IMMIGRANT FERTILITY ADAPTATION AND CHANGE IN LOS ANGELES

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“The Hispanic population in the United States grew by 43% in the last decade, surpassing 50 million and accounting for about 1 out of 6 Americans, the Census Bureau reported Thursday... Analysts seized on data showing that the **growth was propelled by a surge in births in the U.S., rather than immigration,** pointing to a growing generational shift in which Hispanics continue to gain political clout and, by 2050, could make up a third of the U.S. population.”

– Stephen Ceasar, *Los Angeles Times*, March 24, 2011

ABSTRACT. Los Angeles, California has historically been a major destination for migrants coming from high fertility, pro-natalist cultures. Immigration from Mexico has been fairly constant while spikes in immigration from Guatemala, El Salvador, and Vietnam were spurred by civil conflict in the source countries. The fertility behavior of these immigrant groups has attracted the attention of both academic and policy researchers with the primary questions being, a) Will fertility levels of immigrants approach those of the native-born population? and b) If fertility levels do change, will the pace of change occur on the time scale of the individual immigrants or will it take generations? We address these questions and try to provide additional context by using an additional baseline of the home country fertility behavior. We use mixed methods in the research combining the results from statistical models based on the Los Angeles Family and Neighborhood Survey with additional context coming from a set of focus groups with immigrant women from Central America.

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1. INTRODUCTION

Fertility behavior of Hispanic immigrants remains a highly politicized issue in California, and indeed has been one of the key issues that led to propositions eroding access to education and health services for immigrant women and children.[1] Academic research on Hispanic immigrant and foreign born fertility has largely supported the notion that assimilation is not occurring, suggesting that high fertility levels are sustained over time. The resulting image of Hispanic immigrants producing large families over generations has served to fuel politics. However, those guiding research studies generally rely on fertility measures that are not well-suited to studying changes in fertility behavior of immigrant populations. The impacts of disruption and exposure to a new culture have potentially dramatic impacts on both the completed fertility and the timing of births of immigrant women. However, the use of measures suitable for capturing this degree of variation in behavior has been limited by available data. Another shortcoming of the contemporary Hispanic assimilation discourse is the focus on a single population (Mexican immigrants) which frequently serve as a proxy population to represent overall Hispanic fertility behavior. Our approach resolves these shortcomings and the results provide a more complete and nuanced assessment of immigrant fertility behavior.

Past studies have used measures that are not suitable for assessing the dual cultural exposure and conditioning of immigrants. Fertility measures such as the total fertility rate (TFR) and children-ever-born (CEB) have been the primary metrics used to assess fertility change, or attribute fertility burden. TFR is a period measure and the projective nature of its construction implicitly assumes *cultural adaptation of fertility behavior will remain fixed at levels of the surveyed population*. CEB aggregates births prior to immigration with births post-immigration. Because of the crudeness of these metrics, they are of limited value if the research goal is to understand individual fertility adaptation or assimilation. A major methodological novelty of the current paper is to assess changes in parity-specific birth intervals and isolate pre- and post-immigration births. An assessment of birth spacing has direct links to more aggregate measures (TFR and CEB) and will yield results that are in line with current theories of post-immigration behavioral changes that manifest over a range of time scales. This is made possible by relying on a relatively unique data set – Los Angeles Family and Neighborhood Survey (LAFANS) waves I and II – that includes a complete birth history for each woman, and focuses on one of the largest Hispanic immigrant destinations in the US. To evaluate the heterogeneity of the Hispanic foreign-born population, the study will assess whether fertility behavior of Central American immigrants is the same as Mexican immigrants.

2. FERTILITY, IMMIGRATION, AND CULTURE

Several assumptions underlie theories that frame post-immigration changes in fertility behavior: (1) fertility norms in an origin region and a destination region are different; (2) formation of fertility norms are ultimately embedded in a culture and are transmitted from generation-to-generation as part of the acculturation process, even against larger structural features of national society or the economy[2]; (3) fertility norms are multi-dimensional, and (4) evaluating variations in total/completed fertility alone cannot capture the complexity of the process; considering age at first sex, age at marriage, birth spacing and timing, and contraceptive use, among others, is required to fully understand fertility behavior.

Dominant theories in the literature describe possible types of post-immigration changes in fertility behavior that may manifest in the near-, mid- and/or long-term. Near-term, immigrants are usually expected to experience an increase in births (ie, more births, spaced closer together), with closer spacing in births reflecting either family reunification or desire to settle into the new community through the birth of a baby (Lindstrom, 2003; Kulu and Milewski, 2007). Alternatively, the family and lifestyle disruption of international migration can result in increased spacing between births, which may depress fertility temporarily (Bean and Swicegood, 1985; Mayer and Riphahn, 2000). The near-term impacts of immigration on Central American migrants is currently unknown.

A “settling-in” phase comes in the mid-term, 3-10 years after the move from the country of origin. During this period, immigrant fertility behavior might correspond to that of the receiving culture/region (referenced as “adaptation”) or that of the sending culture (referenced as “socialization”) (Carter, 2000; Bean et al., 2000). Having moved beyond the disruption of the actual relocation at this point, families may “catch-up” on any births missed and attain their pre-established fertility goals (Carter, 2000; Mayer and Riphahn, 2000).

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[1] In California, and Los Angeles specifically, the historically high levels of immigration have been a source of public outcry, and have sparked political movements culminating in anti-immigrant propositions such as 187 (restricted public services), 209 (removed affirmative action for public education), and 227 (removed bilingual education).

[2] Development agencies believe this partially explains why reducing fertility is far harder than reducing mortality.

In the long-term, the fertility behavior of the children, or grandchildren, of immigrants may continue to reflect the norms of the source country. Researchers who support theories related to socialization, adaptation or assimilation anticipate that the fertility behavior of second- or third-generation immigrants raised and educated in the US will mirror the behavior of other US-born women (without a foreign-born parent or grandparent) (Alba and Nee, 1997; Parrado and Morgan, 2008). Some results indicate, however, that second and third generations maintain higher fertility levels than those of their host culture, leaving researchers to speculate that either the economic disadvantage of an immigrant heritage or the "persistence of sub-cultural norms" impacts fertility behavior (Portes and Rumbaut, 2001; Frank and Heuveline, 2005).

3. METHODOLOGY, RESEARCH QUESTIONS, AND DATA

The theory base informs testable hypotheses for near-, mid-, and long-term fertility behavior. Short-term, we can test whether observed patterns are more consistent with decreased/increased birthing and longer/shorter spacing between births. Conditional on near-term behavior, mid-term, we can assess whether short birth spacing and continued birthing diverge from Mexico and Central American norms. Long-term, we can examine the birthing patterns of second- and third-generation women. A critical point is that all of those hypotheses posit changes in relation to a "baseline" population that serves as the cultural norm. An additional insight of the present paper is that the baseline can refer to the dominant culture where the immigrants now reside (Los Angeles in this case) or the norm could refer to the *home* region that served as the point of acculturation for the immigrants prior to their departure. The dominant approach among researcher has been to focus on tests of the first variety – *convergence hypotheses* – in the present paper we additionally construct tests of the second variety – *divergence hypotheses*.

3.1. Methodology.

A primary innovation in this paper is the use of birth intervals. Given a complete birth history calendar (exact dates for each live birth), we can measure the birth intervals for each birth parity: marriage to first birth (parity $0 \to 1$), first birth to second birth (parity $1 \to 2$), ...etc. The figure below contains lifelines for four hypothetical women with demographic events roughly in accord with the behavioral theories we propose to test. The Central American woman has the largest number of births (6) and the birth spacing is very close. This would be characteristic of a pro-natalist setting combined with either poor access to, or poor knowledge of, modern birth control methods. For *Immigrant 1* this implies longer exposure to Central American fertility norms (socialization), and we have indicated a longer birth interval between parities 2 and 3 to indicate the disruptive effect of the migration. Because of early socialization, *Immigrant 1* decreases spacing between parities 3 to 5 to achieve an ideal family size close to the source region family size norms. In contrast, *Immigrant 2* has fewer years of socialization to high fertility norms and she adjusts both birth spacing and ideal family size towards the norms for US native born women.

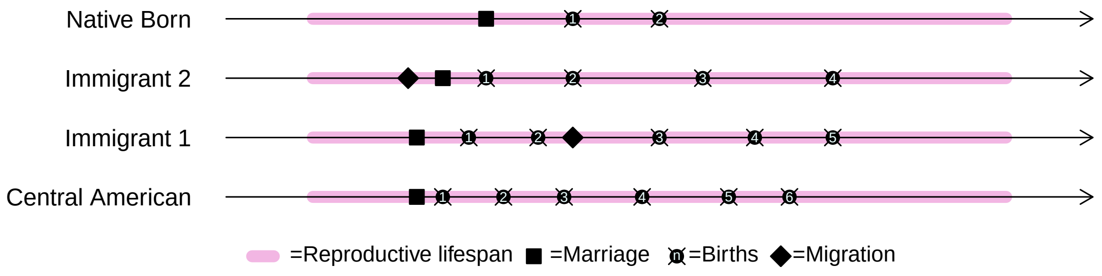

FIGURE 1. Examples of birth timing and spacing

From a statistical modeling perspective, the birth intervals can be viewed as durations from a stochastic counting process with intensity $\lambda(t)$. In our setting, the intensity is the expected number of births of order $j+1$ in the interval $[0,t]$ for a sample of women who have already had their jth birth. The intensity can be decomposed into the hazard rate ($\alpha(t)$) times the number of women at risk of their $j+1^{st}$ birth ($Y(t)$). This allows us to analyze the birth interval data focusing on either the hazard rate $\alpha(t)$ or the survival function $S(t) = exp\left(-\int_0^t \alpha(s)ds\right)$. We use Kaplan-Meier survival curve estimators and Nelson-Aalen cumulative hazard function estimators to visually describe differences in birth interval spacing among different subpopulations, and to conduct pairwise tests of differences between subpopulations. While pairwise comparisons are of interest, we will also use regression models to control for relevant compositional differences among subgroups and to introduce continuous covariates. For regression analysis, we use two different frameworks (Aalen et al., 2008): Cox's proportional hazard model,

$$\alpha_i(t) = \alpha_0(t)\exp(\boldsymbol{\beta}^T \mathbf{x}_i(t)),\ \mathbf{x}_i(t) = \{x_{i1}, \ldots, x_{ik}\},$$

and, Aalen's nonparametric additive hazard model,

$$\alpha_i(t) = \boldsymbol{\beta}(t)^T \check{\mathbf{x}}_i(t),\ \check{\mathbf{x}}_i(t) = \{1, x_{i1}, \ldots, x_{ik}\}.$$

Cox's model remains the dominant framework used to analyze duration data in demography and public health. It is an important starting point but also imposes unnecessary restrictions. Aalen's model has several appealing properties: 1) hazard functions are allowed to cross (this may result from the *disruption* hypothesis), 2) effects are time-varying (allowing us to assess our hypotheses that posit effects over different time scales), and 3) straightforward extension of the model to study birth histories as a series of recurrent events. The covariate effects, $\beta_j(t)$ for $j > 1$, in the Aalen model have the natural interpretation of excess risk relative to the baseline hazard ($\beta_1(t)$) at time t due to a one unit increase in the j^{th} covariate. After fitting regression models (of either type) we can construct *adjusted* survival curves to create visual comparisons that account for compositional differences among subgroups.

3.2. **Research Questions and Hypotheses.** Two research questions we answer utilizing complete birth histories are described in the boxed section below. The hypotheses are written in terms of the hazard rate introduced above. A higher hazard (higher likelihood of birth) is consistent with shorter birth intervals. The parenthetical superscripts on the hazard rate refer to: NB= native born, FB=foreign born, SR=source region, 1=first generation, 2=second generation, and 3=third generation. The hypotheses are classified into near-term (NT), medium-term (MT), and long-term (LT) time scales.

(1) Are fertility levels of immigrant communities from source region *R* **converging towards** native-born fertility levels in Los Angeles?
  NT: For $t < t^*$, $H_o : \alpha(t)^{(NB)}_{j,j+1} = \alpha(t)^{(FB)}_{j,j+1}$ against $H_a : \alpha(t)^{(NB)}_{j,j+1} > \alpha(t)^{(FB)}_{j,j+1}$ (disruption).
  MT: For $t > t^*$, $H_o : \alpha(t)^{(NB)}_{j,j+1} = \alpha(t)^{(FB)}_{j,j+1}$ (adaptation) against $H_a : \alpha(t)^{(NB)}_{j,j+1} < \alpha(t)^{(FB)}_{j,j+1}$ (socialization).
  LT: $H_o : \alpha(t)^{(1)}_{j,j+1} > \alpha(t)^{(2)}_{j,j+1} > \alpha(t)^{(3)}_{j,j+1}$
(2) Are fertility levels of immigrant communities from source region *R* **diverging from** the prevailing levels in source region *R*?
  NT: For $t < t^*$, $H_o : \alpha(t)^{(SR)}_{j,j+1} = \alpha(t)^{(FB)}_{j,j+1}$ against $H_a : \alpha(t)^{(SR)}_{j,j+1} > \alpha(t)^{(FB)}_{j,j+1}$ (disruption).
  MT: For $t > t^*$, $H_o : \alpha(t)^{(SR)}_{j,j+1} = \alpha(t)^{(FB)}_{j,j+1}$ (adaptation) against $H_a : \alpha(t)^{(SR)}_{j,j+1} < \alpha(t)^{(FB)}_{j,j+1}$ (socialization).
  LT: $H_o : \alpha(t)^{(SR)}_{j,j+1} > \alpha(t)^{(1)}_{j,j+1}$ (some adaptation).

3.3. **Data.** We will use Waves I and II of the Los Angeles Family and Neighborhood Survey (L.A. FANS) to test the hypotheses under research questions 1 and 2. The L.A. FANS is a longitudinal design based on a stratified random sample of Los Angeles neighborhoods. The neighborhoods are operationally defined by census tracts which were selected randomly from three strata defined by poverty status: not poor, poor, or very poor. The resulting sample from the first wave includes 65 neighborhoods and approximately 2,500 households. Within sampled households, the survey was administered to both the head of household and the primary care giver (this is important since it ensures a large sample of women). The first wave of the panel was administered in 2000-02 and the second wave was administered 2008-2010. Public use samples are available for both waves. The second wave follows up with all of the original respondents (even if they have left the country) and enrolls a new set of respondents to the survey.

Variables in the data include fertility (birth month and year for up to 16 children) and reproductive health, country of birth, time spent in the US (month/year of entry into the US), education levels of father and mother, work / residential histories for two years prior to the survey, and neighborhood characteristics. While the first wave of the data has been used in education and healthcare research, to our knowledge, none of the data has been used to analyze fertility or reproductive health determinants. The second wave was released only in 2011. The source region (immigrant sending region) resolution in this data set is as good as can be expected from the sample size. The source regions with sufficient sample size to analyze include Mexico and Central America [3]

4. RESULTS

To be completed.

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[3] Costa Rica, El Salvador, Guatemala, Honduras, Nicaragua, and Belize are each separately identified but the sample size will only support analysis of the region as a whole.

5. PRELIMINARY FIGURE

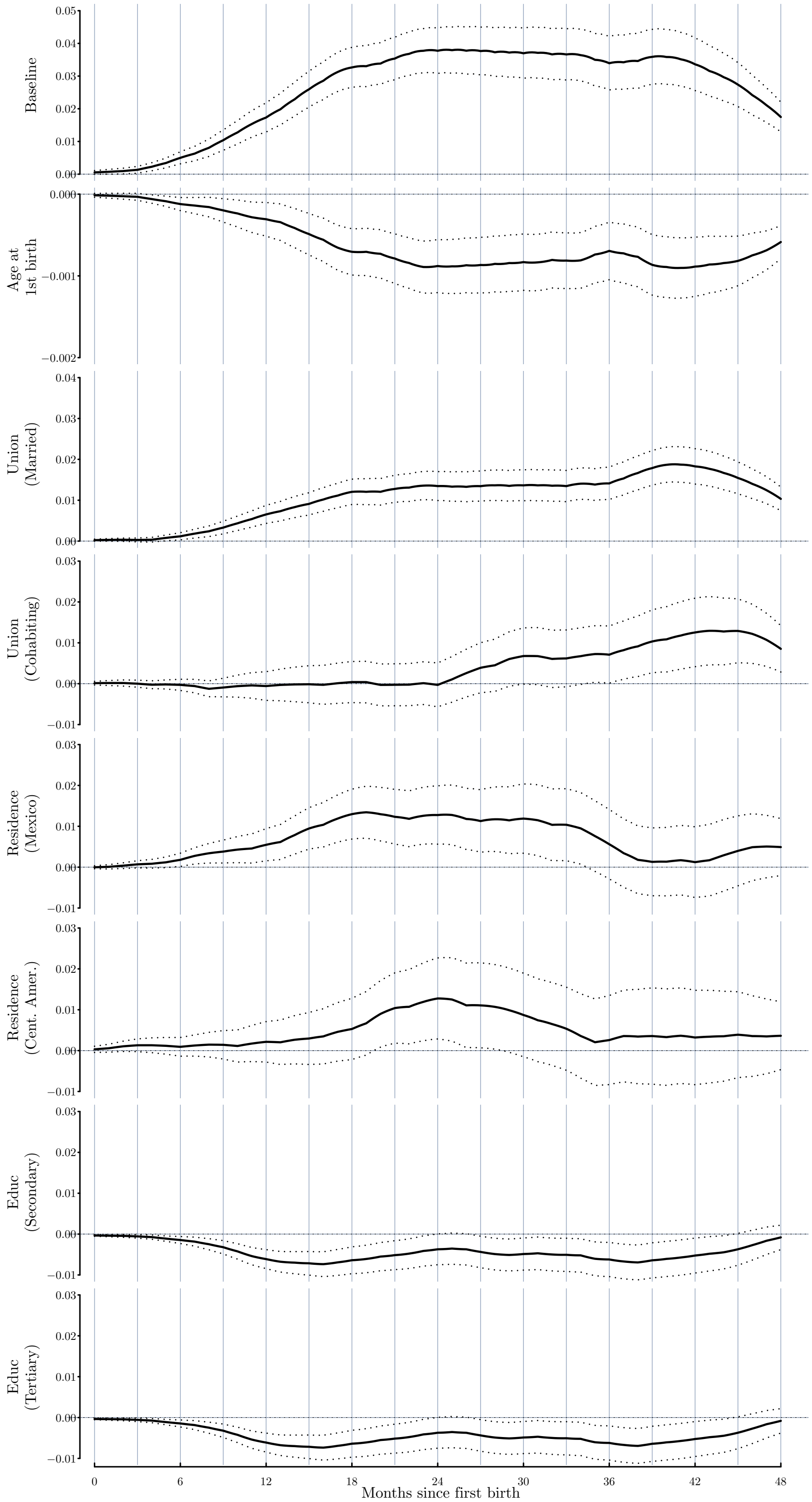

FIGURE 2. Additive regression functions for transition from parity 1 to 2.