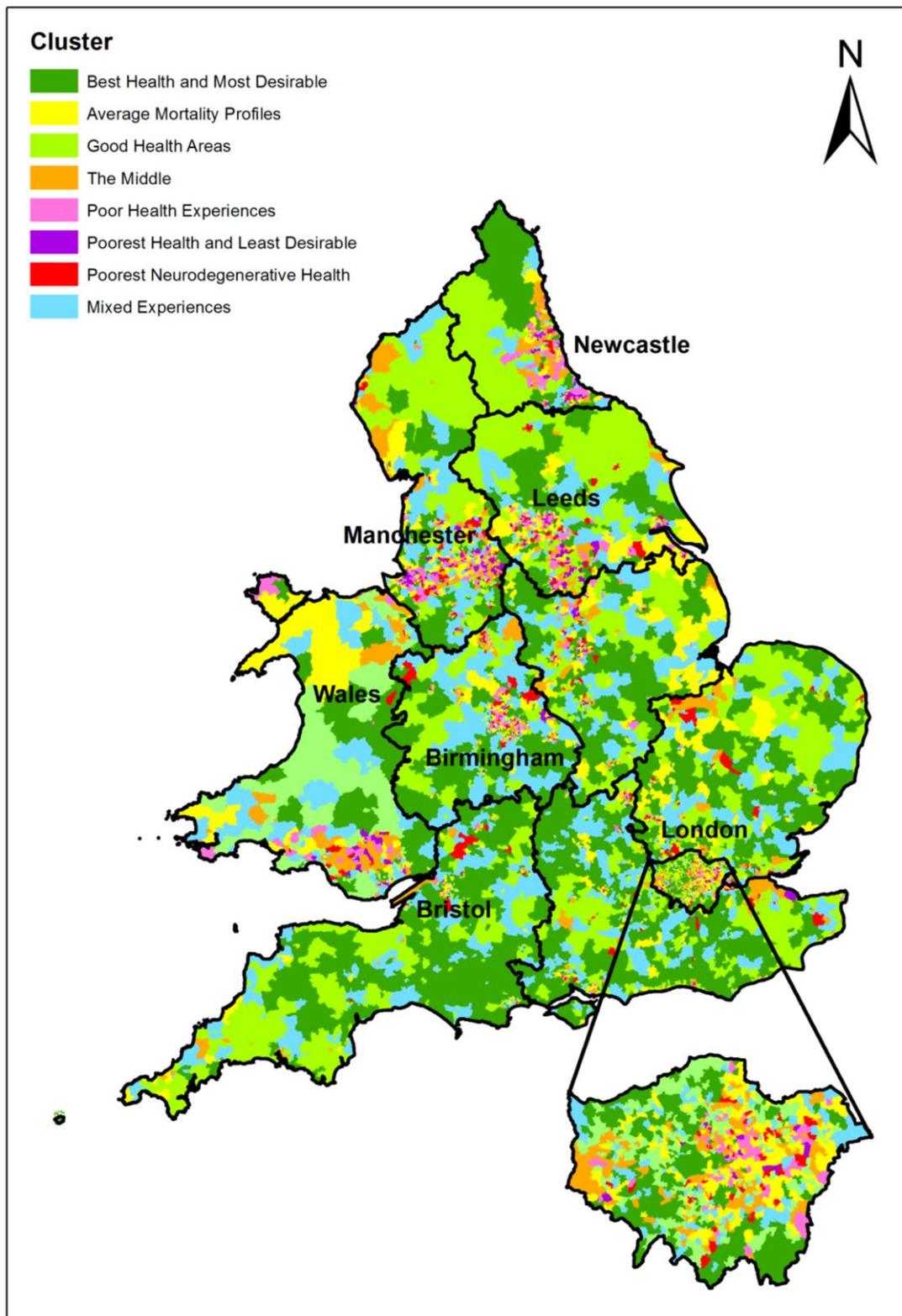
Figure 1: The spatial distribution of cluster location for the mortality classification of England and Wales, 2006-2009 (with London inset). Note: Areal units are Middle Super Output Areas (n=7194, mean population size 7860).

Table 1: Demographic characteristics of individuals in the British Household Panel Survey (2006-2008) split by cluster type.

Cluster	Did not migrate (n)	Migrated in (n)	Migrated out (n)	Female (%)	Poor health (%)	Mean Age	Mean Income
Best Health and Most Desirable	4829	244	234	55.4	24.2	50.3	18079
Average Mortality Profiles	3646	184	199	54.1	33.0	48.7	14618
Good Health Areas	4312	220	192	52.5	29.2	49.9	15303
The Middle	3023	160	186	54.7	34.1	46.9	13747
Poor Health Experiences	2098	100	80	56.4	36.9	47.2	12274
Poorest Health and Least Desirable	1210	67	73	55.1	43.2	49.0	12457
Poorest Neurodegenerative Health	856	75	87	55.4	34.8	45.9	15159
Mixed Experiences	3416	209	208	52.9	26.6	48.2	16887

Anonymous (2013) demonstrated that the classification was a useful means for grouping areas together, accounting for greater variation in life expectancy than offered by traditional techniques for disseminating data using a similar number of groups (e.g. Government Office Regions). The neighbourhood classification builds on previous research which tended to focus on binary or tertiary measures to capture the different area types that individuals migrated between which offer less detail (*c.f.* Anonymous, 2000; Popham et al. 2011; Riva et al. 2011).

The outcome variable in the analysis was self-reported health status. Respondents in the BHPS were asked to rate their health on a Likert scale ('Excellent' (22.3%), 'Good' (47.1%), 'Fair' (21.4%), 'Not Good' (7.1%) or 'Not Very Good' (2.1%)). For this analysis the measure was collapsed into its binary version ('Excellent' or 'Good' (69.4%) versus 'Fair' to 'Not Very Good' (30.6%)). This was chosen as the measure has been demonstrated to be associated with neighbourhood influences (Pickett & Pearl, 2001; Riva et al., 2007).

Statistical Analysis

Population subgroups such as the young or the affluent are more likely to migrate (Catney & Simpson, 2010; Champion, 2012; Evandrou et al., 2010). Migration is not randomly assigned, rather selective based upon personal circumstances. Therefore the covariate distributions of the data for those who migrate and those who do not will be different. It is not possible to simply fit a regression model to analyse the effect migration has on health, as this would break the assumption of the model that there is no bias present in the data (Ho, Imai, King, & Stuart, 2007; S. M. Iacus et al., 2012). Put simply, results of any comparisons made between those who migrate and those who do not may just be an artefact of the differences in their demographic composition (as you are not comparing 'like-for-like'). However, this has been ignored in past migratory research (e.g. Anonymous, 2000; Cox et al. 2007; Kahlmeier et al. 2001; Larson et al. 2004).

Matching methods offer a solution to the issue. Iacus et al. (2012) offers a definition of this approach; "Matching is a non-parametric method of controlling for the confounding influence of 'pre-treatment' control variables in observational data." (p1). Essentially, the approach is measuring a change in status (of which migration is one possible change in status by altering an individual's neighbourhood) of a group of individuals through the comparison of a 'control group'. Despite the advantages of this approach, the methodology has not been used much, especially within public health and geographical research.

The method pairs data that experiences a change in status (referred to as 'treatment') to the rest of the data to create an equivalent control group based on a set of confounders (S. M. Iacus et al., 2012). The benefit of this approach is that bias is reduced and the 'treatment' and 'control' groups become (or very close to) identical in relation to individual characteristics (Ho et al., 2007; S. M. Iacus et al., 2012). By matching across multiple variables, the process

controls for the effects of each variable allowing the analysis to focus more on the change in status (i.e. migration), which is the main difference between the two groups. There are fewer assumptions with this approach, therefore any analyses will be less model dependent (S. M. Iacus et al., 2012).

Migration represents a change in status for individuals that can be tested. Between two time points, some individuals will migrate and others not. Matching allows the analysis to focus on whether those who migrate have significantly different health when compared to those who did not migrate and whether this effect varies by the type of area of origin and destination. The pairing of individuals is conducted at a time point prior to anyone migrating, to allow a comparison of individuals who then migrated from an area type to those who remained the same area type.

Coarsened Exact Matching (CEM) was used to pair individuals that migrated between year A and year B through the creation of a 'control' group (S. M. Iacus et al., 2012). The method has been demonstrated to lead to the creation of a more balanced control group that is comparable to individuals in the 'treatment' group than other matching methods (Stefano M. Iacus, King, & Porro, 2011). It is also faster and requires less user interaction than other methods.

Matching occurs through selecting variables to pair observations with. Variables are temporarily transformed into a series of (meaningful) categorical groups to match data more efficiently (S. M. Iacus et al., 2012). Individuals who migrated can be paired to other individuals who did not migrate but displayed the same characteristics based upon these groupings. There is a trade-off between a greater number of groups a variable is categorised into providing more accurate matches, yet also being less likely to get exact matching for all cases (S. M. Iacus et al., 2012).

Age, sex and annual income (£) were used since previous research has demonstrated differences in migration patterns by these factors (Bailey, 2012; Catney & Simpson, 2010; Champion, 2012; Evandrou et al., 2010). No further variables were included to minimise the amount of noise added to the process, as it becomes more difficult to find exact matches across a greater range of variables (Iacus et al. 2011; 2012). Age was split into age bands (16-24, 25-34, 45-54, 55-64, 65-74, 75-84, 85+). Income was divided into ten thousand pound bands up to £50,000, where everything above was included as a group. Sex did not need to be further categorised..

Logistic regression was then used to analyse the association between poor health and migration status. Age, sex and income did not require including in the model since their effects are eliminated through the matching process (i.e. the impact of migration is independent to these factors as the analysis can compare 'like-for-like').

Recently the statistical community in the UK and USA has suggested that p values should not be reported. We do report quite a few in the tables and text that follows, but if these are seen to be descriptive rather than confirmatory we hope that they remain useful.

Results

Analysing the impact of migrating out of a cluster on health status

To explore the role of migration on health between different area types, the analysis began by looking at the effect of migrating out of particular clusters. Subsets of data were created, splitting up individuals by cluster location at time point A (i.e. origin). This allowed the pairing of migrants against those which remained in the same area, making fairer comparisons by accounting for area type. Separate logistic regressions analysing poor health

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using migration status for each subset were run (as well as all clusters combined) and are

presented in Table 2.

Table 2: Results from nine logistic regressions (each on a subset of cluster location at time A

and a final one of all individuals) analysing migration out of a cluster (at time A) as a

predictor of self-reported poor health status (time B) after matching.

Model (by cluster subset at time A)	Effect of Migration on Poor Health (time B)				
	Odds ratio	Standard Error	Significance	N	Log-Likelihood χ^2
1. Best Health and Most Desirable	1.005	0.133	0.970	468	0.00 (p=0.970)
2. Average Mortality Profiles	1.081	0.143	0.554	398	0.35 (p=0.555)
3. Good Health Areas	1.516	0.193	<0.001	384	10.17 (p=0.001)
4. The Middle	1.026	0.143	0.852	372	0.05 p(=0.860)
5. Poor Health Experiences	1.411	0.242	0.044	160	3.95 (p=0.047)
6. Poorest Health and Least Desirable	1.104	0.228	0.631	146	0.23 (p=0.633)
7. Poorest Neurodegenerative Health	0.970	0.227	0.897	174	0.02 (p=0.897)
8. Mixed Experiences	0.821	0.125	0.195	416	1.74 (p=0.188)
9. All clusters	1.129	0.059	0.020	2518	5.30 (p=0.021)

Table 3: Results from two logistic regression models predicting self-reported poor health status (time B) by destination of migration and other covariates, separately for origin; (a) the cluster 'Good Health Areas' and (b) 'Poor Health Experiences'.

Variable	(a) Good Health Areas			(b) Poor Health Experiences		
	Odds ratio	Standard Error	Significance	Odds ratio	Standard Error	Significance
Destination:	('Best Health and Most Desirable' is the reference in each model)					
Average Mortality Profiles	2.967	1.522	0.034	1.056	0.915	0.950
Good Health Areas	1.381	0.470	0.343	1.388	1.651	0.783
The Middle	1.452	0.816	0.507	1.678	1.481	0.558
Poor Health Experiences	4.736	3.431	0.032	0.542	0.349	0.342
Poorest Health and Least Desirable	3.502	2.637	0.096	1.094	0.927	0.915
Poorest Neuro-degenerative Health	1.887	1.432	0.402	0.438	0.565	0.523
Mixed Experiences	2.248	0.180	0.123	0.277	0.290	0.220
Age	1.019	0.002	<0.001	1.031	0.003	<0.001
Male	0.990	0.072	0.887	0.754	0.075	0.005
Income	0.99998	2.95×10^{-6}	<0.001	0.99998	5.48×10^{-6}	<0.001
Constant	0.164	0.058	<0.001	0.385	0.250	0.141
N	384			160		

Log-Likelihood χ^2	25.47 (p=0.005)			43.43 (p<0.001)		

A statistically significant effect of migration was observed for migration from any cluster type (model 9), where migration was associated with increased likelihood of poor health (this is the average effect of migration). By cluster origin, statistically significant relationships were found for migrating from the clusters 'Good Health Areas' (model 3; p<0.001) and 'Poor Health Experiences' (model 5; p=0.044). People who originally resided in either of these clusters were found to have greater probability of reporting their health as poor if they had migrated from these areas (as opposed to those who remained). These effect sizes were large; being 52 and 41 per cent more likely to report poor health if they were in the clusters 'Good Health Areas' and 'Poor Health Experiences' respectively. However, no other clusters reported significant relationships (models 1, 2, 4, 6-8).

The models for 'Good Health Areas' and 'Poor Health Experiences' were then extended by splitting the binary migration status variable to include the destination of migrants (Table 3). The analysis only considers migrants and hence no matching was employed (age, sex and income were included in the model as confounders). The reference cluster for comparing area types for each model is the cluster 'Best Health and Most Desirable', since it displays the best mortality profile and thus show the effect on health of not migrating to area with the best health outcomes.

Model 'a' considered just the individuals who migrated from the cluster 'Good Health Areas'. Two cluster destinations reported significant effects ('Average Mortality Profiles' p=0.034 and 'Poor Health Experiences' p=0.032) which demonstrated that individuals that migrated to these two clusters instead of the cluster with the best health and social

characteristics reported poorer health. The effect sizes are fairly large as well (odds ratios of 2.967 for 'Average Mortality Profiles' and 4.736 for 'Poor Health Experiences'). Although the other variables were non-significant, their effect sizes follow the same expected direction. However, the model for individuals who migrated from the cluster 'Poor Health Experiences' produced few insightful findings (model b). The results for the confounders followed expected directions.

Analysing the impact of migrating into a cluster on health status

The analysis from the previous section was repeated by taking subsets of individuals at time point 'B' and comparing individuals who migrated into an area against those that were already located there. The approach allows the analysis of cluster destination, rather than origin, to explore if the results are consistent (using the same procedure for matching). The results can be seen in Table 4. There were no significant associations by cluster destination.

Analysing health status as a predictor of migration (and destination of migration)

The relationship analysed may have been mis-specified in that health may instead influence individuals to migrate (Larson et al., 2004). To test this, individuals were matched on their health status prior to migration (i.e. health status at time point 'A'). The same covariates were used in the matching process. Research has shown that self-rated health status varies socially and demographically and matching will help to eliminate any differences (Anonymous, 2009; Lindeboom & van Doorslaer, 2004). The results of a logistic regression testing this association are presented in Table 5. A significant relationship was shown (p=0.001), with individuals who reported their health as poor being 20.1% more likely to migrate by the next year than compared to those of good health.

Table 4: Results from nine logistic regressions (each on a subset of cluster location at time B and a final one of all individuals) analysing migration into a cluster (at time B) as a predictor of self-reported poor health status (time B) after matching.

Model (by cluster subset at time A	Effect of Migration on Poor Health (time B)				
	Odds Ratio	Standard Error	Significance	N	Log-Likelihood χ^2
1. Best Health and Most Desirable	1.054	0.139	0.693	488	0.17 (p=0.685)
2. Average Mortality Profiles	1.149	0.157	0.310	368	0.72 (p=0.396)
3. Good Health Areas	1.270	0.160	0.059	440	3.46 (p=0.063)
4. The Middle	1.315	0.191	0.060	320	3.6 (p=0.058)
5. Poor Health Experiences	1.162	0.204	0.392	200	0.88 (p=0.348)
6. Poorest Health and Least Desirable	1.127	0.245	0.583	134	0.26 (p=0.61)
7. Poorest Neurodegenerative Health	0.951	0.242	0.842	150	0.01 (p=0.908)
8. Mixed Experiences	1.083	0.155	0.577	418	0.38 (p=0.538)

				5.3
9. All clusters	1.129	0.059	0.020	2518	(p=0.021)

Table 5: Results from a logistic regression analysis of poor health status (at time A) as a predictor of migration (by time B).

Variable	Odds Ratio	Standard Error	Significance
Poor health	1.201	0.065	0.001
Constant	0.069	0.002	<0.001
N	2518		
Log-Likelihood χ^2	11.3 (p<0.001)		

The migration variable was then disaggregated to include the destination of migrants to test evidence of health selective migration. The analysis did not consider individuals who did not migrate. A multi-nomial regression was run on the matched dataset and the results are presented in Table 6. Health status prior to migration was used to explain destination of migration (i.e. cluster membership).

Each coefficient in the model was both positively associated and significant (all p<0.001). With the reference cluster being the cluster with the best mortality profile (i.e. lowest mortality rates across the majority of the variables), individuals with poor health that migrated were more likely to migrate to any of the other clusters in comparisons to the reference cluster. The strength of each coefficient was related to the mortality profile of that cluster, with the effect size larger where the cluster represented poorer health outcomes. If the analysis examines only people who actually migrated to a different cluster (i.e. no intra-

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cluster migration), there is little change in the result suggesting that it is a fairly strong relationship.

Table 6: Results of a multinomial regression analysis of poor health status (at time A) as a predictor of destination of migration (at time B).

Cluster	Variable	Coefficient	Std. Error	P
Best Health and Most Desirable	(base outcome)			
Average Mortality Profiles	Poor health	0.440	0.048	<0.001
	Constant	-0.399	0.025	<0.001
Good Health Areas	Poor health	0.267	0.047	<0.001
	Constant	-0.183	0.024	<0.001
The Middle	Poor health	0.552	0.050	<0.001
	Constant	-0.627	0.027	<0.001
Poor Health Experiences	Poor health	0.608	0.056	<0.001
	Constant	-1.009	0.031	<0.001
Poorest Health and Least Desirable	Poor health	0.824	0.065	<0.001
	Constant	-1.609	0.039	<0.001
Poorest Neuro-degenerative Health	Poor health	0.607	0.077	<0.001
	Constant	-1.894	0.044	<0.001
Mixed Experiences	Poor health	0.238	0.051	<0.001
	Constant	-0.432	0.025	<0.001
N	1259			
Log-Likelihood χ^2	198.97 (p<0.001)			

Discussion

This study has presented a new approach for exploring the role of neighbourhood through measuring the impact of migrating between different area types on health. Using migration as a means for altering the area type individuals reside in, a pseudo-experimental design can be employed. This was achieved through using an under-utilised methodology in geography and public health research. Matching helped reduce bias in the data (ignored in previous research in the area), allowing for a more accurate and stronger analysis. It is hoped that the experience of its usage here will help to promote the use of the methodology more widely in public health and geographical research.

The results demonstrated little evidence of area effects as observed through migration. Our inconsistent findings suggest that the type of area individuals moved to did not have an effect on individual health. Disaggregating the analysis to account for both origin and destination of migrations presented some evidence that may suggest the important role of area type (Table 3), however this was not consistent throughout our analysis. This may not be surprising given that the area effects do not often have direct impact upon individual health (Berkman & Glass, 2000). Therefore it is unlikely that any effect would become apparent in the short term (Johnson, Schoeni, & Rogowski, 2012). Future research should build upon this approach by extending these cross-sectional findings longitudinally.

The significant results in Table 2 would appear to be migratory effects (as opposed to informing our understanding of neighbourhood effects). Of the significant effects, migrating from either area type increases the probability that an individual reports their health as poor. With the direction of the effect being the same for either cluster, despite different mortality and social profiles, the impact of migration appears more important than the characteristics of

the areas. However, as this effect is not consistent across all the clusters, it may not be that important.

Reversing the relationship specified in the analysis presented gave stronger results (Tables 5 and 6). Note just did poor health influence an individual's decision to migrate, but there were also variations in the strength of the relationship by destination. This provided some evidence of health selective migration, with individuals of poor health more likely to migrate to the clusters with poorer mortality profiles (and associated lower social characteristics). Possible mechanisms through how this operate include migrating to be nearer to services or family and downsizing through loss of income or the ability to work (Larson et al., 2004). This effect may partly explain the sporadic significant results when the relationship was specified the other way round.

The results support the findings of past research (Bentham, 1988; Anonymous, 2000; Cox et al., 2007; Popham et al., 2011; Riva et al., 2011; Wannamethee, Shaper, Whincup, & Walker, 2002). This study builds upon this work through using data over single years, as opposed to comparing data over long time periods that are less able to account for neighbourhood characteristics. The process of health selective migration is not occurring over the life course overall, but plays out over the short term as well. These studies also fail to account for the level of bias in comparing migrants to non-migrants, and often only use simple measures for disaggregating area type (i.e. the clusters offer greater detail than binary or tertiary measures).

Our results point towards migration as one possible explanation for how geographical inequalities in health persist. Individuals with poor health 'drift' to areas with poor health characteristics, resulting in the polarisation of health patterns (Riva et al., 2011). Through migratory patterns, this social sorting of individuals in terms of their health becomes visible (Bailey, 2012). With the poorer health areas also being more likely to contain higher levels

of poverty (Anonymous, 2013), the resulting polarisation is also indirectly in terms of social conditions as well, with those of poorer health ending up in those less socio-economically disadvantaged areas. Although our investigation was less concerned with focusing on this aspect, our results present interesting findings which require further investigation.

Limitations

Low sample size of migrants is an important limitation to the analysis. Although the total number of migrations (8.6%) was fairly representative, as the measure becomes disaggregated by cluster type to account for origin and destination sample size becomes problematic (see Supplementary Table 1). This is important as migration between the extremes is not common (Anonymous, 2000; Supplementary Table 1) and there were some migrations within cluster types as well. The issue limits the power of our models to test relationships and can be seen in the wide standard errors. This may explain the lack of significant findings when testing the role of neighbourhood. However, there were few data sets available that collected information both on health and migration. Future studies should look to develop the approach using larger data sets where available.

The measure of health used is self-reported health status, which is a subjective assessment made by an individual on their own health. As such, it restricts the observations that can be made about health since perceived health may not reflect actual health. However, the measure has been shown to be associated with other measures of actual health suggesting that it is a useful proxy for health (Idler & Benyamini, 1997; Jylhä, 2009). The variable was also split into its binary measure to improve the accuracy of observations as the individual categories become less abstract to individuals (i.e. it is difficult to understand if your health is either 'fair' or 'not good' but combined into the same group they incorporate poor health

which is more important). However as a binary measure, the results can become bounded as there is no possibility of an individual's health becoming poorer if it was already 'poor' (and *vice versa*). Any analysis will therefore lose out on variation in outcomes restricting the quality of the results. Future research should consider other health variables that tackle these issues.

Whilst the matching of individuals based upon migration status was useful, not all migrations are the same. Individuals migrate for different reasons (e.g. in search of employment, upgrading to a new house, to be nearer family). Although the BHPS contains information on reason for migration, the majority of the data was missing. Without knowing why people moved, we cannot really have a true experimental design to the analysis. For example, Tunstall et al. (2010) showed that where migration was for negative reasons (e.g. divorce, bereavement), there was a stronger observed negative effect of migration on health. Future research should look to incorporate this information as it may hide the role of neighbourhood.

Although matching improves the internal validity of results, there are issues of external validity and generalisability. Individuals who migrated were, on average, younger and of lower annual incomes. Whilst matching provides a stronger method of analysis as data compares 'like-for-like', the findings will be less generalisable to the wider population.

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