Reassessing the migrant health gap across multiple origin and destinations

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Abstract

The "healthy migrant effect" (HME) refers to migrants' health advantage relative to non-migrants in destination countries with similar socioeconomic profiles. This advantage is often attributed to positive health selection in origin countries. Yet, evidence remains inconclusive, and few studies simultaneously compare migrants to both origin and destination populations.

Using all 11 rounds (2002–2024) of the European Social Survey, we construct a dyadic dataset of 11,565 migrants across 39 countries to reassess the migrant health gap. We apply a two-step predictive modeling strategy to estimate counterfactual health levels for each migrant based on non-migrant populations in both their country of origin and destination.

Our findings reveal that the healthy migrant effect is context-dependent. Migrants tend to show a singular advantage: they are healthier than non-migrants in either origin or destination, but rarely both. As such, this challenges the expectations of the selection hypothesis. Moreover, the direction of the gap reflects national health levels: migrants to healthier destinations tend to exceed their origin populations in health, while those from healthier origins tend to fall below their origin populations but remain healthier than their destination population. These results challenge the notion of universal migrant health advantages and highlight the importance of considering health differences relative to both origin and destination societies in migration research.

1 Extended Abstract

The healthy migrant effect (HME) refers to the observation that migrants have health advantages relative to non-migrants in the destination with similar observed socioeconomic characteristics. This advantage is commonly attributed to selection processes operating in the country of origin. According to the selection hypothesis, individuals who choose to migrate possess characteristics that set them apart from those who remain — notably in age, gender, educational level, and health [5]. Indeed, in the HME literature, the general expectation is that international movers are selected from the upper tail of the health distribution of the origin country, which in turn ensures that migrants end up in the upper tail of the destination health distribution[5, 2].

Despite extensive research on the healthy migrant effect (HME) [1], little is known about how migrants' health compares to non-migrant populations in both their origin and destination countries simultaneously. Existing studies typically focus on a single reference group — either the destination or the origin — and thus capture only part of the picture. Even those using multiple origins or destinations are limited to examining health gaps relative to one side at a time, rather than assessing migrants' position between the two. In Europe, findings from these single-context analyses are mixed: the direction and magnitude of the HME vary across destination countries [9, 7] and across origins [3, 4].

The inconclusive evidence calls for a revisit of the pattern of the health gap: is there a double advantage (healthier than both origin and destination), a singular advantage (healthier than one but not the other), or no advantage? This question is particularly relevant in the European context, where health levels among non-migrants differ significantly across countries. Analyses limited to destination populations may therefore obscure selection effects — as the benchmark to be in better health than some destinations are very high. That is, migrants can be positively selected relative to their origin yet show no health advantage in destinations with high overall health, and vice versa.

To assess the health gap, we use all available rounds (1-11) collected from 2002 to 2024 of the European Social Survey (ESS) to construct a dyadic dataset. The original dataset consisted of 512,242 observations; however, several restrictions were applied to refine the sample. Consequently, the analytical sample contains 11,565 migrants. First, we excluded people under 25 and over 70 years of age. Second, we define migrants as individuals who themselves have migrated with two parents born in a country other than the one in which the migrant resides.

The analysis employs a two-step predictive modeling strategy analogous to the *estimated dependent variable* (EDV) method, combined with counterfactual benchmarks based on non-migrant samples (as in [6]). This approach allows us to compare migrants' self-reported health simultaneously with origin and destination populations while respecting the cross-classified data structure. In the first step, we estimated counterfactual health expectations for migrants from the health patterns of non-migrants, establishing two reference points: (1) an **origin benchmark** representing the expected health if remaining in the origin country and a (2) **destination benchmark** representing the expected health level if the same individual exhibited the health typical of non-migrants in their current country of residence with similar characteristics. Technically, for each country c, we fitted a weighted regression among non-migrants:

$$\text{Health}_i = \beta_0^{(c)} + \beta_1\,\text{Age}_i^{(c)} + \beta_2\,\text{Age}_i^{2(c)} + \beta_3\,\text{Edu5}_i^{(c)} + \theta\,\text{Male}_i^{(c)} + \varepsilon_i^{(c)}. \tag{1}$$

The covariates included age, age squared, educational attainment, and gender. As such, we adjust the benchmarks to the composition of the migrants. In addition, survey-round fixed effects and ESS sampling weights were applied to account for temporal variation, unequal sampling probabilities, and cross-national population differences. The predicted values and their standard errors were then reshaped into long format, yielding three stacked observations per individual: one observed and two counterfactuals. The standard errors quantify uncertainty in the first-stage predictions and were incorporated into the second-stage regressions through weights:

$$w_i = \frac{1}{\sqrt{\omega_i^2 + \delta^2}}$$

Where ω_i^2 denotes the measurement-error variance in the first-stage predictions and δ^2 is the common residual variance estimated from the unweighted second-stage regression. In other words, we obtain a FGLS estimator which we use to weight the final models; again, mirroring the EVD approach [8]. Furthermore, as we use stacked data, the final models have clustered standard errors at the individual level.

First, we confirm in Figure 1 that there is a significant difference in health across the countries in our data. As there is a significant difference in most country pairs, our data is acceptable for our endeavor since migrants are moving between countries where the non-migrant population has different average health adjusted for age, age squared, sex, and educational level.

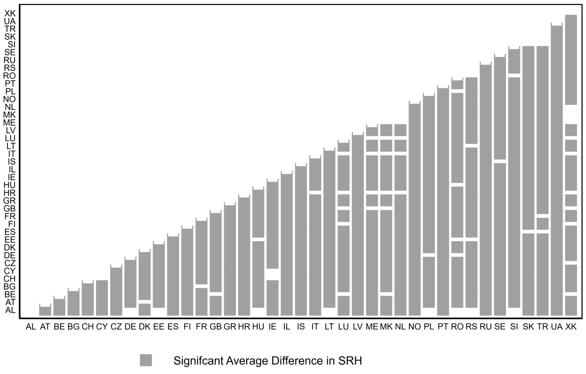


Figure 1: Country pairs with statistically significant differences in health. Note: Pairwise comparisons of means among non-migrant respondents, showing country pairs with statistically significant differences at the 95% confidence level

As seen in Figure 2, the pattern of the health gap varies depending on whether migrants are going to countries where the population has better or worse health than their origin. In both cases, there is no double advantage. In fact, there is a negative average gap to destination among migrants going to destinations where the population has higher health, and a negative gap to origin when the destination has worse health than the origin.

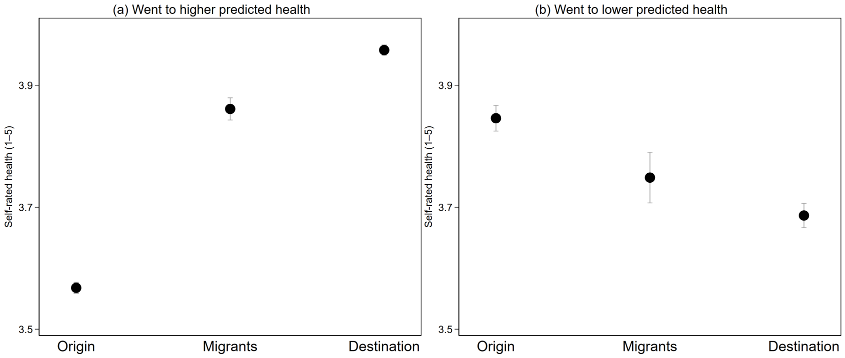
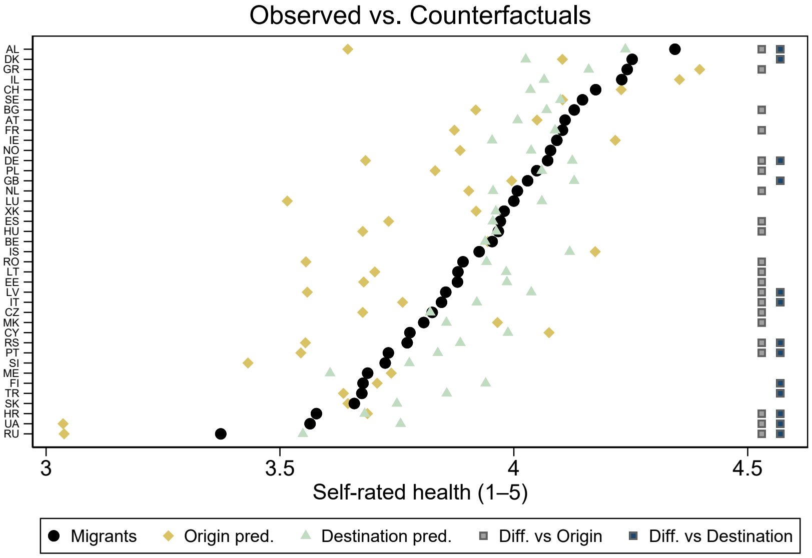


Figure 2: Comparison of migrants' health with non-migrants in origin and destination countries. Results from second-stage regressions with stacked data; standard errors are individual-clustered and corrected using FGLS.

The health gap between origin and destination varies across Europe. In Figure

3, we group the migrants by origin country, demonstrating that the gap to the origin is more prominent than the gap to the destination. Furthermore, the gaps are not mutually inclusive; there are a variety of health gap patterns. In addition, as visualised by the black squares, there are more significant health gaps between the migrants observed health to origin than the destination.



Side squares indicate where health differ from Origin/Destination predictions at p<0.05.

Our preliminary findings suggest that the healthy migrant effect is not uniform across Europe. Instead of a consistent “double advantage,” migrants most often exhibit a singular comparative advantage: they are healthier than non-migrants in either their country of origin or destination, but seldom both. This pattern underscores that the migrant health gap is shaped by contextual differences in population health rather than by a universal selection effect.

By jointly benchmarking migrants against both origin and destination non-migrants, our study offers the first systematic comparison of migrants’ relative health across multiple origin–destination pairs. The results highlight the importance of considering cross-national health variation when assessing selection mechanisms in migration research, especially considering who the reference group is. In addition, we move beyond analyses that focus solely on the migrant health gap relative to destination populations by comparing the health of migrants to non-migrants in the origin simultaneously.

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