Center for Studies in Demography and Ecology

Residential Trajectories: Using Optimal Alignment to Reveal the Structure of Residential Mobility

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Introduction

There are many reasons to believe that patterns of residence play a crucial role in determining individual life course outcomes. In the cross-section, there is evidence that both specific places (e.g., New York city) and types of places (e.g., small rural towns, suburbs of big cities) offer unique constellations of educational, occupational, and social opportunities for diverse segments of the population. It further makes sense to think that the possibility of moving geographically might reflect a form of cultural capital that is unevenly distributed throughout the population. For example, some individuals, highly committed to a career or a firm, move frequently in order to further their occupational prospects, while others, tied to locale through kin or inertia, are buffeted by local labor markets (Blair-Loy, forthcoming). Moreover, considered in light of research concerning the segmentation of individuals' social ties to local communities from their attachments to more extended communities over time (Guest and Wierzbicki, forthcoming), we might even conceptualize the existence of distinct residential mobility *regimes*, each characterized by a particular pattern of residential mobility.

Yet despite its potential importance for both demographic and stratification research, the temporal and spatial structure of domestic residential mobility is poorly understood. Currently popular analytic methodologies and available data sources allow researchers to focus careful attention only on certain aspects of the process of migration and residential movement. So, for example, a number of studies published during the past 10-15 years use event-history models and longitudinal survey data to examine how demographic life cycle factors, in combination with other life course transitions (e.g., getting married, having a child, getting a new job), influence the likelihood of a change in residential situations. These studies have focused on the impact of educational attainment (Bailey 1993), changes in household types and family composition (Davies-Withers 1997; Clark, Deurloo, and Dieleman 1994), occupational status (Odland 1997), and race (South and Crowder 1997) on decisions to move, change housing tenure, and migrate to different geographic destinations. Other studies focus more directly on the interdependent nature

of life course processes, examining how the timing of events like marriage (Mulder and Wagner 1993) and changes in household organization or occupational status (Odland 1997; Odland and Shumway 1993) impact the likelihood and timing of changes in a residential situation.

Not surprisingly, the theoretical framework guiding most of these studies is the idea that individuals follow structured social and developmental pathways over their life course (Elder 1985, 1994). Perhaps the most prominent theme in the emerging life course paradigm is that lives "unfold" in patterned ways as individuals age and pass through different life stages. While previous life course migration and mobility studies have examined the determinants of, and interdependencies between, the specific transitions that constitute this "unfolding" over time, few have attempted to examine the full long term *trajectory* or *sequence* of residential movements that typify this unfolding process. Yet the nature of this "unfolding" over time cannot be expressed in terms of a single transition; only a temporally ordered *sequence* of events captures the essence of the life-course insight. Therefore, just as we now recognize the importance of examining the sequence of jobs over time in order to understand occupational careers, it seems crucial to examine actual sequences of residences during different stages of the life course in order to understand the structuring of residential pathways.

Hence our goal in this paper is to demonstrate how an alternative strategy, based on optimal alignment (a method for comparing whole sequences of events), facilitates a more comprehensive understanding of residential migration and mobility patterns. We argue that these techniques allow us to (1) identify empirically common residential trajectories; and (2) examine how individuals' movement patterns and attachments to different sorts of places unfold and evolve over the life course. Our hope is that this exercise will illustrate how the optimal alignment procedure works in practice, and will assist others who wish to experiment with this method in other substantive contexts.

We begin by outlining our approach to the study of longitudinal migration and residential movement patterns, and show how using a sequential approach offers new insight into individuals'

life course patterns of residential movement and place attachment. Second, we address some of the concrete challenges associated with using this method to study residential behavior over time. Finally, we discuss the findings from our analyses of a large sample of residential trajectories defined in terms of the "types of places" in which individuals live. These analyses demonstrate that it is possible to identify distinct sequential patterns of residential movement that match our theoretical expectations of the age-graded roles and transitions that individuals undertake over the life course. Further examination of the population of residential trajectories raises some interesting theoretical and empirical issues concerning different types of residential situations at different points of the life course.

The substantive focus of this paper is on patterns of residential movement as defined by shifts in the "types of places" individuals live in across their residential career. Thinking about a sequence as a trajectory of movement across "types of places" (e.g., rural vs. urban locations) differs from defining such a sequence in terms of actual moves within or across such "types of places", or in terms of shifts across specific "geographic places" over time (e.g., New York to Chicago to Andover, MA). Since our trajectories reflect movement across different sectors of the geographic landscape, we are able to draw from research on individual's attachments to, and attitudes towards rural, suburban, and urban places to support our findings of distinct pathways of residential movement. Yet, by also using summary measures of residential moves and total shifts in specific "geographic place", we have the ability to describe the mobility behaviors of those who follow different "type of place" trajectories, and assess the distinctions between individual's attachments to "type of places" with their attachments to specific locales.

Sequence Versus Transitions

Where the analytic goal is to examine the probability of transition from step *a* to step *b*, stochastic models, including time series, Markov chains, or event-history models are adequate. These methods assess the likelihood of transitions between time 1 and time 2, estimate the time-to transition in the future, or examine the effect of a single previous transition on future outcomes.

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However, traditional event-history approaches, which focus on single-event transitions, are not well suited to the analysis of sequential data, since as a group these models are unable to retain the past complexity carried by individual sequences of events. In short, by focusing on the determinants of a *single transition* all these models ignore the highly scripted nature of many fundamental life course processes.

In contrast to stochastic models of specific transition probabilities, sequence analyses are useful for answering questions about the empirical structure of patterns of behavior. When we believe that the temporal order of different states embedded in the trajectory reflects a (normatively) structured pattern of human behavior, we must use a method that treats the *trajectories* as the units of analysis. This is what we do here, in order to explore the structure and composition of trajectories of movement through the residential landscape. The optimal alignment technique is a "whole sequence" method which enables us to examine whether common or regular patterns exist within a particular set of empirically observed sequences. If we determine that regularity exists in the sequential pattern, we can then ask questions about where such patterns came from and how such patterns may influence other structured patterns or social processes in the future (Abbott, 1995).[1]

Among social scientists, interest in methods designed to analyze sequential processes has grown in concert with the movement toward emphasizing the temporal context of events (Abbott 1995, 1998; Hareven 1978). Sequence-based modeling techniques, which move beyond the variable-based assumptions of standard regression models, make it possible to illustrate the true nature of scripted processes, and assess how shifts in the underlying social and historical context influence the structure of sequential patterns. Interestingly, while the optimal alignment approach has been utilized in social science applications for over ten years, there are still relatively few studies that incorporate this approach.

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[1] Since these methods transform complex longitudinal patterns of events into measures and variables, the results of sequence analyses can be integrated into more traditional statistical analyses.

The optimal alignment approach we employ draws from techniques used in DNA sequence matching (Sankoff and Kruskal 1983); it was first introduced to the social sciences by Andrew Abbott (Abbott and Forrest 1986). Optimal alignment algorithms operate on whole sequences of ordered elements and assesses the resemblance between pairs of sequences in terms of how easy it is to transform one sequence into the other. The procedure returns a matrix of pairwise "distances" which can be clustered to identify natural groupings of sequences.

The most distinctive feature of the optimal matching approach is its emphasis on the identification and analysis of whole sequences rather than the estimation or prediction of the step-by-step transitions contained within the sequence. Most previous applications of these methods in the social sciences have focused on occupational career patterns, ranging from analyses of the typical careers of German musicians (Abbott and Hrycak 1990) to the shift in career systems over cohorts of employees at the Lloyd's Bank in Great Britain (Stovel, Savage, and Bearman 1996). The technique has also been utilized to examine diverse social and political processes, including patterns of Morris dance sequences (Abbott and Forrest 1986), differences in the adoption sequences of welfare policies in developed nations (Abbott and DeViney 1992), and distinctions in the sequences of Black lynching patterns in counties of the Deep South (Stovel 1997). To date, optimal alignment has not been used in any studies of life course migration or residential mobility processes.

In a general sense, use of optimal alignment methods has been limited for a number of reasons. First, since this technique is most useful for understanding scripted social processes, its utility is limited to phenomena which are theoretically expected to follow a finite set of temporally ordered patterns. While sociologists have long argued that certain life course and occupational processes follow such scripts, there are many other processes (e.g., status attainment) that are not often understood in this way. Second, even given identification of appropriate phenomena, one needs longitudinal data to identify and illustrate these sequences over time. Increasingly, such data

are available from surveys such as the Panel Study of Dynamics and National Longitudinal Survey of Youth.

Third, and perhaps most importantly, optimal alignment is not a "traditional" probability-based method; rather, it is a more descriptive technique which draws on theoretical and empirical assessments to guide the modeling exercise. Unlike stochastic longitudinal methods (such as event-history analysis and Markov models) optimal alignment analyses make no assumptions about the causal mechanisms underlying the sequential patterns of behavior, instead relying on subsequent analyses to differentiate those who follow various scripted patterns. As a consequence, it is not always simple to translate the conclusions of alignment analyses to a traditional "causal-model" framework. Finally, some may be reluctant to usee an approach that transforms complex longitudinal patterns (e.g., a sequence of where someone lives for 14 consecutive years) to a single variable (e.g., a residential trajectory with 20 possible categories).

Optimal Alignment

Optimal Alignment refers to a set of dynamic algorithms used to analyze complex sequences of uneven length (see Sankoff and Kruskal 1983; Abbott and Forrest 1986). The basic premise of optimal alignment is straightforward: determine the resemblance between two sequences of elements by minimizing the "cost" of transforming one sequence into the other. Others have explained the details of optimal alignment (Abbott and Hrycak 1990, Stovel, Savage and Bearman 1996), but since these methods remain unfamiliar to many sociologists we briefly outline the basic approach.

Three operations are available for this transformation process: a new element can be *inserted* into one of the sequences; an element can be *deleted* from one of the sequences; or an element in one sequence can be *substituted* for an element of the other sequence. The cost of each of these operations is established in advance; once the costs are established, the algorithm evaluates all possible solutions for each pair of sequences and returns the cost of the most efficient

transformative path as the "distance" between the sequences.[2] Pairs of sequences with small

"distances" are similar to one another, while pairs with larger "distances" are more distinct.

The following example illustrates how optimal alignment compares three hypothetical

sequences:

POSITION	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Sequence 1:	4	4	4	4	5	5	5	5	6	6	6	6	6	1
Sequence 2:	3	3	3	3	3	5	5	5	5	1	6	6	6	6
Sequence 3:	3	4	4	2	2	5	5	6	6	6	6	6		

The goal of this example is to show how the optimal alignment method uses the set of

operations to align and transform pairs of sequences. In the comparison of Sequences 1 and 2 we

find discrepancies in elements 1-5, 9-11, and 14. We could utilize a transformation that entails a

series of only substitutions. This would involve, for example, substituting the 3 3 3 3 in elements

1-4 of the second sequence for the 4 4 4 4 in the first sequence, along with other substitutions later

in the sequence. The cost of each of these individual transformations (e.g., substituting a 3 for 4 in

the second element) is set by the a-priori established costs of the different transformation

operations. If we imagine that the cost of substituting one element for another is the difference in

their numeric values ($S_{ij}=|i-j|$), then the minimum total cost of aligning the sequences is simply the

sum of the individual operations; here the "distance" between the sequences would equal

$(4*|3-4|)+(|3-5|) + (|5-6|) + (|1-6|) + (|6-1|) = 17$.

The algorithm could also conceivably try a transformation strategy that involves insertions,

deletions, and substitutions. In this comparison we could delete the 1 in element 14 of Sequence 1,

shift the remaining 13 elements to the right and then insert a 3 in the first element:

POSITION	1	2	3	4	5	6	7	8	9	10	11	12	13	14	
Sequence 1:	4	4	4	4	5	5	5	5	6	6	6	6	6	1	(original)
Sequence 1a:	3	4	4	4	4	5	5	5	5	6	6	6	6	6	(after insertion and deletion)
Sequence 2:	3	3	3	3	3	5	5	5	5	1	6	6	6	6	

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[2] The minimum cost of transforming one sequence into another is typically referred to as the *distance*
between sequences.   Despite this convention, it is perhaps more appropriate to consider these values

After the insertion and deletion we have a situation where Sequence 1a and Sequence 2 are not aligned at only elements 2-5 and 10, thus requiring fewer substitutions. However, if the cost of using an insertion or deletion is high in part because we are adding essentially unknown elements to an established sequence, then using a combination of insertions, deletions, and substitutions likely produces a less cost efficient transformation. [3] Let's say that the cost of insertion or deletion (i.e., indel cost) in this example is 9. The distance between Sequences 1 and 2 using a combination of indels and substitutions would equal $(2*9) + (4*|3-4|) + (|1-6|) = 27$. In this case the most efficient transformation involves only substitutions, though there are instances where simple insertions or deletions can result in the most cost-efficient path of transforming two sequences of *equal length*.

In the comparison of two sequences of *unequal length* such as Sequences 1 and 3, the algorithm is forced to utilize at least some insertions or deletions:

```
POSITION      1 2 3 4 5 6 7 8 9  10 11 12 13 14
Sequence 1:   4 4 4 4 5 5 5 5 6  6  6  6  6  1
Sequence 3:   3 4 4 2 2 5 5 6 6  6  6  6
```

Once again there are a large number of alignment possibilities. We could use a series of substitutions at elements 1, 4, 5, and 8 to bring the first 12 elements of each sequence into perfect alignment, and then insert a 6 1 at the end of Sequence 3 to complete the alignment. This transformation would result in a cost of $(|3-4|) + (|2-4|) + (|2-5|) + (|6-5|) + (2*9) = 25$. In contrast, we could insert a 4 at the start of Sequence 3, shift the 12 existing elements one position to the right and then insert a 1 in the 14th position (shown below in Sequence 3a).

```
POSITION      1 2 3 4 5 6 7 8 9  10 11 12 13 14
Sequence 1:   4 4 4 4 5 5 5 5 6  6  6  6  6  1
Sequence 3:   3 4 4 2 2 5 5 6 6  6  6  6
Sequence 3a:  4 3 4 4 2 2 5 5 6  6  6  6  6  1  (after insertions)
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dissimilarities, since distance implies the existence of a known equation which can array such a set of points in space.

[3] In many applications the cost of insertions and deletions are fixed at a value slightly higher than the highest substitution cost (see Abbott and Hrycak 1990).

As shown in the comparison of Sequences 1 and 3a, this would place elements 1, 3-4, and 7-14 in perfect alignment and necessitate only three additional substitutions. Such a transformation would also result in a cost of $(|3-4|) + (2*|2-5|) + (2*9) = 25$. The key is that the algorithm tests many different transformations and chooses the pathway that minimizes the cost of making the two sequences identical.

Clearly, since the cost of the transformations determines the quantitative resemblance between pairs of sequences, the development of the cost scheme is integral to the matching process. Ideally, these costs reflect a combination of the researcher's theoretical assumptions about the inherent distinctions between the values or categories and an empirical assessment of the differences between values or categories in sequence elements. In applications such as ours, where there are no accepted measures of quantitative differences between types of places to guide the estimation of the cost of substituting residential locations (e.g., Small Rural for Big City), researchers must rely on their own theoretical assumptions and whatever empirical data are available to facilitate this process. Thus a challenge of optimal alignment is developing a substitution scheme that accurately represents the analytic differences between states of a sequence. A related challenge is identifying an insertion/deletion cost that, when used in conjunction with the substitution matrix, creates reasonable measures of resemblance.

Steps in the Process

Our method for analyzing the structure of residential mobility sequences involves a number of steps. The first task is to define the *range of sequence elements*. Extremely complex element schemes may retain important substantive information, but they also increase the computational intensity of the analyses, and may make it difficult to identify similar sequential patterns. Conversely, overly simple schemes may disguise meaningful variation in sequential pattern. In our application, this involves developing a usable classification of different *types* of residential location.

The second task is to develop a *transformation cost scheme*. This is perhaps the most critical stage in optimal alignment analyses, since the structure of the cost scheme determines the resemblance between pairs of sequences. For us that means constructing a scheme that quantitatively reflects differences between the types of residential locations we have identified.

Once the cost scheme is established, the optimal alignment algorithm is used to *compute the dissimilarities between all pairs of sequences*. Since computation time increases exponentially with the size of the sample, various strategies for drawing sub-samples can be employed to reduce analysis time.[4] Here, we begin by calculating the cost of alignment within eight sub-samples of 200 sequences.

Next, we *use a hierarchical clustering algorithm* on the distance matrices in order to identify groups of observations with similar sequences. The goal here is to identify a set of clusters in which each cluster reflects a distinct residential trajectory. The objective of most hierarchical clustering techniques is to partition proximity data into meaningful subgroups when the number and composition of the subgroups is unknown. Clustering algorithms– single linkage, average linkage, complete linkage, Ward's minimum variance, etc. – differ in how they combine individual cases or smaller clusters into larger partitions, and can produce different solutions that emphasize certain characteristics of clusters (e.g., shape, orientation, volume, etc..) over others. For instance, while average-linkage methods tend to produce a set of clusters with similar variances, a minimum-variance method such as Ward's tends to produce spherical clusters of similar volume.

Newer clustering techniques based on principles of Bayesian inference have been successfully used in scientific applications to guide the choice of both the proper method and the optimal number of clusters (see Fraley and Raftery 1998 for an overview), but at this time this

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[4] Various programs are available for optimal alignment. Andrew Abbott's algorithm Optimize runs relatively quickly and has nice exploratory data features, but cannot handle samples over 150 sequences. Goetz Rowher has included an alignment procedure in the latest release of TDA; we use Stovel's SAS/IML program (1994) which can handle very large samples of sequences. In our study the majority of Optimal Alignment analyses were conducted on a Pentium-75 PC with Windows 95. On a machine of this size, each analysis of

approach is not developed for the analysis of dissimilarity data.[5] Therefore, identifying a coherent, and stable set of meaningful clusters often involves testing various clustering methods and refining solutions through examination of data points (e.g., see Abbott and Hrycak 1990). The empirical challenge is to see if any clustering method identifies discrete groups of observations with substantively similar sequential patterns.

For each cluster we then identify a *typical trajectory* to represent the central pattern of the group of sequences in the cluster. In our study, the set of "typical" sequences comprehensively describes the range of possible residential trajectories. Finally, we again use the optimal alignment algorithm, this time *to classify the remaining observations in the sample* in terms of the typical residential trajectories we have revealed. To do this we calculate the distance between each empirical sequence and all of the "typical" sequences, assigning observations to closest typical trajectory (see Stovel, Savage, and Bearman 1996 for a similar strategy). A subsequent set of criteria is used to identify any sequences that don't empirically fit into one of the established residential trajectories. These sequences are often composed of a complex pattern of shifts across place-types, and are treated as examples of non-patterned trajectories.

Data/Sample

We use the Panel Study of Income Dynamics (PSID) in our study of residential mobility patterns. The PSID is a nationally representative sample that began in 1968 with 5000 households (3000 in a representative cross-sectional sample and 2000 in a low-income sample). The original 5000 households and any households formed by members of the original households have been followed for almost 30 years. The PSID is well-suited for our analyses because it includes detailed

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200 unique sequences took about 15 minutes of computational time. The computational time is reduced to roughly 4 minutes per analysis using a Pentium-410 PC with Windows NT.
[5] These methods are designed for rectangular multivariate data structures; using them on proximity data requires transforming the data with a multi-dimensional scaling algorithm. Our explorations with these techniques suggest that this transformation refracts the relationship between observations in ways that result in distorted clusters.

geographic data on heads of households for the survey years 1968-1985, ranging from state of residence to census tract.

Sample Criteria

The sample for analysis is comprised of all individuals who were a household head at least once during the period between 1968-1985. Since the geographic data is linked to the household head in each year it was easy to identify the residential information for those individuals who were household heads in every survey year. Yet we also wished to identify the residential information for other sample members in the years when they were not the household head. Using PSID indicators of an individual's position in a household (e.g., head, spouse, child, other adult, etc…), in conjunction with the geographic information on the head of the household, we were able to impute address information for non-household heads across years. So, for example, if we have a woman who was the spouse of the household head between 1968-1975 and eventually became household head in 1976, we are able to use the geographic information linked to the head of her household (i.e., the husband) between 1968-1975 to identify her residential location in those eight years. In the case of children who eventually became household heads, we did not start imputing geographic information until they reached age 18, the assumed minimum age at which individuals might consider independent residential moves. This strategy allowed us to construct longer residential sequences for a wider variety of household members, and thus broaden the sample to include more women and younger adults.

Geographic data

Ideally we would like to include the residential place type for all respondents across all 18 years for which the PSID collected geographic data. However, while reconstructing the address datafile, the staff at the Survey Research Center at the University of Michigan found that some of the original address tapes from four survey years (1969, 1975, 1977, 1978) had been overwritten or destroyed. While there is some evidence that the Survey Research Center staff imputed address information for these missing years (based on individuals' information in prior and subsequent

years), our examination of the data indicates that the problem was not fully corrected. Therefore, we have excluded these missing years from the analysis.

This missing data problem has consequences for the way we construct the residential trajectories. Without the missing years, an individual's residential history would represent a series of residential locations over consecutive years. If this were the case, we would know both the absolute number of years in the entire sequence (e.g., 1968-1985 = 18 years of data) and the interval between two consecutive elements in a sequence (i.e., 1 year). However, given the structure of the missing years of data, we decided to consider consecutive "time periods" rather than years. Therefore, while the longest possible trajectory spans 18 years (from 1968-1985), it consists of only 14 data points, covering residential data for 1968, 1970-1974, 1976, 1979-1985. Since many households are picked up mid-stream, this strategy means that sequences vary not only in length, but also in the number of actual years they span. For instance, a 12 time period sequence starting in 1968 spans 15 years, while a 12 time period sequence starting in 1970 spans 14 years. Moreover, the real duration of consecutive sequence elements can differ, depending on where they fall in the sequence of residential locations. Our overall sample consists of 5474 individuals with ten or more consecutive time periods of residential data.

Coding Types of Place

Once we had constructed the sample and the sequences of residential data, we classified each residential location into a *place-type*. We focus on place type (rather than specific geographic place) for two reasons. First, there is growing evidence that individuals may identify with *types* of communities, and that such identities may influence their attachments to, and behaviors within different types of communities and settlements (Hummon 1990; Feldman 1990). Our second reason is more pragmatic: residential trajectories would be far too complex to analyze if we retained every location.[6] Our *place-type* variable has nine categories, classified according to a

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[6] Another possible way to consider residential mobility histories is to simply note when an individual moves. However, this approach ignores the qualitative differences between residential communities and is hard to

geographic-place continuum ranging from Small Rural town to Large Metropolitan Large City (see

Table 1). Particular locations were classified according to their 1980 census place designation,

their 1980 census place population, and their 1983 Metropolitan Statistical Area (MSA)

designation.[7] We used the MSA designation (in conjunction with the census place identifier) to

classify locations as either central city, suburb (i.e., non central-city situated in a metropolitan area),

or rural (i.e., place situated in an non-metropolitan region). Population data were used to

distinguish less populated from more populated locations *within* urban, suburban, and rural areas.

Table 1 reports the population sizes we used to distinguish different rural, suburban and central city

areas. Finally, we used the MSA designation to contrast smaller (i.e., MSA with < 1 million

inhabitants) with larger (i.e., MSA with 1 million or more inhabitants) metropolitan regions,

thereby distinguishing locations in and around huge cities like New York or Los Angeles from

locations situated near smaller cities like Bellingham, WA or Redding, CA.

This coding scheme yields residential sequences containing 10-14 elements which

summarize the string of place-types that comprise a residential career. These residential sequences

are represented by a string of numbers. For instance, the sequence **2 2 2 2 2 2 8 8 8 8 8 1 1 1** (or

conceptualize in sequential terms. At the end of this paper (and in other analyses by the lead author) we
briefly consider the relationship between shifts in place types and the sheer number of moves.
[7] The decision to use 1980 census information and 1983 PMSA/SMSA definitions to classify locations
between 1968-1985 was two fold. First, this ensured that demographic or administrative changes in a place
over time would not result in changes in the categorization of this place along the geographic continuum
within a residential trajectory. For example, the town of Ferndale, WA (a "suburb" of Bellingham, WA) is
now considered metropolitan because of its inclusion in a metropolitan statistical area created in 1980,
although in 1970 it was considered rural. If one of our respondents lived in Ferndale from 1968 to 1985, and
we used both 1970 and 1980 census classifications the sequence would indicate that the respondent had
moved from a Large Rural place to a Small Metro Small Suburb, simply because of changes in the
administrative classification of that location. Hence our approach eliminates the possibility of shifts along
the continuum based solely on changes in the place characteristics (i.e., one actually had to move to shift
along the continuum). Second, the use of the 1983 PMSA/SMSA definition allowed for the inclusion of new
geographic areas that grew in population size or functional prominence between the 1970 and 1980 censuses.
Between 1975 and 1983 the number of MSA's and NECMA's (New England County Metropolitan Areas)
increased from 250 to 314. This tremendous growth represented the emergence of newer geographic areas in
primarily Southern and Western regions of the country that met the criteria for MSA designation. Moreover,
the boundaries of some existing metropolitan areas changed to include adjacent counties with increased
population density or larger commuting flows. Many believe that the post 1980 census designations reflect a
more accurate representation of the "metropolitan" areas of the United States, and sufficiently consider the
tremendous 1970's decentralization of the population (*drawn from personal conversation with Richard
Morrill*).

6(2), 5(8), 3(1)[8]) indicates that an individual spent six time periods in a Large Rural location, the next five time periods in a Large Metropolitan Small City, and the last three time periods in a Small Rural location. Clearly, with nine different *place-type* categories and 10-14 time points, the number of possible unique sequences is quite large. Therefore, the first analytic goal is to reduce the number of complex sequences to a manageable number of typical trajectories.

Sub-Samples

Our research design is based on empirically deriving a population of typical residential trajectories and then evaluating the prevalence of such pathways among different segments of the population. A great deal of literature on migration patterns indicates that mobility rates decline sharply after age 30 (Long 1988; Frey and Kobrin 1982), while other studies have shown that the likelihood of migration to different city and suburban destinations is related to age and household compositional factors (South and Crowder 1997). Thus we expect age at the first time period to influence patterns of movement over the course of the residential sequences. In order to ensure that our population of residential trajectories reflects all age groups, we drew random samples of 200 individuals from each of four age groups: <=25 years old at start of sequence, 26-35 years old at start of sequence, 36-49 years old at start of sequence, and 50+ years old at start of sequence.[9]

Above and beyond the effects of age, however, we hypothesized the existence of both stable (demonstrates a general pattern of residence in the same place-type over the entire sequence) and non-stable (demonstrates patterned changes in place-type over course of the sequence) trajectories. In general, we expected respondents' residential histories to be relatively stable, particularly among older individuals. In fact, fewer than 40% of the individuals in any of the four random samples made any *place-type* transition over the course of their trajectory. Thus, the

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[8] This form of representing a sequence is used to reduce the complexity of interpreting the potentially long sequences of elements. The number in the parentheses represents the coding of the residence on the nine category place-type continuum. The number immediately proceeding that represents the number of time periods spent in that "type of place". For example, 9(1) would indicate that the individual spent 9 consecutive time periods living in a Small Rural place.

absolute number of "transitional" individuals (i.e., individuals who made at least one shift in

place-type over the sequence) present in these random samples was small. To supplement our

analyses of the random samples we drew an additional set of random samples of "transitional"

sequences from each age group. [10] Ultimately, we integrate the results from all eight samples in

order to construct our universe of residential patterns.

Analysis of Residential Trajectories

<u>Substitution Costs</u>

In order to use the optimal alignment algorithm it is necessary to develop a reasonable set

of transformation costs. Constructing the appropriate cost for substituting one type of place for

another is challenging since no one has yet conceived of a scheme for *quantifying* distinctions

between types of places. Therefore, the costs used here reflect a combination of two different

considerations: (1) our theoretical understanding of distinctions in the *character* of places along

our continuum; and (2) the empirical structure of transitions between different *place-types* in the

PSID. Theoretically, the extent to which types of places differ is a function of perceived

differences in the identity, characteristics, and physical/social environment of places with different

sizes and relative location in the spatial landscape. Yet differences between *place types* might also

reflect the likelihood of population movement between different types of places.

The initial framework for our substitution cost matrix is our theoretical understanding of

intrinsic differences in the *character* of places across our residential *place-type* continuum. We

draw from the following observations:

1) The character of residential locations is related to absolute *population size*. Locations with
   small populations are different from those with large populations in terms of *amenities,
   available services, occupational opportunities, and likelihood of social interaction with*

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[9] We selected samples of size 200 for three reasons: (1) these samples are large enough to contain a
heterogeneous mix of residential trajectories; (2) these samples are small enough to allow for reasonably fast
calculations; and (3) drawing samples of 200 leaves enough observations for subsequent analyses.
[10] The samples for the age <=25, age 26-35, and age 36-49 groups consisted of 200 random transitional
sequences. Since the absolute number of age 50+ transitional sequences was small, our sample was
comprised of **all** 250 individuals age 50+.

others. This observation implies that sheer differences in population size should influence substitution costs.

2) The character of residential locations is related to the level of *metropolitan influence*. It is thought that metropolitan areas of different size and prominence offer a different range and diversity of *services, occupational and economic opportunities across a consolidated region*. This suggests that communities situated in non-metropolitan or smaller metropolitan areas are different from those in large metropolitan areas. This implies assigning a high cost to substituting a non-metropolitan for a large metropolitan place, and a somewhat reduced cost to substituting either with a small metropolitan location.

3) The character of a residential locations reflect *distinct ideologies and identities* that residents and non-residents construct and maintain about urban, suburban, and rural communities in the United States (Hummon 1990). Interviews of residents in urban, suburban, and small town communities highlight the differences in individuals' perceptions of the quality of life in different places, and indicate that residents of one class of community often have negative perceptions about the character of other types of communities. This suggests that there is some substantial cost associated with crossing rural, suburban, and urban boundaries.

These observations suggest that substitution costs are a function of differences between places in terms of three dimensions: changes in population from less than 10,000 to more than 250,000, changes in "metropolitan influence" from a non-metropolitan to large metropolitan (i.e., MSA > 1 million) region, and movement across rural, suburban, and urban boundaries. Furthermore, substitutions that involve crossing these rural/suburban/urban geographic boundaries are perhaps costlier than substituting *place-types* within geographic sectors (e.g., within suburban boundaries). These principles yield a rank ordering of the nine categories of the *place-type* continuum with the highest overall cost associated with substituting a Small Rural for a Large Metropolitan Large City location.

To augment these theoretically-derived principles, we examined the empirical distribution of transitions between types of place. If transitions from one *place-type* to another are particularly prevalent, this is evidence of a strong flow of persons from one type of place to another. Even if the character of these places is markedly different, they are linked together by the mobility stream, and therefore should have lower substitution costs.

Table 2 reports the distribution of transitions between types of place, considering *all* changes of *place-type* over the 14 possible time periods. Cell values represent the percentage of

individuals who made the transition to each *place-type*, given a particular origin. For example, among those who were in a Large Rural location and changed *place-types*, 42.0% moved to a Small Rural location, while only 8.9% moved to a LM Large City. These percentages can then be compared with the overall (column) percentages to determine particularly strong or weak migration flows.

Table 3 summarizes the relative transition rates between different types of places. The transition ratios reported in this table are computed by dividing the percentage of individuals beginning in place-type *i* who move to place-type *j* by the percentage of *all* individuals who move to place-type *j*. For example, the percentage moving from Large Rural to Small Rural (42.0%) is divided by the overall percentage moving to Small Rural places (12.9%), resulting in a transition ratio of 3.24. Higher values indicate a greater than average likelihood of transition across place-types. In nearly every instance, the strength or weakness of the migration flow between two place-types is symmetric. In other words, when the transition ratio associated with moves from place-type *i* to place-type *j* is higher, we should expect the opposite ratio for moves from place-type *j* to place-type *i* to also be high.

The examination of the transition-specific migration flows reveals several features which supplement our theoretical understanding of the distinctiveness of different place-types. First, we observe relatively high rates of migration between suburban and central city locations within different sized metropolitan areas. Specifically, ratios are higher for transitions between Small Metropolitan Small Suburbs and Small Metropolitan City Locations, and between Large Metropolitan Suburbs and Large Metropolitan City locations. Second, we observe higher than average transition ratios for moves between rural locations and small metropolitan central city locations (for example, the transition ratio from Small Rural to Small Metropolitan Large City is 1.71). Third, in general the transition ratios for moves between rural and city places are higher than ratios for moves between rural and suburban places. Hence if similarity were based solely on transition-specific migration rates, rural places would be considered more similar to city locations

than to suburban locations, a conclusion which is inconsistent with our theoretical understanding of the character of types of places.

Our final substitution matrix (see Table 4) combines our theoretical assumptions with insights drawn from the transition analysis. Specifically, the empirical analysis of transition ratios demonstrated the ease of suburban-city movement within, rather than across, different sized metropolitan areas, so we increased the cost of suburban-to-city moves which cross the boundary between small and large metropolitan areas. Similarly, we adjusted our preliminary cost for substituting rural and small metropolitan urban locations to reflect relatively high transition rates between these place-types. We are confident that the final cost matrix represents a reasonable balance between our theoretical assumptions and empirical assessments of similarity across locations.[11]

Indel Costs and Sequence Length

A general rule of thumb for optimal matching models is to fix the insertion and deletion (indel) costs at slightly above the greatest individual substitution cost in the matrix (Abbott and Hrycak 1990). This means that when sequences are of roughly equal length, most transformations will likely rely on substitution rather than insertion or deletion. When sequences are of substantially different length, however, inserting or deleting elements can contribute significantly to the overall distance calculation. In substantive contexts where distinctions in length are essential to the examination of different sequential patterns, this approach makes a great deal of sense. For example, Stovel et. al. (1996) utilize variations in sequence length to distinguish lifelong Lloyd's Bank employees from those with shorter tenures, and demonstrate changes in the likelihood of

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[11] In the process of developing this cost scheme, we repeatedly adjusted the relative balance between our initial theoretical model and the empirical migration rates, testing a number of alternative cost matrices. Consistent with past research, small variations in the individual costs (such as increasing the cost of moving from a Rural to Suburban location, or decreasing the cost of moving from a small to large metropolitan region) did not result in drastically different distance values (Abbott and Forest, 1986). Moreover, the conclusions drawn from analyses using the initial matrix based solely on "character" differences were very similar to those found using our final cost scheme. However, we did find that using a substitution matrix based solely on the empirical distribution of transitions limited our ability to identify consistent stable and non-stable

short and long tenure careers across successive cohorts. In the present application, however, variations in length are the result of truncated data rather than a reflection of substantively meaningful variation in career trajectories. Therefore, we would like to minimize the impact of length differences on our classification of trajectories. Consider the following example:

S1: (10 time periods of SM Small Suburb)   3 3 3 3 3 3 3 3 3 3
S2: (14 time periods of SM Small Suburb)   3 3 3 3 3 3 3 3 3 3 3 3 3 3
S3: (10 time periods of LM Large Suburb)   5 5 5 5 5 5 5 5 5 5

In this example, sequences S1 and S2 both exhibit a pattern of stable residence in SM small suburban locations; the two sequences differ only in length. The simplest alignment of the two sequences involves inserting four 3's in S1 (or deleting four 3's from S2). When the indel cost is fixed, the distance between S1 and S2 equals **(4*indel cost)/14**. Given our substitution matrix, a typical fixed indel cost might be 2.7, which yield a distance of **0.77**. In contrast, aligning S1 and S3 involves the substituting all ten 5s for 3s (or vice versa). If substituting a 5 for a 3 costs 0.6 per substitution, this yields a distance of **(10*.6)/10 = .60**.

This cost scheme suggests that S1 and S3 are more similar to each other than are S1 and S2, even though the substantive patterns for S1 and S2 are literally identical (i.e., individuals with stable residence in a SM Small Suburban place). Clearly, the fixed indel cost is drawing sequences together on the basis of similar lengths, rather than similar patterns. To minimize this effect we developed a strategy of *variable* indel costs that uses fixed indel costs for pairs of sequences of equal length, and a reduced indel cost -- roughly ¼ of the fixed cost -- for pairs of sequences of varying length. Returning to the example above, the indel will remain fixed at 2.7 for pairs of sequences of equal length, but will fall to .45 when sequence length varies. Upon using these modified specifications, the distances better reflect obvious resemblance within the sequential patterns.

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patterns of movement, and produced heterogeneous clusters comprised of individuals with very different trajectories.

Results

   We analyzed each of the eight age-graded samples of sequences using the optimal

alignment algorithm and the cost scheme we developed. We then clustered each of the eight

distance matrices (using the Ward minimum variance method) to identify unique groups of

common residential patterns. Within each sample we selected a cluster solution which a) restricted

the population of trajectories to a manageable size for subsequent analyses; b) avoided solutions

that produced any clusters composed of only a single observation; and c) included a number of

relatively homogeneous "non-stable" clusters. While there has been much conjecture over

techniques for choosing the number of clusters (for overview see Milligan and Cooper, 1985), we

did not utilize one of the various "heuristics" for cluster choice, but rather allowed the constraints

noted above to guide the choice of cluster solutions.

   For each sample this produced a robust solution of 13-15 clusters in which the

"within-cluster" distance (i.e., average distance between two individuals in the same cluster) was

substantially lower than the "between-cluster" distance (i.e., average distance between an

individual and any individual assigned to a different cluster). T-tests indicated that in each of the

samples the overall "within-cluster" distance was significantly different from the overall

"between-cluster" average.

   In reality, even the most coherent clusters are composed of sequences which are similar in

general but different in detail. Therefore, in order to characterize each cluster we need a way to

identify a representative sequence for that cluster. We define the "typical" sequence to be the

sequence with the *lowest average within-cluster distance*. An example demonstrating the process

of identifying the "typical" sequence is shown in Appendix A

   Tables 5a-5d report the cluster solutions revealed in the four age-graded random samples.

All of the solutions included a cluster for each of the nine possible stable residential trajectories

(e.g., Stable SM Small City, stable LM Large Suburb). In addition, another 4-6 non-stable clusters

emerged in each analysis, reflecting trajectories with a single shift across the rural-suburban-urban

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continuum (e.g., first 7 time periods in LM Large City and last 7 time periods in Small Rural). For the most part, these non-stable trajectories contained intra-metropolitan shifts across urban and suburban boundaries. These typical patterns suggest that it is empirically rare that individuals simultaneously cross urban-suburban boundaries, and move between small and large metropolitan areas. [12]

The results of the cluster analyses on the four age-graded transitional samples are shown in Tables 5e-5h. These analyses support the existence of the non-stable trajectories identified in the random samples, and suggest the existence of several additional typical residential trajectories. Some of these new patterns involve single shifts, but others reveal the existence of more complex patterns involving multiple shifts across the rural-suburban-urban continuum. For example, in both the **age <=25** and **age 26-35** samples we find small clusters with the following distinct patterns: a) rural -> city -> rural; and b) city -> suburb -> city. Further analysis of the general "city -> suburb -> city" pattern indicates unique trajectories for those living in smaller vs. larger metropolitan areas. Thus, in subsequent analyses we construct two different "city -> suburb -> city" trajectories to retain these distinctions across the size of the metropolitan area.

Recall that the objective of our initial alignment analysis was to construct a *population* of typical residential trajectories, using the variety of patterns revealed in the smaller samples. This population should include all general trajectories that were similar across the four age groups as well as any unique patterns that emerged in particular age classes. However, in order to conduct our subsequent classification of residential sequences, we need to summarize each trajectory in the population with a single typical sequence. Where typical sequences are identical across age groups this presents no problems. But where the same *general* pattern emerges in two or more samples,

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[12] Examples of crossing both urban-suburban boundaries, and from a small to large metropolitan area would involve moving from Seattle (a LM Large City) to Zillah, WA (a SM Small Suburb situated just outside Yakima, WA) or moving from Yakima (SM Small City) to Lynnwood, WA (a LM Small Suburb just outside Seattle). The probability of such movement is substantially less likely than the probability of intra-metropolitan movement from, for example, Seattle to Lynnwood or Zillah to Yakima.

but the *details* of the typical sequence differ, we selected the average or most common pattern.[13] Further, we standardized the length of each sequence in the population of typical sequences to the average sequence length of 13 elements since we had no theoretical reason to think that some residential scripts are shorter than others.

Integrating the typical sequences from all samples results in the 25 residential trajectories shown in Table 6. This family of residential trajectories represents a wide range of sequential patterns: in total there are nine completely stable trajectories, 12 non-stable trajectories consisting of one shift across the rural-suburban-urban continuum, and four non-stable trajectories consisting of multiple shifts across the continuum.

Once we had developed a comprehensive population of residential trajectories, we again turned to the optimal alignment algorithm to assign each of the 5474 individuals one of 25 trajectories. Rather than calculating distances between all pairs of sequences in a small sample, here we calculated the distance between each empirical sequence and each of the 25 typical sequences, thereby *substantially* reducing the computational intensity of the task. Using these distances, we assigned each individual residential career to the closest typical trajectory (see Stovel et. al., 1996 for a similar strategy).

While this approach classifies individuals in terms of the "closest" pattern, we had some concerns with the assignment process. First, there were instances where shorter length non-transitional sequences (e.g., 10(9)) were assigned to closer "non-stable" groups. This occurred, in part, because of the shortcomings associated with the indel costs noted earlier. To correct this problem, all individuals with completely non-transitional sequences were forced into one of the nine stable trajectories.

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[13] For example, it is unclear whether the "best" typical sequence for the general LM Suburb to City pattern is **6(5), 8(9); 7(4), 7(9);** or **8(5), 6(9)**. In this instance we have selected the central pattern of **7(4), 7(9)** to represent the typical LM Suburb -> City trajectory. Additional analyses indicate that slight modifications in the specifications of the typical sequence – e.g., using **6(5), 8(9)** rather than **7(4), 7(9)** – do not alter the assignment of individuals to different residential trajectories.

Second, we noticed that many individuals who made more than two shifts across the place-type continuum over the full time period were still being placed into a stable trajectory. Likewise, there were individuals who had spent less than 50% of the time periods in the place category that they were subsequently assigned to (e.g., individuals who spent only 6 of 14 time periods in a Large Rural place yet were assigned to the Stable Small Rural pattern). These seemed like questionable assignments, and thus we adopted a strategy that took into account the percentage of time periods spent in different size categories among individuals originally assigned to a "stable" pattern, and reassigned individuals if this percentage dropped below a specific criterion.[14]

Third, it was evident that there were a number of individuals who demonstrated sequences that were substantively and empirically distinct from any of the established patterned trajectories. These individuals typically followed more complex transitional sequences comprised of multiple shifts across the place-type continuum (e.g., 3(1),2(4),5(9),2(1),1(4)). The optimal alignment analyses indicated that these individuals were "quantitatively distant" from all of the 25 patterned residential trajectories. Since the goal was to identify and examine groups comprised of individuals following similar structured patterns of residential movement, it was not appropriate to include these individuals simply on the basis that their pattern was closest to a given typical sequence. Thus, 198 individuals, or 3.6% of the total sample, were categorized as following a "non-patterned" trajectory.

Table 7 presents selected characteristics of respondents in each of the 25 residential trajectories. As we would expect, we observe the greatest sequence homogeneity in the nine stable trajectories. For each of the stable trajectories, the average distance from any one sequence to that group's typical sequence is less than .100, while in contrast the average is roughly three times higher in all of the non-stable trajectories. Again as expected, the most heterogeneous groups are those with the most complex sequences (e.g., those reflecting multiple shifts across the rural-suburban-urban continuum (e.g., LM City/Suburb/LM City)). In addition, we find that the

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[14] This modification resulted in a shift of 297 individuals, or 5.4% of the total sample.

average distance to the typical sequence is substantially among those who followed non-patterned trajectories. The large disparity evident in this group validates our decision to reassign these individuals out of the coherent, structured residential trajectory groups.

Yet even within the more homogenous clusters a fraction of the sequences involve two or more place-type shifts. Interestingly, among these "stable" groups the likelihood of multiple shifts is 20% or higher in the Large Rural, LM Large Suburbs, and LM Small City trajectories, and less than 11% in some of the larger groups such as Small Rural and LM Large City. The fact that "stable" does not necessarily mean absence of movement across the continuum suggests that even some residential careers that involve shifts in place type are closer to the pure "stable" trajectories than to any of the other typical patterns. We speculate that such individuals are demonstrating a pattern of stable commitment to a particular place type even given small or temporary deviations away from complete stability. For example, it seems reasonable to classify an individual who spends the first seven time periods in city, shifts to a suburb for 1 time period, and then shifts back to the city for 6 time periods as someone demonstrating a commitment to residence in an urban location.

Table 7 also reports both the lifetime number of residential moves and actual geographic place changes among individuals following different trajectories to emphasize that place-type stability is often distinct from geographic mobility. For instance, while members of the Stable LM Large City group have a homogeneous set of residential careers consistent with the typical sequence, their geographic mobility is quite distinct from that of members of the other stable groups. While this group of urbanites moves more than any other stable group (an average of 2.35 moves over a 13 time period sequence), they have the fewest changes in census place or county – 0.38. Clearly, attachment to a particular city often requires multiple intra-city moves during the course of a residential career. This contrasts sharply with the pattern demonstrated by members of the stable SM Small Suburbs cluster, who are more stationary in terms of both the place-type and their specific residence (i.e., fewer moves and changes of place or county).

Table 8 considers the prevalence of each residential trajectory across our four different age groups. These descriptive profiles indicate both the validity of this population of systematic trajectories, and the potential utility of these new measures for studies of individual patterns of residential movement over the life course. For simplicity, we have consolidated the population of residential trajectories to a set of 12 combined trajectories reflecting general patterns of movement across the rural-suburban-urban continuum (although the picture is unchanged when we examine all 25 typical trajectories). As we would expect, our younger respondents are more likely to have "non-stable" residential trajectories. Over 30% of the individuals in the **age <=25** group followed a "non-stable" trajectory in comparison to only 11.3% of the individuals in the **age 50+** group. Further analysis of individuals in "stable" trajectories illustrate some expected patterns with respect to individuals' residential locations. In particular, while younger "stable" individuals are more likely to maintain consistent residence in a Large City, those in the older age segments are more likely to remain in either Suburban or Rural areas. For example, almost 39% of the **age 36-49** individuals categorized into a "stable" trajectory maintain consistent residence in the suburbs, while over 34% of the **age 50+** individuals classified as "stable" maintain consistent residence in a rural area.

An analysis of the distribution of "non-stable" individuals across the various "non-stable" trajectories also shows differences across age groups. First, "non-stable" individuals in the **age <=25** group demonstrate the greatest likelihood of following a "Rural -> City" or "Rural-Suburb/City/Rural-Suburb" trajectory. Conversely, respondents over 35 are the least likely to follow such patterns. Second, older "non-stable" respondents (over 35) are more likely to follow a "Suburb -> Rural" trajectory than younger individuals. Last, the likelihood that a "non-stable" individual will travel a "City/Suburb/City" trajectory is very similar across the three youngest age segments - roughly 6-8% of all "non-stable" individuals in each group. This suggests that non-stable middle-age individuals are just as willing as younger individuals to make shifts in and out of suburban areas.

These profiles illustrate that the prevalence of various residential trajectories varies systematically across age graded segments of the population. While the distinctions in the likelihood of pathways are not dramatic, this does suggest that some systematic patterns of geographic movement are more prominent at different stages of an individual's life course. These findings are consistent with the notion that individuals occupy different roles and positions -- in this instance different residential situations -- throughout various stages of their life course, and that the cumulative progression through such positions may be influenced by demographic characteristics such as age, gender or race.

Discussion

In this study we have used an alternative longitudinal methodological approach to demonstrate the existence of a set of systematic patterns of residential movement across the geographic landscape. This procedure, drawing on theoretical and empirical assessments of the distinctions across different place-types and residential locations, allows us to better understand the structured nature of residential mobility patterns over time, and to look beyond the factors that influence the year to year mobility transitions across various stages of the life course. By treating the whole residential sequence as a unit of analysis, we are able to identify a set of residential trajectories that typify the forms of long term mobility processes exhibited by diverse groups of individuals.

In this paper we perform a simple analysis to show how an individual's characteristics such as age shapes the likelihood of following different residential trajectories. Subsequent analyses could conceivably demonstrate that the prevalence of residential trajectories is related to, or influenced by, a wide set of sociodemographic variables such as race, gender, education, family composition, and marital status. Moreover, it is now possible to utilize these residential trajectories to adjust our understanding of how past residential experience impacts subsequent mobility processes. Residential mobility studies have consistently demonstrated that individuals with a greater past mobility are more likely to move in the future (Lansing and Mueller 1967; Morrison

1967; South and Crowder 1997). Traditionally, past mobility is measured in terms of the number of moves since age 18, or some assessment of whether the individual moved in a specified time period prior to the survey year (e.g., yes/no moved in past 3 years). Our trajectories, which retain both qualitative and quantitative aspects of residential mobility, make it feasible to assess how variations in the composition and scripted nature of such "past residential mobility" influences future behaviors and attitudes such as moving, getting married, having child and forming attachments to residential communities.

Further explorations could also use the population of residential trajectories to illustrate the interdependent nature of life course sequential processes over time. It is reasonable to believe that for many individuals, residential sequences are closely intertwined with other life course patterns, including marriage, family composition, and home ownership. Hence this study not only introduces the tools and methods to construct alternative life course sequences such as marriage or family structure trajectories, but also proposes a specific population of residential possibilities.

The basic notion of using sequence methods to identify residential trajectories can be extended to facilitate enhanced study of other longitudinal migration and mobility processes. For instance, we could attempt to construct trajectories based on more complex scheme of categorizing places – perhaps one that considers not only population and geographic characteristics, but also contextual characteristics of places such as income or home ownership levels. Moreover, we might modify our understanding of residential situations and define individuals' situations not in terms of "where one lives", but rather in terms of the composition of those in the household or the physical characteristics of the dwelling. The idea of identifying structured patterns of movement could also be applied to the study of specific populations such as immigrants and used to assess whether immigrants of different backgrounds follow similar patterns of movement across the US geographic landscape after entry into the country.

Most importantly, this paper outlines a framework for others interested in using optimal alignment methods in their own investigations of scripted life course processes. We have

illustrated some of the methodological challenges associated with the optimal alignment approach such as the development of theoretically and empirically derived transformation costs, the integration of dissimilarity matrices from a set of sub-samples, and the utilization of concurrent hierarchical clustering techniques. We subsequently demonstrated the method's ability to identify common residential patterns from a population of complex sequences. The process by which we identified specific place-types for sequence elements, constructed substitution costs across such place-types, chose typical trajectories from clusters of similar sequences, and categorized individuals into proper residential trajectories is analogous to the steps others will face when using this approach. For example, the scholar interested in evaluating the existence of household composition careers faces many challenging questions (e.g., What are the possible "states" of household composition? How do I quantify the differences between such states? How should the length of careers influence cost assessments?). Hopefully we have suggested some strategies for addressing and answering these difficult questions.

TABLE 1: Place-Type Continuum

Coding	Description of Type of Place	Examples	Number of Geographic Places (1980) [b]	% Sample Time Period 1	% Sample Time Period 10
1	Rural /Non-Metropolitan Area <10K Population Size or Missing Population (SMALL RURAL)	Omak, WA Sistersville, WV Mendicino, CA	12,579 (55.8%)	18.6%	18.5%
2	Rural /Non-Metropolitan Area 10K+ Population Size (LARGE RURAL)	Walla Walla, WA Paris, TX Ames, IA	510 (2.3%)	5.8%	5.8%
3	Suburb/Small Metropolitan Area < 25K Population Size or Missing Population (SM SMALL SUBURB)	Cheney, WA Durham, NH Sonoma, CA	5,424 (24.1%)	9.8%	11.1%
4	Suburb/Large Metropolitan Area < 25K Population Size or missing population (LM SMALL SUBURB)	Des Moines, WA Ashland, MA Great Neck, NY	2,987 (13.3%)	9.0%	9.9%
5	Suburb/Large Metropolitan Area 25K+ Population Size (LM LARGE SUBURB) [a]	Renton, WA Walnut Creek, CA Mt. Lebanon, PA	519 (2.3%)	6.9%	8.5%
6	Central City/Small Metropolitan Area < 100K Population Size (SM SMALL CITY)	Yakima, WA Nashua, NH Sarasota, FL	310 (1.4%)	8.2%	7.9%
7	Central City/Small Metropolitan Area 100K+ Population Size (SM LARGE CITY)	Spokane, WA Austin, TX Charlotte, NC	94 (0.4%)	11.1%	10.7%
8	Central City/Large Metropolitan Area < 250K Population Size (LM SMALL CITY)	Everett, WA Cambridge, MA Marietta, GA	69 (0.3%)	2.3%	2.4%
9	Central City/Large Metropolitan Area 250K+ Population Size (LM LARGE CITY)	Seattle, WA Pittsburgh, PA Chicago, IL	38 (0.2%)	28.3%	25.2%

a - A small percentage of the suburbs classified in category 5 are situated in Small Metropolitan Areas (some examples are Pekin, IL, Edison, NJ, and Miami, OH). Less than 10% of the Small Metropolitan area suburbs had a population of 25K+.
b – Source for classifying the 22,529 places was *1980 Census of Population and Housing: Geographic Identification Code Scheme – PHC80-R5 (1983)*

Small Metropolitan Area
  – MSA/PMSA/NECMA with Population in 1980 of < 1 Million
  – Examples: Tacoma WA, Stockton CA, New Haven CT, Worcester MA, Toledo OH

Large Metropolitan Area
  – MSA/PMSA/NECMA with Population in 1980 of 1 Million or more (41 areas)
  – Examples: Seattle WA, San Francisco CA, New York NY, Boston MA

TABLE 2: Likelihood of Place-Type Transition Across Time Periods

<div style="text-align:center">Destination – Time Period 2</div>

Origin – Time Period 1	Small Rural	Large Rural	SM Small Suburb	LM Small Suburb	LM Large Suburb	SM Small City	SM Large City	LM Small City	LM Large City
Small Rural	N/A	29.6%	18.8%	6.9%	4.3%	8.6%	17.4%	1.9%	12.5%
Large Rural	42.0%	N/A	9.8%	6.8%	5.3%	11.1%	13.0%	3.1%	8.9%
SM Small Suburb	18.2%	4.8%	N/A	7.2%	8.1%	25.5%	21.8%	4.0%	10.4%
LM Small Suburb	8.8%	5.0%	10.7%	N/A	31.1%	6.3%	4.5%	5.7%	27.8%
LM Large Suburb	8.6%	3.0%	8.1%	32.9%	N/A	6.0%	7.2%	9.0%	25.3%
SM Small City	12.2%	8.6%	36.7%	9.4%	7.3%	N/A	14.1%	1.9%	9.7%
SM Large City	15.2%	8.4%	34.2%	7.4%	10.1%	10.9%	N/A	2.3%	11.6%
LM Small City	8.6%	5.0%	13.8%	18.6%	23.3%	4.3%	6.3%	N/A	20.2%
LM Large City	10.1%	4.4%	6.8%	30.4%	28.8%	6.4%	7.5%	5.7%	N/A
ALL	12.9%	7.9%	14.7%	14.0%	13.6%	9.2%	10.1%	4.3%	13.4%

Sample: only includes those who changed place category from one time period to the second time period

TABLE 3: Transition Ratios Across Time Periods

<div style="text-align:center">Destination – Time Period 2</div>

Origin – Time Period 1	Small Rural	Large Rural	SM Small Suburb	LM Small Suburb	LM Large Suburb	SM Small City	SM Large City	LM Small City	LM Large City
Small Rural	N/A	3.76	1.28	0.50	0.31	0.94	1.71	0.45	0.94
Large Rural	3.24	N/A	0.67	0.49	0.39	1.21	1.29	0.72	0.67
SM Small Suburb	1.41	0.62	N/A	0.52	0.59	2.78	2.15	0.94	0.78
LM Small Suburb	0.68	0.64	0.73	N/A	2.28	0.69	0.45	1.33	2.08
LM Large Suburb	0.67	0.38	0.55	2.36	N/A	0.65	0.71	2.11	1.89
SM Small City	0.94	1.10	2.50	0.67	0.53	N/A	1.40	0.45	0.72
SM Large City	1.18	1.07	2.33	0.53	0.74	1.19	N/A	0.54	0.87
LM Small City	0.66	0.63	0.94	1.33	1.71	0.47	0.63	N/A	1.51
LM Large City	0.78	0.55	0.46	2.18	2.11	0.70	0.74	1.34	N/A

TABLE 4: Substitution Cost Matrix

	Small Rural	Large Rural	SM Small Suburb	LM Small Suburb	LM Large Suburb	SM Small City	SM Large City	LM Small City	LM Large City
Small Rural	0.00								
Large Rural	0.30	0.00							
SM Small Suburb	0.90	0.60	0.00						
LM Small Suburb	0.90	0.60	0.30	0.00					
LM Large Suburb	1.20	0.90	0.60	0.30	0.00				
SM Small City	1.70	1.40	0.80	1.10	0.80	0.00			
SM Large City	2.00	1.70	1.10	1.40	1.10	0.30	0.00		
LM Small City	2.10	1.80	1.50	1.20	0.90	0.70	0.40	0.00	
LM Large City	2.40	2.10	1.80	1.50	1.20	1.00	0.70	0.30	0.00

TABLES 5a-5h Summaries of Cluster Analysis

TABLE 5a

SAMPLE: Random Age <=25	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "Stable SM Small City"	14	13(6)	0.08	0.88
2 – "Stable SM Small Suburbs"	16	14(3)	0.16	0.83
3 – "Stable LM Small Suburbs"	13	14(4)	0.26	0.81
4 – "Stable Small Rural"	31	12(1)	0.12	1.18
5 – "Stable SM Large City"	14	14(7)	0.24	0.99
6 – "Stable LM Large City"	44	13(9)	0.19	1.19
7 – "Stable LM Large Suburbs"	7	14(5)	0.21	0.80
8 – "Stable Large Rural"	11	14(2)	0.22	1.01
9 – "SM City -> Suburbs"	8	6(6), 7(3)	0.41	0.82
10 – "LM City -> Suburbs"	12	6(9), 5(5)	0.39	0.93
11 – "Stable LM Small City"	6	11(8)	0.29	0.97
12 – "LM Suburbs -> City"	8	1(9), 6(4), 5(9), 2(4)	0.50	1.01
13 – "Rural -> SM City"	4	5(2), 7(6)	0.51	0.96
14 – "Rural -> Suburbs"	7	5(1), 9(4)	0.48	0.92
15 – "SM City -> Rural"	5	6(6), 8(1)	0.52	1.03
OVERALL **	200		**0.24**	**1.02**

** T-Value = 43.98 df=199 p < .001

TABLE 5b

SAMPLE: Random Age 26-35	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "Stable SM Small Suburbs"	21	14(3)	0.10	0.88
2 – "Stable SM Small City"	13	14(6)	0.10	0.92
3 – "Stable Small Rural"	34	14(1)	0.12	1.32
4 – "Stable LM Suburbs"	25	14(4)	0.23	0.89
5 – "Stable LM City"	47	14(9)	0.11	1.25
6 – "Stable Large Rural"	10	14(2)	0.33	1.08
7 – "Stable SM Large City"	18	14(7)	0.16	0.98
8 – "SM Suburbs -> City"	8	1(6), 6(3), 7(6)	0.46	0.95
9 – "SM City -> Suburbs"	7	5(6), 1(7), 1(6), 7(3)	0.42	0.89
10 – "LM City -> Suburbs"	9	6(9), 8(5)	0.37	0.99
11 – "LM Suburbs -> City"	3	1(9), 1(4), 3(5), 9(9)	0.36	1.17
12 – "SM City -> Rural"	3	6(7), 1(6), 7(2)	0.59	1.08
13 – "LM City -> Rural"	2	9(9), 5(1)	0.97	1.12
OVERALL **	200		**0.20**	**1.08**

** T-Value = 43.78 df=199 p < .001

TABLE 5c

SAMPLE: Random Age 36-49	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "Stable Small Rural"	29	14(1)	0.05	1.33
2 – "Stable LM Large City"	52	14(9)	0.06	1.26
3 – "Stable LM Small Suburbs"	17	14(4)	0.09	0.93
4 – "Stable SM Small Suburbs"	26	14(3)	0.15	0.95
5 – "Stable SM Large City"	17	14(7)	0.08	1.07
6 – "Stable SM Small City"	12	14(6)	0.05	0.98
7 – "Stable LM Large Suburbs"	16	14(5)	0.24	0.89
8 – "Stable Large Rural	11	14(2)	0.16	1.12
9 – "Stable LM Small City"	5	14(8)	0.06	1.07
10 – "LM Suburbs -> City"	4	5(4), 9(9)	0.39	1.17
11 – "LM City -> Suburbs"	6	7(9), 7(4)	0.46	1.04
12 – "Suburbs -> Rural"	3	6(5), 8(1)	0.42	1.24
13 – "Rural -> City"	2	7(1), 7(7)	0.96	1.11
OVERALL **	200		**0.13**	**1.12**

** T-Value = 54.24 df=199 p < .001

TABLE 5d

SAMPLE: Random Age 50+	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "Stable SM Small Suburbs"	18	14(3)	0.05	0.85
2 – "Stable SM Small City"	12	14(6)	0.06	0.96
3 – "Stable Small Rural"	46	14(1)	0.06	1.22
4 – "Stable SM Large City"	15	14(7)	0.05	1.07
5 – "Stable LM Large City"	55	14(9)	0.07	1.32
6 – "Stable LM Large Suburbs"	14	14(5)	0.14	0.83
7 – "Stable LM Small Suburbs"	9	14(4)	0.11	0.84
8 – "Stable Large Rural"	9	14(2)	0.06	1.03
9 – "LM City -> Suburbs"	7	6(9), 7(5)	0.28	0.94
10 – "Stable LM Small City"	3	14(8)	0.33	1.12
11 – "Suburbs -> Rural"	2	7(4), 7(1)	0.13	1.04
12 – "LM City -> Rural"	2	7(9), 7(1)	0.23	1.17
13 – "SM City -> Suburbs"	3	1(9), 6(7), 7(4)	0.34	0.85
14 – "Rural -> SM City"	3	6(1), 1(9), 2(4), 1(9), 1(4)	0.58	1.09
15 – "SM Suburbs -> City"	2	10(3), 4(9)	0.56	0.96
OVERALL **	200		**0.10**	**1.11**

** T-Value = 57.03 df=199 p < .001

TABLE 5e

SAMPLE: Transitional Age <=25	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "LM Small Suburbs"	22	2(5), 11(4)	0.21	0.82
2 – "Small Rural"	20	1(2), 13(1)	0.30	1.14
3 – "SM Large City"	27	2(1), 12(7)	0.39	1.00
4 – "LM City"	24	1(3), 13(9)	0.27	1.17
5 – "LM Large Suburbs"	15	3(5), 2(4), 8(5), 1(4)	0.37	0.82
6 – "LM City -> Suburbs"	12	6(9), 7(4)	0.32	0.93
7 – "SM Small Suburbs"	17	2(3), 1(5), 11(3)	0.38	0.88
8 – "City -> Suburbs"	9	1(3), 4(7), 9(5)	0.42	0.87
9 – "LM Suburb -> City"	12	4(4), 8(8)	0.36	1.03
10 – "Large Rural"	8	4(1), 9(2)	0.44	1.01
11 – "SM Small City"	14	2(3), 2(6), 1(3), 7(6)	0.35	0.91
12 – "LM City -> Rural"	4	6(9), 8(1)	0.35	1.15
13 – "Rural -> SM City"	5	5(1), 8(7)	0.45	1.05
14 – "Suburbs -> Rural"	7	1(1), 6(3), 3(1)	0.50	0.97
15 – "Rural -> City -> Rural"	4	4(1), 1(2), 1(1), 1(9), 1(1), 1(9), 1(1)	0.86	1.07
OVERALL **	200		**0.35**	**0.98**

** T-Value = 47.08 df=199 p < .001

TABLE 5f

SAMPLE: Transitional Age 26-35	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "SM City -> Suburbs"	16	3(7), 11(3)	0.29	0.93
2 – "Rural -> Suburbs"	7	7(2), 7(4)	0.47	1.07
3 – "Rural -> SM City"	7	5(1), 9(7)	0.36	1.09
4 – "LM City -> Suburbs"	26	6(9), 8(4)	0.42	0.97
5 – "LM City"	32	1(8), 13(9)	0.33	1.16
6 – "Small Rural"	27	2(2), 12(1)	0.32	1.24
7 – "LM Suburbs"	29	1(5), 13(4)	0.34	0.93
8 – "LM Suburbs -> City"	12	1(9), 1(4), 3(5), 9(9)	0.50	1.12
9 – "LM City -> Rural"	5	8(9), 3(1), 1(7), 1(9)	0.45	1.13
10 – "LM City -> Rural"	10	5(9), 9(2)	0.46	1.07
11 – "SM City"	12	1(6), 6(7), 1(6), 6(7)	0.38	0.97
12 – "SM Suburbs -> City"	12	1(6), 6(3), 7(6)	0.43	0.95
13 – "Rural -> City -> Rural"	2	4(1), 5(9), 3(1), 2(2)	0.54	1.21
14 – "City -> Suburbs -> City"	3	1(5), 3(9), 3(3), 5(7), 2(5)	0.71	1.04
OVERALL **	200		**0.38**	**1.06**

** T-Value = 52.40 df=199 p < .001

TABLE 5g

SAMPLE: Transitional Age 36-49	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "LM City -> Suburb"	19	6(9), 8(5)	0.36	0.92
2 – "Rural"	32	5(1), 1(2), 8(1)	0.25	1.19
3 – "LM Large City"	26	13(9), 1(4)	0.29	1.21
4 – "LM Small Suburbs"	19	13(4), 1(3)	0.31	0.82
5 – "Suburbs -> Rural"	12	9(4), 5(1)	0.39	0.96
6 – "SM City"	19	3(6), 10(7)	0.37	0.99
7 – "SM City -> Suburbs"	12	6(7), 8(3)	0.36	0.88
8 – "LM City -> Rural"	8	5(9), 9(1)	0.60	1.04
9 – "LM Large Suburbs"	14	8(5), 1(4), 5(5)	0.34	0.81
10 – "SM Small Suburbs"	7	1(2), 13(3)	0.24	0.88
11 – "LM Small City"	10	1(4), 13(8)	0.21	1.05
12 – "SM Suburbs -> City"	11	6(3), 7(6)	0.44	0.95
13 – "LM Suburbs -> City"	6	9(5), 5(8)	0.35	0.91
14 – "SM City -> Rural"	5	6(6), 8(2)	0.38	0.90
OVERALL **	200		**0.33**	**1.00**

** T-Value = 44.27 df=199 p < .001

TABLE 5h

SAMPLE: Transitional Age 50+	N	Typical Sequence	Average Within Cluster Distance	Average Between Cluster Distance
Cluster				
1 – "LM City -> Suburb"	25	6(9), 8(5)	0.33	1.05
2 – "SM Small Suburbs"	19	1(6), 13(3)	0.40	0.88
3 – "Suburbs -> Rural"	13	7(4), 7(1)	0.30	0.97
4 – "Rural"	29	8(1), 2(2)	0.32	1.06
5 – "SM City"	28	13(6), 1(7)	0.37	1.04
6 – "LM Small Suburbs"	21	5(4), 1(5), 8(4)	0.33	0.83
7 – "LM City -> Rural"	4	3(9), 11(1)	0.14	1.12
8 – "LM City"	30	13(9), 1(8)	0.48	1.23
9 – "LM Suburbs -> City"	11	5(4), 9(9)	0.38	1.12
10 – "LM Large Suburbs"	18	1(4), 13(5)	0.27	0.83
11 – "SM City -> Rural"	12	7(7), 7(1)	0.40	1.10
12 – "SM City -> Suburbs"	14	6(6), 8(3)	0.47	0.94
13 – "Rural -> Suburbs"	7	7(1), 7(5)	0.30	1.01
14 – "SM Suburbs -> City"	8	10(3), 4(7)	0.49	0.93
15 – "Rural -> City"	11	8(1), 6(7)	0.50	1.14
OVERALL **	250		**0.37**	**1.02**

** T-Value = 62.37 df=249 p < .001

TABLE 6: Population of Residential Trajectories

ID	Residential Trajectory	Typical Sequence	Example in Washington
1	Stable Small Rural	13(1)	Omak
2	Stable Large Rural	13(2)	Walla Walla
3	Stable SM Small Suburbs	13(3)	Cheney
4	Stable LM Small Suburbs	13(4)	Sumner
5	Stable LM Large Suburbs	13(5)	Renton
6	Stable SM Small City	13(6)	Yakima
7	Stable SM Large City	13(7)	Spokane
8	Stable LM Small City	13(8)	Everett
9	Stable LM Large City	13(9)	Seattle
10	SM City -> SM Suburb	6(6), 7(3)	Yakima -> Selah
11	LM City -> LM Suburb	7(9), 6(4)	Seattle -> Woodinville
12	SM City -> Rural	6(6), 7(1)	Richland -> Dayton
13	LM City -> Rural (long city)	9(9), 4(1)	Seattle -> Roslyn
14	Suburb -> Rural	6(4), 7(1)	Puyallup -> Mossyrock
15	SM Suburb -> SM City	6(3), 7(6)	Prosser -> Kennewick
16	LM Suburb -> LM City	5(4), 8(9)	Bothell -> Seattle
18	Rural -> LM City	6(1), 7(9)	George -> Seattle
19	Rural -> LM Suburb	6(1), 7(4)	Onalaska -> Yelm
20	LM City -> Rural (long rural)	4(9), 9(1)	Seattle -> Sequim
21	Rural -> SM City	5(1), 8(7)	Colville -> Spokane
22	Rural/City/Rural	5(1), 4(9), 4(1)	Anacortes -> Seattle -> Sequim
24	Suburb/City/Suburb	4(4), 3(9), 6(4)	Buckley -> Seattle -> Puyallup
25	SM City -> LM Suburb	6(7), 7(5)	Tacoma -> Federal Way
26	LM City/Suburb/LM City	4(9), 4(5), 5(9)	Seattle -> Renton -> Seattle
27	SM City/Suburb/SM City	4(7), 4(3), 5(7)	Spokane -> Mead -> Spokane

TABLE 7: Summary of Residential Trajectories

Residential Trajectory	% of overall sample (unweighted)	Average Distance to Typical Sequence	% with 2+ shifts in place-type	Average Number of Moves [a]	Number of Changes in Place or County
STABLE TRAJECTORIES					
Stable Small Rural	15.5%	.056	10.8%	1.81	0.78
Stable Large Rural	4.5%	.070	20.8%	1.96	0.79
Stable SM Small Suburbs	7.6%	.061	10.5%	1.29	0.64
Stable LM Small Suburbs	6.9%	.076	18.5%	1.69	1.21
Stable LM Large Suburbs	5.1%	.093	23.8%	1.89	1.36
Stable SM Small City	5.9%	.067	13.3%	2.01	0.53
Stable SM Large City	8.4%	.067	12.2%	2.13	0.49
Stable LM Small City	1.8%	.083	21.6%	2.07	0.81
Stable LM Large City	22.3%	.061	8.3%	2.35	0.37
NON-STABLE TRAJECTORIES					
SM City -> SM Suburb	2.3%	.287	53.6%	3.48	2.28
LM City -> LM Suburb	3.2%	.274	41.6%	2.99	1.99
SM City -> Rural	0.7%	.289	63.4%	3.57	2.59
LM City -> Rural (long city)	0.4%	.286	52.2%	4.40	2.57
Suburb -> Rural	1.9%	.304	60.4%	3.36	2.67
SM Suburb -> SM City	1.7%	.282	59.3%	3.62	2.66
LM Suburb -> LM City	1.6%	.299	58.1%	3.65	2.43
Rural -> LM City	0.3%	.253	52.6%	3.85	1.95
Rural -> LM Suburb	1.2%	.304	60.6%	3.81	2.80
LM City -> Rural (long rural)	0.6%	.302	54.3%	3.21	2.14
Rural -> SM City	0.9%	.296	50.0%	3.91	2.54
Rural/City/Rural	0.1%	.337	100.0%	5.63	3.71
Suburb/City/Suburb	0.7%	.322	100.0%	4.09	3.64
SM City -> LM Suburb	1.4%	.321	50.6%	3.28	2.40
LM City/Suburb/LM City	0.9%	.333	100.0%	4.39	3.06
SM City/Suburb/SM City	0.5%	.316	100.0%	5.12	3.35
NON-PATTERNED TRAJECTORY	3.6%	.577	84.8%	5.01	3.97
Overall	100.0%	.127	23.9%	2.38	1.13

a – standardized to reflect average number of moves over a residential sequence of 13 time periods

TABLE 8: Distribution of Residential Trajectories by AGE

Combined Trajectory	IDS	<=25	26-35	36-49	50+	Overall
N of Cases with weight > 0		2053	886	1217	1032	5188
Weighted N of Cases **		46,890	19,097	27,091	27,628	120,706
Stable Rural	1,2	17.8%	19.8%	19.9%	29.6%	21.3%
% of stable		**28.1%**	**26.6%**	**23.6%**	**34.3%**	**28.4%**
Stable Suburb	3,4,5	19.6%	24.5%	32.8%	24.3%	24.4%
% of stable		**31.0%**	**33.0%**	**38.9%**	**28.2%**	**32.5%**
Stable Small City	6,7	13.2%	14.1%	17.3%	18.0%	15.4%
% of stable		**20.9%**	**19.0%**	**20.5%**	**20.9%**	**20.5%**
Stable Large City	8,9	12.7%	15.9%	14.4%	14.4%	14.0%
% of stable		**20.0%**	**21.4%**	**17.1%**	**16.7%**	**18.6%**
TOTAL STABLE		63.3%	74.3%	84.4%	86.3%	75.1%
City -> Suburbs (% of overall)	10,11,25	11.6%	8.8%	4.2%	4.4%	7.8%
% of non-stable		**38.4%**	**37.9%**	**33.9%**	**38.9%**	**37.9%**
City -> Rural (% of overall)	12,13,20	2.6%	2.7%	1.1%	1.6%	2.0%
% of non-stable		**8.6%**	**11.6%**	**8.9%**	**14.2%**	**9.7%**
Suburb -> City (% of overall)	15,16	5.6%	4.2%	1.9%	1.5%	3.6%
% of non-stable		**18.5%**	**18.1%**	**15.3%**	**13.3%**	**17.4%**
Suburb -> Rural (% of overall)	14	2.5%	2.0%	3.0%	1.9%	2.4%
% of non-stable		**8.3%**	**8.6%**	**24.2%**	**16.8%**	**11.6%**
Rural -> City (% of overall)	18,21	2.4%	1.4%	0.4%	0.4%	1.3%
% of non-stable		**8.0%**	**6.0%**	**3.2%**	**3.5%**	**6.3%**
Rural -> Suburb (% of overall)	19	1.6%	1.4%	0.8%	0.9%	1.2%
% of non-stable		**5.3%**	**6.0%**	**6.5%**	**8.0%**	**5.8%**
R-S/CC/R-S (% of overall)	22,24	1.8%	1.1%	0.0%	0.2%	0.9%
% of non-stable		**6.0%**	**4.7%**	**0.0%**	**1.8%**	**4.3%**
CC/Suburb/CC (% of overall)	26,27	2.2%	1.4%	1.1%	0.4%	1.4%
% of non-stable		**7.3%**	**6.0%**	**8.9%**	**3.5%**	**6.8%**
TOTAL NON-STABLE		30.2%	23.2%	12.4%	11.3%	20.7%
NON-PATTERNED TRAJECTORY		6.5%	2.5%	3.2%	2.4%	4.2%

** Data Weighted by Individual Weights in final year of sequence

Appendix A: Identifying "Typical" Sequences

Cluster 1 (Small Metropolitan City -> Suburb) n=5

Sequences

S1:	6 6 6 6 6 6 3 3 3 3 3 3
S2:	6 6 6 6 6 6 6 5 5 5 5 5 5
S3:	7 7 7 7 7 5 5 5 5 5 5 5 5 5
S4:	1 6 6 6 6 6 6 3 3 3 3 3 3
S5:	6 6 6 6 6 6 3 3 3 3 3 3

Symmetric Distance Matrix

	S1	S2	S3	S4	S5
S1	--	0.392	0.517	0.142	0.040
S2	0.392	--	0.208	0.350	0.404
S3	0.517	0.208	--	0.556	0.529
S4	0.142	0.350	0.556	--	0.104
S5	0.040	0.404	0.529	0.104	--
Avg within-cluster Distance	**0.273**	**0.339**	**0.452**	**0.289**	**0.269**

Typical Sequence – S5   **6 6 6 6 6 6 3 3 3 3 3 3**

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