

Identifying Gendered Patterns in Family Formation Trajectories among Immigrants

Abstract

Gender is one of the strongest stratification variable in contemporary societies. Hence, the way in which migration and family dynamics are associated, is necessarily affected by the gendered nature of the migration experience itself. Using retrospective data from the Mexican Migration Project and the Latin American Migration Project, I reconstruct full sequences of marital and birth histories for men and women with and without migration experience. Sequence analysis and cluster analysis techniques allow me to uncover typologies of family formation and dissolution. These typologies differ by gender, country of origin and migration status. Based on a holistic description of these typologies this paper highlights the interaction between migration and gender in shaping family outcomes. This interaction is highly dependent on the conditions at the moment of migration which support the hypothesis of migration as a disruptive event in particular for women's trajectories.

Key words: *life-course perspective, fertility, sequence analysis, migration.*

1 Introduction

International migration is topical in contemporary social sciences (Özden et al. 2011, Castles & Miller 2014). The causes and consequences of contemporary migration flows

are new, in the sense that they differ from those associated to historical migration flows (slavery, colonization, shortage of labor force) (Garcia & Le Bras 2017). Even if we were to argue that the movement of people from one place to another has accompanied human civilization since long time ago, it is the particularities of nation-states economic and political relationships, the particular forces driving migration flows and the consequences of them, what makes contemporary migration topical.

How will the family—a central institution for modern societies—be affected by this phenomena is a pressing question for family demographers and sociologists. The question is in fact a threefold question depending on the place we raise it: from the perspective of the sending country, from the perspective of the receiving country or from both. How will family systems in contemporary receiving countries be affected by the arrival of migrants? How will family systems adjust to the increasing number of emigrants—in sending countries? How will both family systems—in the country of origin and in the country of reception—accommodate to the emergence transnational links? (Portes 2001). Studies on migration and studies on the family are numerous, however there are three focuses typically unexplored when it comes to understand family formation and dissolution dynamics among immigrants. This study aims to explore these aspects.

First, family formation studies among immigrants typically focus on women (Fargues 2011, Lindstrom & Saucedo 2002, Glick et al. 1997, Davis 2011, Parrado 2011, Castro-Martin & Rosero-Bixby 2011, Parrado & Flippen 2012); or when they include the men, their experiences are analyzed separately. However, there are at least two reasons to consider a joint study of family-related outcomes: (1) sex or, more generally gender, has been one of the strongest stratification conditions of modern and contemporary societies. From differences in sex ratios at birth to more 'socially determined' outcomes such labor-market inequalities or life expectancy at birth, difference in social outcomes between these two groups are pervasive (Héritier 1996). (2) at least during the last two centuries, the most prevalent family form has been associated to childbearing within a legal form that recognizes the union of a couple, e.g. marriage (Aries 1962). For these two reasons, family formation studies ought to be conducted with gender lens.

The second aspect, often neglected by classic demographic studies, is the fact that demographic events occur and change in close conjunction. Mortality and fertility interplay is perhaps the best example of the interaction between demographic phenomena. Even for this well-known association, it is no uncommon to forget how relevant changes in mortality were for fertility transitions all over the world (Mason 1997). A similar assessment can be done when it comes to study family and migration. Only until recently, scholar have

begun to jointly study these phenomena (Castro-Martin & Rosero-Bixby 2011, Parrado 2015, Kulu & Hannemann 2016).

Third, migration studies are typically conducted from the perspective of the country of reception, a perspective that I termed immigration perspective, i.e. migration studies that rely on information (about migrants) collected in the country of reception. Currently, countries where demographic surveys are available to study family dynamics are typically countries with positive migration balances, in short, receiving countries (Organization of American States 2011, Castles & Miller 2014). Instead, sending countries have less data, in particular they lack of longitudinal studies. In the case of Latin America, there are exceptions for this general statement such as the case of Mexico, Brazil or Chile, where data infrastructure is better developed compared to other countries in the region; yet only the Central American country has rich information on migrants. This situation prevent scholars from conducting comparative research from the perspective of the sending country, i.e. from a emigration perspective.

Over three past decades, demographers and sociologists have begun to assemble data on migrants from a transnational perspective. The Mexican Migration Project (MMP), the Latin American Migration Project (LAMP), and the The Migrations between Africa and Europe Project (MAFE) are examples of these attempts. These efforts have uncover interesting dynamics for which other type of sources are blinded. As of today, it has become clear that the so-called immigration perspective is not sufficient to understand the migration experience and its associations with other demographic outcomes.

This study builds on such efforts in order to provide a holistic description of family formation and dissolution life-paths for Latin American men and women who either migrated to the US or pertain to a household in which at least one member migrated. I pooled the data from the MMP and the LAMP to cover eight countries and over twenty-thousand life-histories of men and women. Using retrospective information on childbearing and marital status I identified differences and similarities between the typical trajectories of family formation and dissolution of men and women, with and without migration experience. These comparison highlights: (1) the gendered nature of the migration experience, (2) the strong influence of migration in shaping the calendar of family formation events, and its difference by sex and (3) the importance background conditions proxied by the country of origin.

2 Previous studies and theoretical background

Studying fertility and family-related outcomes among immigrant populations possess important methodological and conceptual challenges (Kulu 2005, Kulu & Milewski 2007, Kulu & Hannemann 2016). In terms of measurement, for example, even for a well-known measure of fertility such as the Total Fertility Rate, it is not clear how to determine the contribution of migrants to the fertility of the country of reception. A simple—and widespread—solution is to only count the births that occurred after arrival, yet this approach often lead to overestimate the TFR of migrants for two reasons: (1) fertility rates before migration are typical low and they pick after migration regardless of the age at migration, (2) migrants arrive at different ages. Combined, these two conditions produce particularly inflated age-specific fertility rates, and consequently overestimates for the TFR (Parrado 2011). Focusing on complete fertility rates or computing fertility index that account for the time since migration are suitable ways to get an accurate estimate of the actual fertility level among migrants (Toulemon & Mazuy 2004, Laurent Toulemon & Mazuy 2004). This situation is not specific to fertility measures. In general, every outcome that is measured among immigrant populations is likely to suffer of this bias if the event at stage is correlated with the migration experience.

Conceptually, the definition of who is a migrant has created numerous debates. While using data in the context of reception the identification of different types of migrants can be done using information on the year of arrival and the country of birth. Two fundamental variables can be constructed: age at migration and time since migration. These two variable permit to distinguish the so-called 1.5-generation, i.e. people who migrated before age fifteen, from people who migrated after this age (first migrant generation). Along with the parents' country of birth this variable permit to separate people in terms of the context in which they experienced primary socialization: 1st-generation, people who experienced primary socialization in the country of origin (less exposure to the cultural norms and social institution of the country of reception), 2nd-generation, people that were born in the country of reception of the 1st-generation ('full' exposure to cultural norm and social institutions of the host society) and the 1.5-generation, located in between these two groups (Pailhé 2015).

Using the same information migrants can be classified as recent migrants (those who arrived less than five year ago), or old migrants (those with five or more years of residence in the country of reception). These two distinctions are crucial to appropriately understand demographic related outcomes as they are closely related with the amount

of exposure migrants have experienced in a given moment. However, the immigration perspective—while informative and necessary—need to be complemented as by definition it misses an important part of the migrant population. First, data collected in the host country does not include those migrants who returned to their country of origin. Second it does not account for those 'migrants to be', i.e. people who did not migrate but that could potentially influence family-related decisions among migrants. These two sets of people can only be observed in transnational data collections such as the MMP and LAMP.

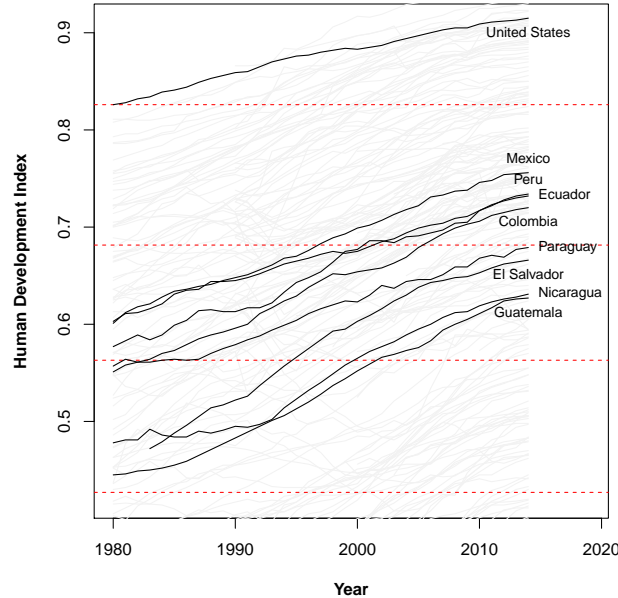
Moreover, conceptual problems on how to identify migrants or when to count events for demographic calculation among this population can be overcome by having a life-course approach to family dynamics. Within a life-course approach family and fertility related outcomes are understood not as events, but as sequences of cumulative occurrences within individuals' lives (Ryder 1965). For these reasons, this study focuses on cohorts that have already passed their reproductive period (above age 40). This restriction has pros and cons. As for the first, focusing on cohort permits the implementation of a fully life-course approach as all the reproductive period of individual is observed and included in the analysis. As for the cons, sample sizes are smaller and results correspond to relatively old cohorts, i.e. results can not speak to current trends on family formation and dissolution among recent cohorts.

2.1 The Latin American case

Figure 1 displays country-specific trends in the Human Development Index across nine countries in the Americas. Cross-national differences in development levels between the US and Latin American sending countries—in particular those included in this work—are large. Along with cultural differences across these nations, differences in human and economic development posit Latin America and the US as very different contexts for family formation. Not surprisingly, family-related outcomes differ substantially among the non-migrant populations of Latin American countries and the US. All in all, these samples of countries offer sufficient heterogeneous context to test hypotheses on how initial differences in macro-level conditions may or may not influence patterns of family formation. It is expected that the more similar the countries in terms of their stage of development, the more similar the patterns of family formation will look like.

Besides the high heterogeneity among these eight countries in terms of development, they also differ substantially in their migration history to the US, migration rates over the last four decades and the stock of migrants currently living in the US. Figure 2 presents

Figure 1: Trends in Human Development for eight Latin American countries and the US, 1980 to 2015



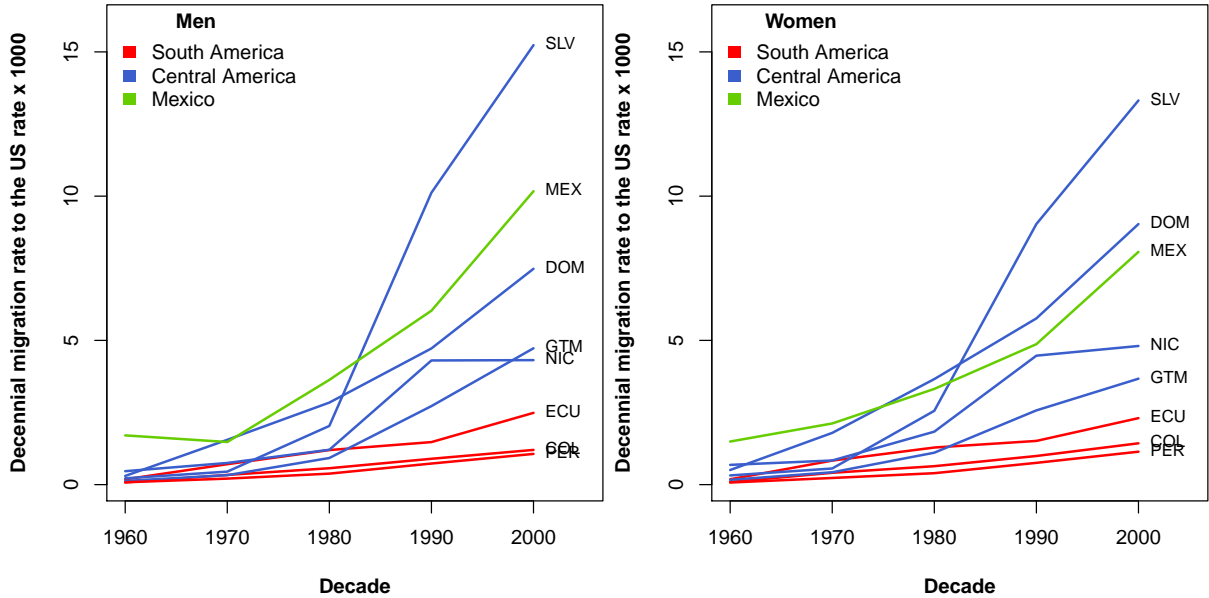
estimates of out-migration rates by country of origin and sex since 1960 to 2010.

From rapidly raising migration rates in El Salvador to relatively stable and low rates for Peru and Colombia, the second half of the twenty century witnessed a sharp increased in migration flows for men and women (Organization of American States 2011). These migration rates along with the changing dynamics of US migratory regulations translated into different stock of migrants for each country, ranging from around 500 thousand Nicaraguan nationals, to 9.5 million Mexican nationals living in the United States by 2000 (Massey et al. 2014). The total population of Latin American immigrants from these eight countries living in the US is estimated in 15.3 million in 2010. If we added returned migrants, we can think of this as a sizable population for which family trajectories ought to be described and understood.

3 Data

Together the Mexican Migration Project (MMP) and the Latin American Migration Project (LAMP) cover twelve countries of Central and South America: Mexico, Colombia, *Costa Rica*, Dominican Republic, Ecuador, El Salvador, Guatemala, *Haiti*, Nicaragua, Paraguay, Peru y *Puerto Rico*. These two project have been collecting transnational information since 1982 and 1998 respectively. They shared fundamental methodological

Figure 2: Out-migration rates to the US for eight Latin American countries, 1960-2000



Note: author's calculations based on Global Bilateral Migration Database (2011) and UN population prospects (2015)

and theoretical grounds for which information across countries is highly comparable. I focus on eight countries—excluding those with italics—to keep comparability with a parallel research effort on domestic migration in these eight Latin American countries.

Using the retrospective information from people in these eight sample I reconstruct the sequence of family-related events, namely, births, unions, marriages, separations and divorces from ages 15 to 39. In order to have complete trajectories I restrict the analysis to men and women above age 39. Table 1 displays the total number of men and women for which birth histories are available. Given the design of the MMP and LAMP, birth histories are only collected for the head of the households.

Using retrospective information on births and marital status, I reconstruct the sequence of family-related events for each of these individual from age 15 to 39. There are twenty possible states that results from the interaction of four parity levels (0, 1, 2, 3+) and five marital status categories (single, cohabiting, married, separated/divorced, remarried). I used five different colors to distinguish marital status and different intensities to differentiate parity levels. Figure 3 display ten randomly selected sequences of the women data set.

Table 1: Total sample size by birth cohort and region of birth for women (top panel) and men (bottom panel) from the MMP and the LAMP

<i>Women</i>						
	Birth cohort					
Region	30-40	40-50	50-60	60-70	70-80	Total
Mexico	661	692	557	263	50	2223
Central America	157	190	257	94	0	698
South America	188	266	339	326	72	1191
Total	1006	1148	1153	683	122	4112

<i>Men</i>						
Region	30-40	40-50	50-60	60-70	70-80	Total
Mexico	2642	3795	3655	1995	442	12529
Central America	276	399	663	278	0	1616
South America	326	535	695	623	163	2342
Total	3244	4729	5013	2896	605	16487

4 Methods

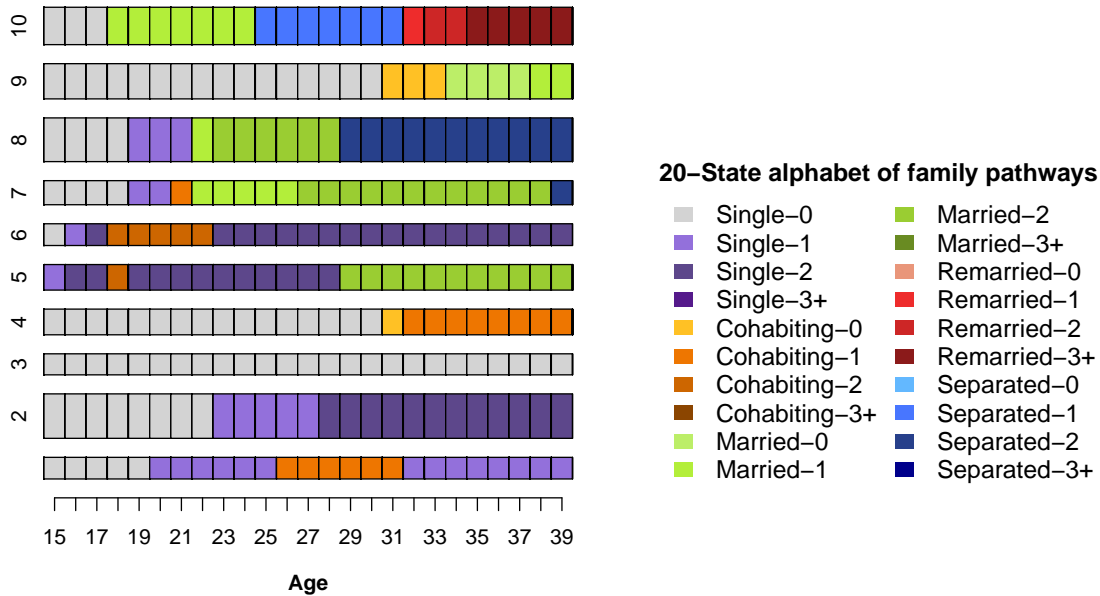
This paper uses two statistical techniques: (1) sequence analysis (SA), hierarchical cluster analysis (CA). SA techniques are used to measure dissimilarity levels across individual trajectories of family formation. Hierarchical cluster techniques are used to identify typical trajectories of family formation and dissolution.

4.1 Sequence Analysis

To compare sequence of categorical states (e.g. single, married, divorced) it is necessary to measure the dissimilarity between pairs of sequences. A measure based on the comparison of sequences' features is typically used to assess between-sequences proximity/similarity. As complex objects, sequences can be compared in several dimensions. In the social sciences, there are at least five aspects in which sequences can be compared: (1) experienced states (including features to account for the relative proximity between states), (2) distribution of the states, (3) timing of events, (4) duration of states and (5) sequencing (Studer & Ritschard 2016). There is not distance measure that can account for all the dimensions simultaneously. Typically, distance measures neglect one aspect when fully account for another. Researchers need to select one approach based on the research question of interest.

Perhaps because of the relatively recent application of SA to sociological research, there

Figure 3: Ten randomly selectec sequence of family formation/dissolution events and labes for the twenty states of the sequences



are both skepticism on its usefulness (Wu 2000) and optimism on its future development and potential contributions (Abbot & Tsay 2000, Aisenbrey & Fasang 2010, Fasang & Liao 2014, Aisenbrey & Fasang 2017). Most of the criticism against SA have been focused on the use of Optimal Matching (OM) to construct distance measures. Classic OM techniques do not account for four out of five socially meaningful aspects in which sequence can be compared. Moreover, OM requires the definition of substitution-, deletion- and insertion-costs (often termed as edit-operation costs), which do not have a meaningful sociological interpretation by themselves (Elzinga & Studer 2015). Despite these critiques, most of the initial studies that used SA relied on OM to measure dissimilarity among sequences. In response to these critiques, recent studies have developed alternative ways for computing distance measures that are more sensitive to the five aspects and do not depend on edit operations (see Studer & Ritschard (2014) for an overview of distance measures). These studies have provided three important improvements.

First, alternative OM-based distance measures have been proposed to better account for the timing of events by using age-specific information (Lesnard 2010). Coined as *dynamic Hamming matching* (HAM), this particular OM variant is highly sensitive to the timing of the event as the edit-operation costs are based on age-specific transition matrices. This variant is particularly appealing to study family formation events as the

timing of events is a crucial—not unique—feature of family dynamics.

Second, recent studies have introduced a sub-sequence-based distance measure that incorporates: differences in the sequencing of the events (i.e. the order in which events take place over the life-course), the timing and the duration of the events (i.e. when do events take place and how long do individual remain in a given state), and the potential proximity between states (i.e. the fact that some states can be similar to others). The general approach proposed by these authors is called Sub-sequence Vector Representation (SVR) (Elzinga & Studer 2015). SVR measures are more sensitive to the ordering of the events than to their timing.

Third, these studies have conducted simulations to assess the sensitivity of different distance measures to the above mentioned five aspects. Results from these studies show the high level of flexibility of both OM-based (including HAM) and SVR approaches with respect to alternative distance measures (Studer & Ritschard 2016). Yet, the criticism against OM on the lack of sociological sense of edit-operation costs remains.

As an emerging/alternative technique SA requires some validation before their results can be fully considered as evidence of social dynamics with some explanatory power. Concerns about the validity of SA arise from the fact that the researcher has to select a metric and the parameters associated to it. Even though simulation studies have shown that clustering algorithms are robust to the selection of the metric, this selection could seem rather arbitrary (Robette & Bry 2012).

Given the nature of the sequences considered in this study I will use the Dynamic Hamming Distance as it is particularly sensitivity to two aspects of sequences: (1) the timing of events and (2) the strong age-specific patterns of the demographic phenomena included in the sequence.

4.2 Cluster analysis

Clusters will be identified using agglomerative hierarchical clustering (HC) implemented in the R package `WeightedCluster` (Studer 2013)³. I preferred this technique over non-hierarchical clustering for three reasons. First, hierarchical clustering does not require the specification of the number of groups, i.e. the researcher can select the number of groups based on the clustering structure of the data. Second, hierarchical clustering permits the construction of classifications threes which allows me to compare the clustering structure across sub-populations (native-born vs foreign-born). Third, hierarchical clustering is more stable than non-hierarchical clustering as it does not depend on initial conditions.

³Specifically I used the function `hclust` using Ward's methods

I will use the *pseudo* - R^2 to measure the proportion of the discrepancy explained by the clusters as a measure for the goodness of the clustering (Studer et al. 2011). The marginal increase of this quantity serves to set a cutoff point in the selection of the numbers of groups to analyze. Given that the SVR metric includes more features than the HAM metric, it is expected that the *pseudo* - R^2 for clusters based on the SVR metric would be lower than the *pseudo* - R^2 for clusters based on the HAM.

5 Preliminary results

This section is based on the visual inspection of two descriptive graphs elaborated for the sequences of family formation/dissolution by sex, region and migration status. The two graphs are: (1) a frequency plot showing the most representative sequences within each group, (2) a modal state graphs showing the most prevalent state at all ages. These descriptive figures indicate that there are important differences across regions, between men and women and by migration status. However, a cluster analysis ought to be conducted before we can actually talk about typical trajectories. For now, these conclusions are speculative.

5.1 Typical trajectories of family formation and dissolution

Figures 5 and 4 display the frequency plots for men and women respectively, without (0) and with (1) migration experience for two regions and Mexico. A visual inspection of these plots suggests:

1. Trajectories of family formation and dissolution among women are more heterogeneous compared to the trajectories of men, at least in terms of the events that are present in the sequences.
2. For both men and women without migration experience a typical trajectory of childlessness and no marital union is observed (light gray color from the beginning to the end of the observation period). This typical trajectory does not appear among men and women with migration experience.
3. There are important levels of regional variation in the two patterns described above. For instance, cohabitation is more prevalent in Central America, while marriages seems to be more stable in Mexico.

Figure 4: Frequency plot for the family formation/dissolution sequences for women with (1) and without (0) migration experience

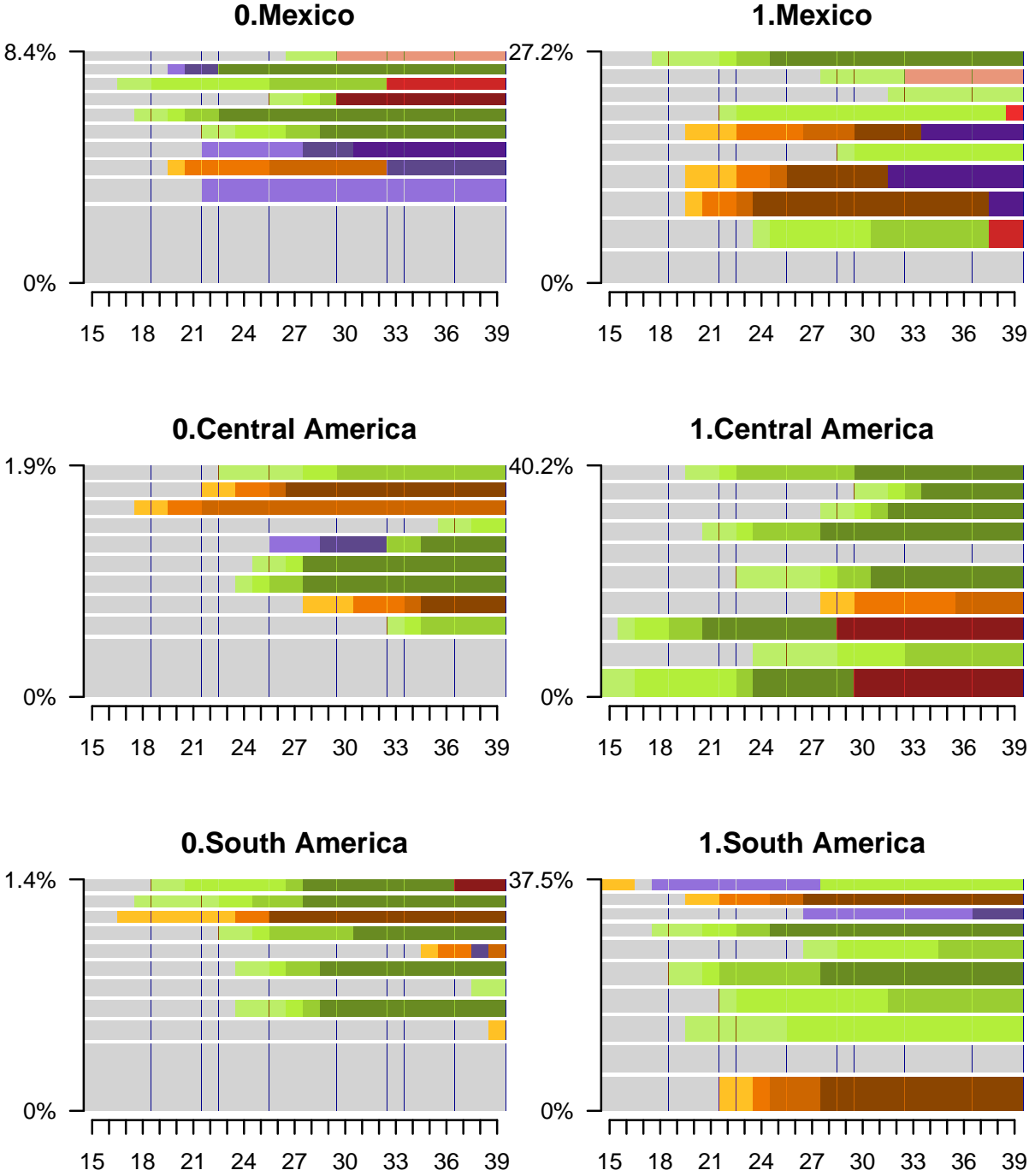
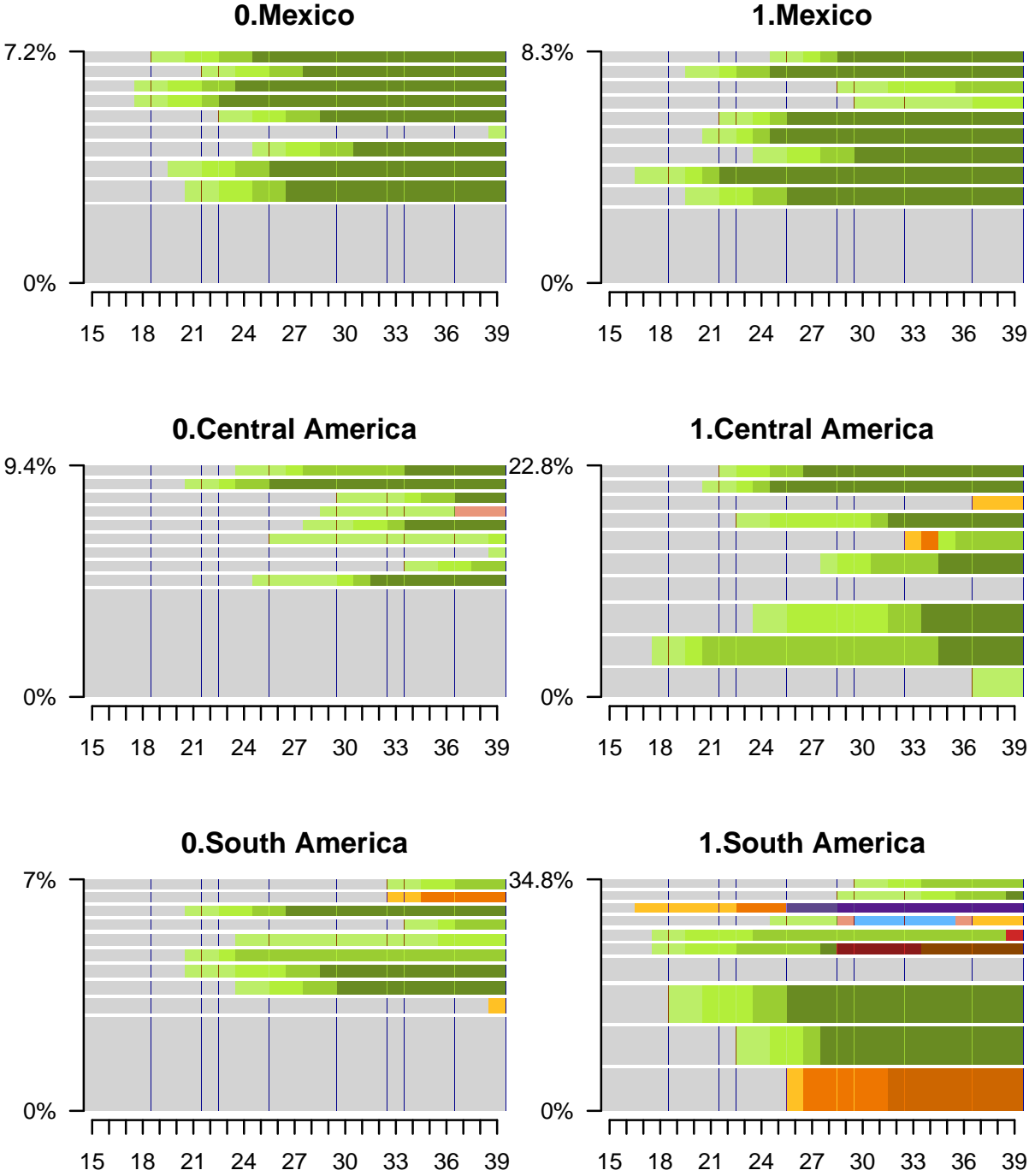


Figure 5: Frequency plot for the family formation/dissolution sequences for men with (1) and without (0) migration experience



5.2 *The disruptive potential of the migration experience*

Figures 7 and 6 display the modal state plots for men and women respectively, without (0) and with (1) migration experience for two regions and Mexico. A visual inspection of these plots suggests:

1. Among women with migration experience the area covered by the light gray (single without children) is bigger than among women without migration experience. This suggests that the migration experience can potentially delay transition to family formation. A similar pattern is observed among men. Yet, a strong difference appears among women from South American countries. For this last group, the modal state between 27 and 33 years is married with one kid, for which the migration experience can also be associated with the delay of the transitions to high parity levels.
2. There are important levels of regional variation in the shapes of the curves of the single without children state, i.e. in the patterns of transition to family formation. Also, modal states differ by region and sex, which indicates the plausibility of more detailed analysis.

6 Further steps

1. Define an appropriate strategy to compare the sequences of family formation and dissolution (Studer & Ritschard 2016)
2. Implement this strategy and test the extent to which the comparison of sequences is robust to the selection of different metrics and clustering strategies.
3. Perform a clusters analysis to identify typical trajectories of family formation and dissolution among men and women, by country (region of origin) and migration status.
4. Describe and compare these patterns in terms of the events experienced over the life-course, the ordering of such events, their timing and the evolution of heterogeneity over age.
5. Correlate these typologies of family trajectories with three types of variables: family background, typical SES variables and conditions at the moment of migrations in order to test the *socialization*, *adaptation* and *disruptive-nature* hypotheses respectively.

Figure 6: Modal states for the family formation/dissolution sequences for women with (1) and without (0) migration experience

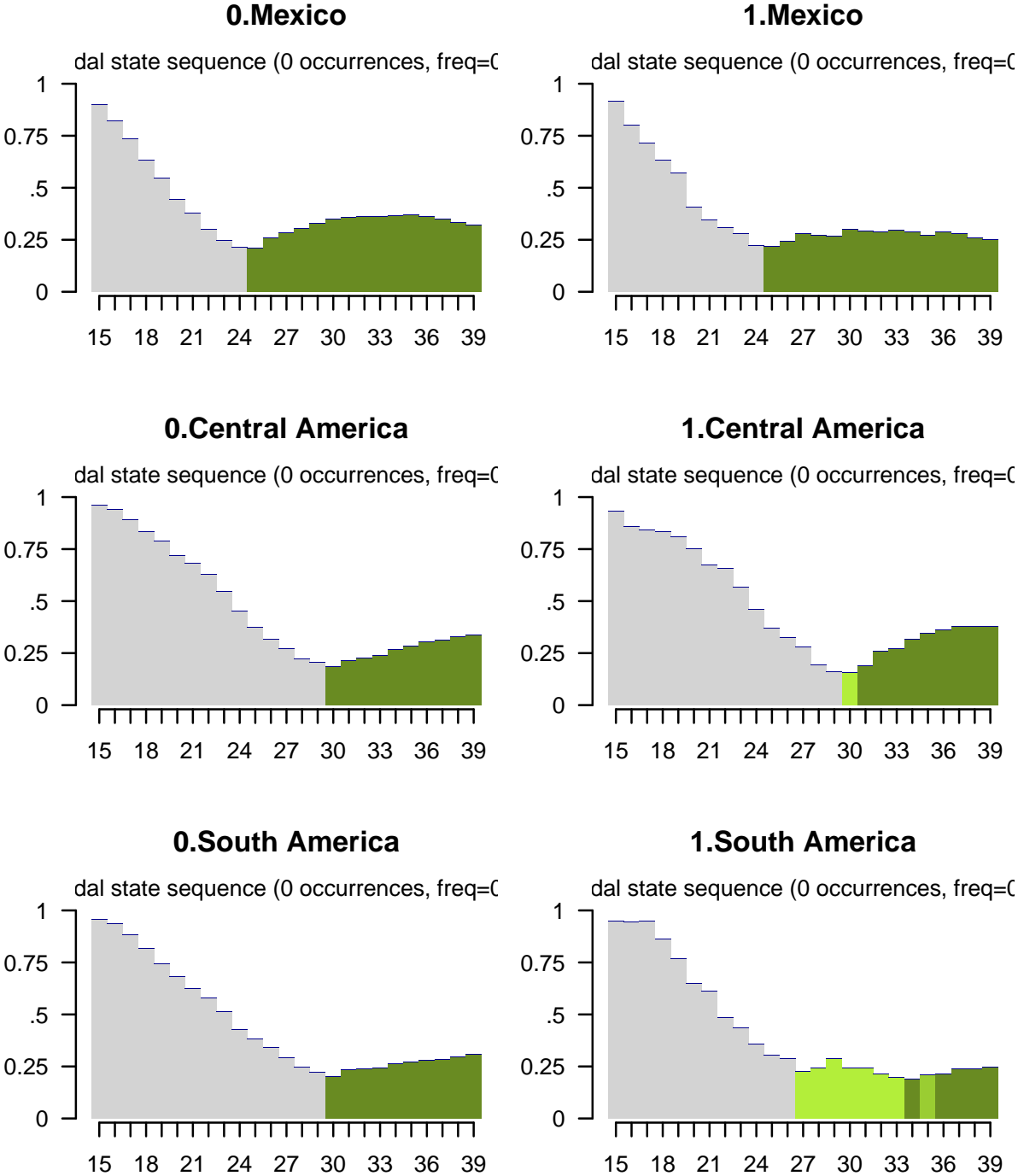
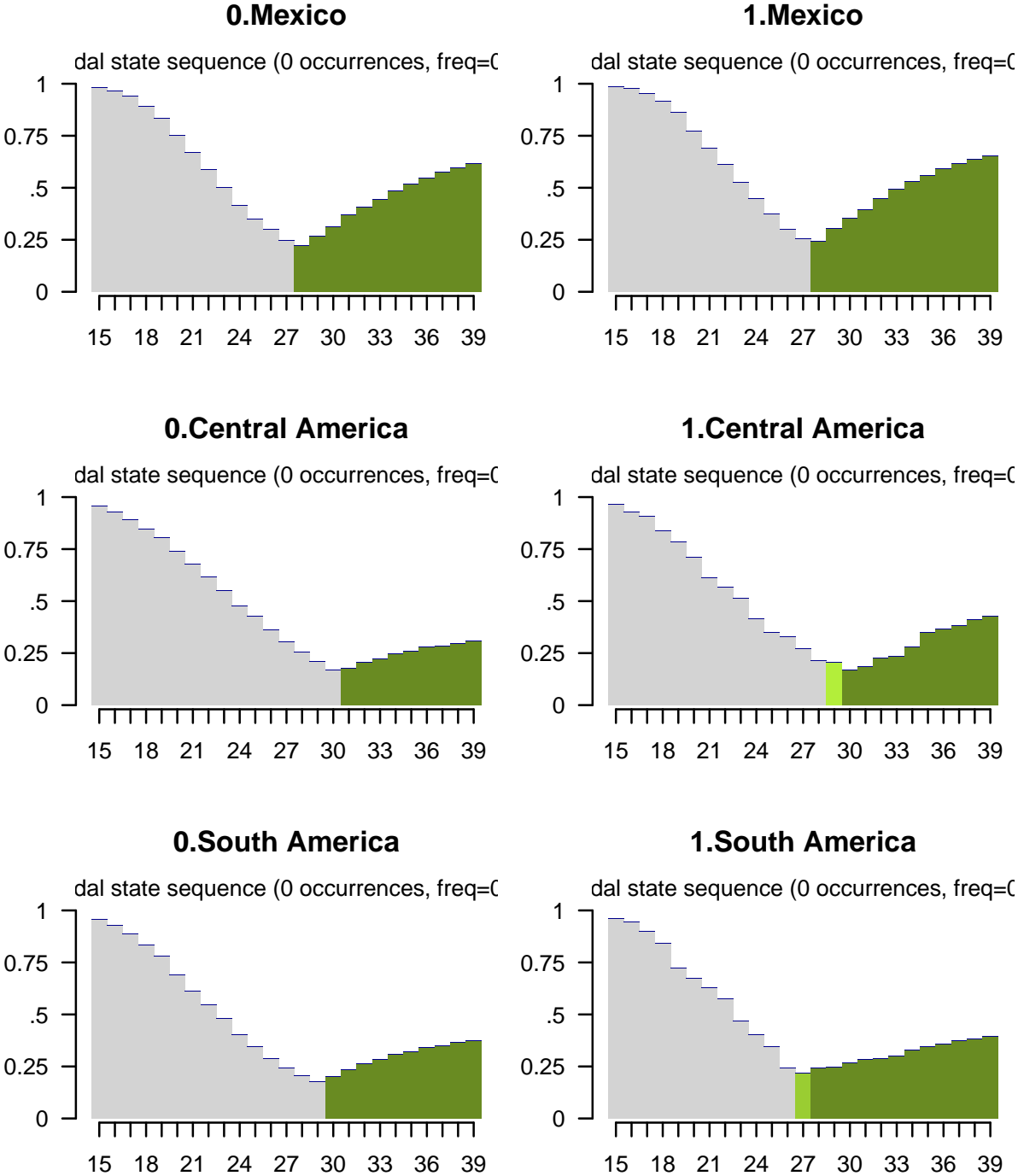


Figure 7: Modal states for the family formation/dissolution sequences for men with (1) and without (0) migration experience



References

- Abbot, A. & Tsay, A. (2000), 'Sequence Analysis and Optimal Matching Methods in Sociology', *Sociological Methods & Research* **29**(1), 3–33.
- Aisenbrey, S. & Fasang, A. (2017), 'The Interplay of Work and Family Trajectories over the Life Course : Germany and the United States in Comparison', *American Journal of Sociology* **122**(5), 1448–84.
- Aisenbrey, S. & Fasang, A. F. (2010), 'New Life for Old Ideas: The "Second Wave" of Sequence Analysis Bringing the 'Course' Back Into the Life Course', *Sociological Methods & Research* **38**(3), 420–462.
- Aries, P. (1962), *Centuries of childhood*, Penguin Books, New York.
- Castles, S. & Miller, M. J. (2014), *The Age of Migration: international population movement in the modern world*, fifth edn, Teh Guildford Press, New York.
- Castro-Martin, T. & Rosero-Bixby, L. (2011), 'Maternidades y fronteras. La fecundidad de las mujeres inmigrantes en España', *Revista Internacional de Sociología* (1), 105–137.
- Davis, J. (2011), 'Decoupling Migration Effects from Income Effects on Reproduction in Central American Migrant-Sending', **45**(2), 325–347.
- Elzinga, C. H. & Studer, M. (2015), 'Spell Sequences, State Proximities, and Distance Metrics', *Sociological Methods & Research* **44**(1), 3–47.
- Fargues, P. (2011), 'International migration and the demographic transition: A two-way interaction', *International Migration Review* **45**(3), 588–614.
- Fasang, A. E. & Liao, T. F. (2014), 'Visualizing Sequences in the Social Sciences: Relative Frequency Sequence Plots', *Sociological Methods & Research* **43**(4), 643–676.
- Garcia, D. & Le Bras, H. (2017), *Archéologie des migrations*, 1 edn, La Découverte, Paris.
- Glick, J. E., Bean, F. D. & Van Hook, J. V. W. (1997), 'Immigration and Changing Patterns of Extended Family Household Structure in the United States: 1970-1990', *Journal of Marriage and the Family* **59**(1), 177–191.
- Héritier, F. (1996), *Masculin/Feminin I. La pensée de la différence*, Odile Jacob, Paris.
- Kulu, H. (2005), *Hypotheses and Fertility : Competing*, Vol. 21.
- Kulu, H. & Hannemann, T. (2016), 'Introduction to research on immigrant and ethnic minority families in Europe', *Demographic Research* **35**(July), 31–46.
- Kulu, H. & Milewski, N. (2007), 'Family change and migration in the life course: An introduction', *Demographic Research* **17**, 567–590.

- Laurent Toulemon & Mazuy, M. (2004), ‘Comment prendre en compte l’âge à l’arrivée et la durée de séjour en France dans la mesure de la fécondité des immigrants?’, *Documents de travail- INED* **120**, 1–34.
- Lesnard, L. (2010), *Setting Cost in Optimal Matching to Uncover Contemporaneous Socio-Temporal Patterns*, Vol. 38.
- Lindstrom, D. P. & Saucedo, S. G. (2002), ‘The Short-and Long-Term Effects of U.S. Migration Experience on Mexican Women’s Fertility’, *Social Forces* **80**(4), 1341–1368.
- Mason, K. (1997), ‘Explaining fertility transitions’, *Demography* **34**(4), 443–454.
- Massey, D. S., Durand, J. & Pren, K. A. (2014), ‘Explaining undocumented migration to the U.S.’, *International Migration Review* **48**(4), 1028–1061.
- Organization of American States (2011), *International migration in the Americas: First report of the continuous reporting system of international migration in the Americas 2011*, Migration and Development Program, Washington, D.C.
- Özden, Ç., Parsons, C. R., Schiff, M. & Walmsley, T. L. (2011), ‘Where on earth is everybody? The evolution of global bilateral migration 1960-2000’, *World Bank Economic Review* **25**(1), 12–56.
- Pailhé, A. (2015), ‘Partnership dynamics across generations of immigration in France: Structural vs. Cultural factors’, *Demographic Research* **33**(1), 451–498.
- Parrado, E. (2011), ‘How High is Hispanic/Mexican Fertility in the United States? Immigration and Tempo Considerations’, *Demography* **48**(3), 395–409.
- Parrado, E. A. (2015), Migration and Fertility, in ‘International Encyclopedia of the Social and Behavioral Sciences’, Elsevier, pp. 397–406.
URL: <http://linkinghub.elsevier.com/retrieve/pii/B978008097086831128X>
- Parrado, E. a. & Flippen, C. a. (2012), ‘Hispanic Fertility, Immigration, and Race in the Twenty-First Century’, *Race and Social Problems* **4**(1), 18–30.
- Portes, A. (2001), ‘Introduction: the debates and significance of immigrant transnationalism’, *Global Networks* **1**(3), 181–194.
- Robette, N. & Bry, X. (2012), ‘Harpoon or Bait? A Comparison of Various Metrics in Fishing for Sequence Patterns’, *Bulletin of Sociological Methodology/Bulletin de Méthodologie Sociologique* **116**(1), 5–24.
- Ryder, N. B. (1965), ‘The cohort as a concept in the study of social change.’, *American Sociological Review* **30**(6), 843–861.
- Studer, M. (2013), ‘WeightedCluster Library Manual: A practical guide to creating typologies of trajectories in the social sciences with R’, *LIVES Working Papers*, 24 .

- Studer, M. & Ritschard, G. (2014), A comparative review of sequence dissimilarity measures, Technical report.
- Studer, M. & Ritschard, G. (2016), ‘What matters in differences between life trajectories: A comparative review of sequence dissimilarity measures’, *Journal of the Royal Statistical Society* **179**(2), 481–511.
- Studer, M., Ritschard, G., Gabadinho, A. & Müller, N. S. (2011), ‘Discrepancy Analysis of State Sequences’, *Sociological Methods & Research* **40**(3), 471–510.
URL: <http://journals.sagepub.com/doi/10.1177/0049124111415372>
- Toulemon, L. & Mazuy, M. (2004), Comment prendre en compte l’âge à l’arrivée et la durée de séjour en France dans la mesure de la fécondité des immigrants ?, Technical report.
- Wu, L. (2000), ‘Some Comments on ’Sequence Analysis and Optimal Matching Methods in Sociology: Review and Prospect’’, *Sociological Methods & Research* **29**(1), 41–64.