Sibling Patterns in Spatial Mobility Trajectories

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1. Introduction

Migration is often conceptualized as an individual choice, yet family remains one of the most powerful forces shaping spatial mobility across the life course (see Mulder, 2007). While previous research has extensively examined how family context influences internal migration decisions—particularly through proximity to parents and children (e.g, Michielin et al., 2008; Pettersson & Malmberg, 2009; Smits, 2010; to name a few) or in response to changes in family structures (see Kulu & Milewski, 2007)—less attention has been paid to within-family dynamics such as socialization, resource transmission, and the potential influence of siblings' behavior. Siblings are of particular interest not only because they share key background characteristics, enabling researchers to better isolate within-family effects, but also because they may serve as agents whose own mobility, and place of residence, influences that of other family members (Li & Huang, 2025; Mulder et al., 2020)

The aim of the paper is therefore to better understand the role of family process in shaping individual internal migration trajectories by studying similarity across siblings. To achieve this aim, we ask three main questions. First, is similarity in migration trajectories stronger in the context of family members? Second, under what conditions (family characteristics and shared childhood experiences) are siblings' trajectories more similar to one another? And third, to what extent these conditions explain greater sibling similarity?

To answer these questions, this paper leverages rich Finnish register data to explore the internal migration trajectories of siblings. We conceptualize migration trajectories as long-term processes anchored in a place of origin, defined as the municipality of residence at age 17. This reference point allows us to measure spatial mobility in terms of distance from the origin, thereby capturing how subsequent moves (such as onward, return, or circular migration) relate to the family's original location.

We apply sequence analysis to reconstruct migration trajectories between ages 18 and 43 for individuals who turned 18 between 1988 and 1998. These cohorts offer complete histories, sibling linkages, and sufficient temporal coverage to capture diverse spatial mobility patterns. In the second phase, we adopt a within-dyad approach to sequence analysis to assess the degree of alignment in migration trajectories across siblings, compared to randomly paired individuals from the same birth cohorts. Average similarity among siblings reflects the extent of within-family trends in internal

migration patterns. In contrast, average similarity among unrelated dyads captures broader cohort-specific migration trends. By comparing these, we assess the extent to which migration trajectories are shaped by within-family mechanisms, beyond societal or structural forces. In the final phase, we examine family-level factors (family and sibship structure and shared background characteristics and early-life experiences), that may underlie convergence or divergence in siblings' trajectories.

Adopting a life-course perspective (Elder et al., 2003), this study views migration as part of a network of linked lives, where individual trajectories are interconnected with those of family members (Coulter et al., 2016; Findlay et al., 2015). By examining siblings' geographical trajectories in relation to one another, the analysis highlights how spatial mobility is shaped not only by individual aspirations or structural opportunities, but also by the relational contexts of families. Siblings' movements reflect shared histories, mutual influences, and the enduring effects of family-based resources, norms, and expectations. This perspective moves migration research beyond individual decision-making, and shows that spatial mobility is a relational process structured by family interdependencies.

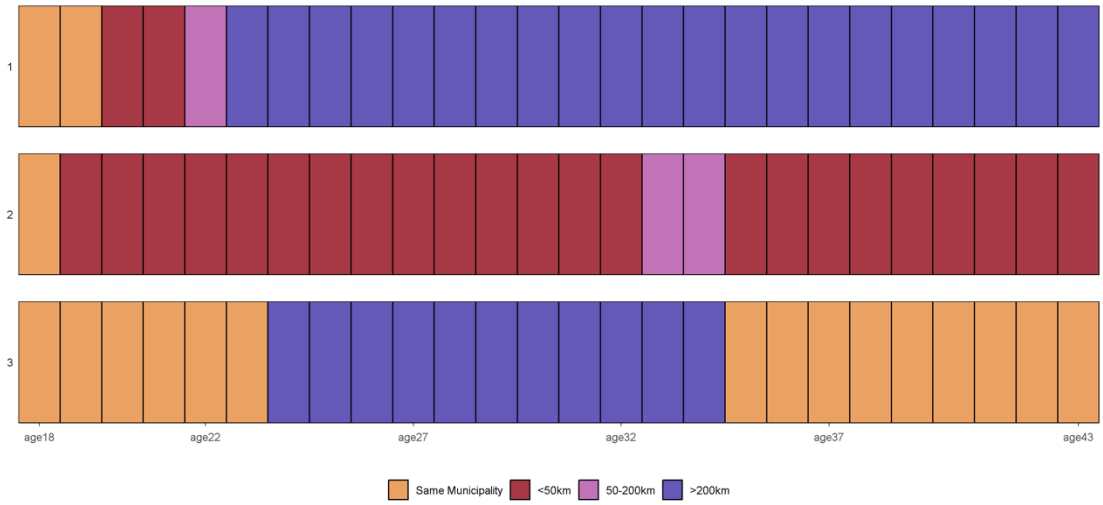
2. Data and method

To address our aims, we utilize Finnish population register data covering all citizens and permanent residents from 1987 to 2023. The data provide annual information on each individual's municipality of residence, allowing us to trace complete residential histories across the life course. Our analytical sample includes all individuals who lived in Finland at age 17 and who turned 18 between 1988 and 1998. This design ensures that each cohort can be followed continuously from age 18 to 43, providing full migration histories over a 26-year window. Individuals who emigrated (or died) before age 43 were excluded (since further migration episodes could not be traced when individuals living abroad) so that trajectories are complete and reflect internal migration only. The final study population comprises 550,941 individuals.

For each person, we measured the annual distance between their municipality of residence and their municipality at age 17, using Euclidean distances between municipal centroids. Distances were grouped into four ordered categories representing increasing spatial separation: residence in the same municipality (including co-residence), short-distance moves (less than 50 km), medium-distance moves (50–200 km), and long-distance moves (over 200 km). These categorical measures provide a concise

representation of individuals' geographical trajectories between ages 18 and 43. Figure 1 exemplify 3 different individual trajectories.

Figure 1 - Example of individual trajectories.



Source: Statistics Finland, own calculation.

Using anonymized parental identifiers, we identified full and half siblings within the population. From each family with at least two children, one individual was randomly selected as the *Ego* (n = 115,891). Note that, since our focus is on migration trajectories, and immobility is considered a qualitatively distinct trajectory, we limit our selection of Egos to individuals who undertook at least one change of state in their migration career, therefore individuals with no siblings in the sample, or those from families where all children were immobile could serve only as Alters. Each Ego was then paired with an Alter in two distinct ways to create two samples of dyads. In the *sibling dyad* sample, each Ego was matched with one randomly selected (full) sibling. In the *unrelated dyad* sample, the same Ego was matched with a randomly selected Alter from the broader population (neither a sibling nor a half-sibling).

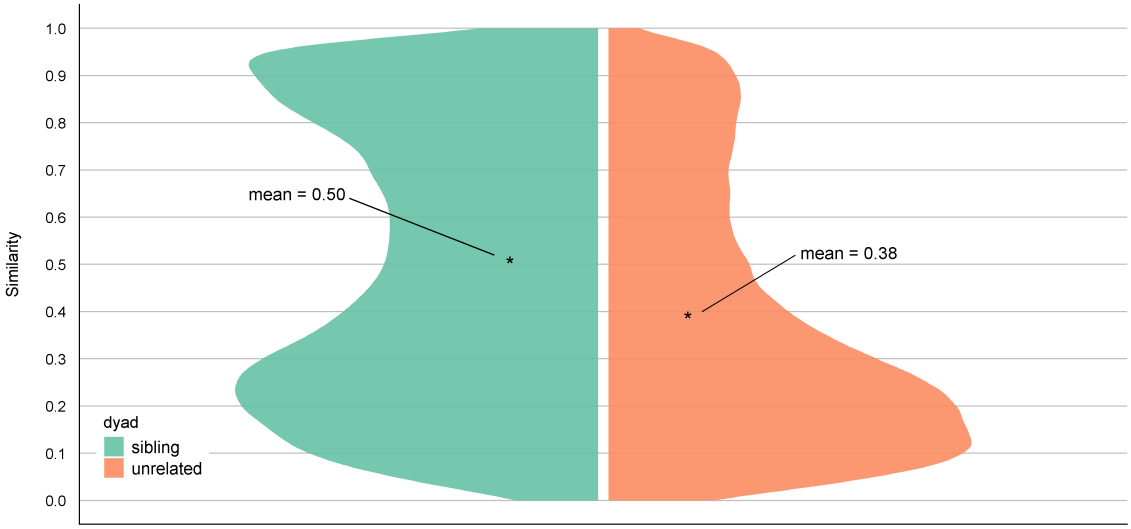
We apply sequence analysis, a method widely used to study ordered life-course processes, to summarize and compare these spatial trajectories. Specifically, we use the Optimal Matching (OM) algorithm to compute dissimilarities between sequences. OM quantifies how different two trajectories are in terms of their timing, duration, and order of moves, by calculating the minimal "cost" required to transform one sequence into another through insertions, deletions, or substitutions of states. Following standard practice, the cost of insertions and deletions was set to 1, and substitutions to 2.

Pairwise OM distances were computed for each dyad, producing a continuous measure of similarity in siblings' and unrelated individuals' migration trajectories. These raw distance scores were then normalized to range between 0 and 1, where 1 represents identical trajectories and 0 represents maximal dissimilarity. Average normalized similarity among sibling dyads indicates the extent of within-family alignment in migration behavior, while the corresponding average for unrelated dyads reflects broader cohort-specific mobility patterns (RQ1). Then we measure using linear regression analysis, among the related dyads only, what family characteristics matter for sibling similarity (RQ2). Finally, we examine whether these characteristics explain the difference between related and unrelated dyads (RQ3).

3. Preliminary results and next steps

Figure 2 shows two density function of dyadic similarity scores across the related (green) and unrelated dyads (orange), and in line with expectation, illustrates that the average similarity of siblings is greater from the average similarity of unrelated dyads (meanSib = 0.5 and meanUnrelated = 0.38) (RQ1). To answer RQ2, using regression analysis we will identify, within the sibling sample, what family characteristics are associated with greater dyadic similarity. Then, to address RQ3, based on the identified characteristics we will match Egos with unrelated Alters who share similar characteristics, to explore whether these explain the greater similarity among siblings.

Figure 2 – Dyadic similarity in geographical mobility: sibling vs. unrelated dyad



Source: Statistics Finland, own calculation.

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