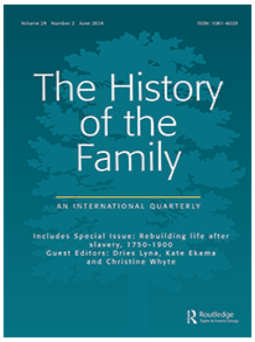

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Trends in assortative mating in the United States, 1700–1910. Evidence from FamiLinx data

Giulia Corti[a], Saverio Minardi[b] and Nicola Barban[b]

[a]Center for Demographic Studies (CED-CERCA), Barcelona, Spain; [b]Department of Statistics "P. Fortunati", University of Bologna, Bologna, Italy

ABSTRACT

Couple formation and assortative mating significantly influence societal structures, as marriages between individuals from diverse geographical or social backgrounds promote intra-family diversity. Understanding these patterns is crucial for grasping the demographic processes that shape contemporary societies. However, the scarcity of comprehensive data has impeded progress in this area. This paper aims to fill this gap by investigating assortative mating trends in the United States among birth cohorts from 1700 to 1910, utilizing data from FamiLinx, an online crowdsourced genealogical database. We focus on two primary dimensions: migration background (including natives, first and second-generation migrants) and age at marriage. Our analysis yields three major findings. First, we document significant changes in assortative mating trends over time, reflecting the dynamic nature of mate selection and its responsiveness to societal shifts. Second, we uncover substantial heterogeneity in assortative mating patterns across different social groups, indicating varying social dynamics and preferences. Third, we illustrate how these trends can be differently interpreted depending on whether the perspective is individual or familial. Additionally, we explore the advantages and limitations of using online genealogical data for historical studies of assortative mating, highlighting its potential for offering new insights while acknowledging the challenges posed by data quality and representativeness.

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KEYWORDS
Assortative mating; online genealogical data; historical demography; United States

1. Introduction

Couple formation is a significant demographic phenomenon with multiple implications. At the individual level, having a partner influences various aspect of one's social and economic trajectory (Van Bavel, 2021) and often serves as a prerequisite for biological reproduction. At the societal level, couples play a crucial role in shaping the distribution of characteristics and inequalities among families, influencing their transmission across generations (Schwartz, 2013).

Extensive research has demonstrated that individuals do not randomly choose their partners; instead, they tend to exhibit similarities in various traits. This phenomenon is

CONTACT Giulia Corti gcorti@ced.uab.es

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known as assortative mating. Findings from different fields have highlighted the extent to which partners tend to resemble each other in socioeconomic aspects (e.g. education, income, and occupation) (Greenwood et al., 2014; Kalmijn, 1994; Schwartz, 2013), ethnic backgrounds (Chiswick & Houseworth, 2011), physical attributes (Little et al., 2006) and genetic traits (Robinson et al., 2017).

While the patterns and causes of assortative mating have been extensively studied in the social sciences, social history, and historical demography, there is still limited knowledge about long-term trends. Nevertheless, a comprehensive understanding of the historical transformations in assortative mating is essential to unravel how contemporary societies have emerged. Marriage merges families, increasing or limiting within-family diversity and social cohesion, and influencing the distribution of social characteristics and genetic traits (Thiessen & Greeg, 1980). Moreover, the combination of partner's characteristics significantly influences the distribution of socioeconomic resources across households. Different levels of assortative mating are associated with other socio-demographic phenomena such as fertility (Conley et al., 2016; Nitsche et al., 2018) or health (Guner et al., 2018). Finally, the characteristics of parents determine the family background and life prospects of subsequent generations, influencing social mobility and stratification.

Despite its relevance, studying long-term mating patterns has traditionally been challenging due to the demanding data requirements. However, recent developments and the availability of crowdsourced online genealogies offer new and unprecedented opportunities to study historical demographic processes across geographically diverse populations. Genealogical data have already been utilized to examine longevity (Cozzani et al., 2023; Kaplanis et al., 2018; Minardi et al., 2023) and fertility (Blanc, 2021; Hsu et al., 2021). We contribute to this emerging body of literature by demonstrating, for the first time, how crowdsourced genealogical data can be leveraged to study assortative mating.

This paper documents long-term assortative mating trends in the United States from the 18th to the early 20th centuries, utilizing FamiLinx genealogical data. Specifically, we focus on assortative mating based on migration background and age. On the one hand, assortative mating by geographical origin is used as an indicator of the openness of a society, and it can be studied to assess the evolution of societies and the integration of migrants into them (Kalmijn, 1998). On the other, assortative mating by age is used as a proxy of changes in partner choice; the reduction in the age gap between partners is often interpreted as the rise of personal criteria over instrumental ones over time, which can be read as a further indicator of the changing meaning of the institution of marriage over time (Van de Putte et al., 2009). Thus, we believe that assortative mating by geographical origin and age are important dimensions to investigate when studying the evolution of a society over time. And genealogical data can be an interesting source to pursue such an investigation.

Our findings highlight the dynamic and multidimensional nature of assortative mating. First, changes in assortative mating did not follow a consistent trajectory over time but were concentrated within particular birth cohorts. Second, persistent variations existed in assortative mating between individuals defined by their migration histories and gender across different periods. Finally, results indicate the remarkable persistence in the intergenerational reproduction of mating behavior across history.

2. Assortative mating by migration background and age: concepts and previous studies

2.1. Migration background

Assortative mating based on place of origin is particularly interesting when examining the interaction between different social groups. High intermarriage rates indicate extensive contact and mutual acceptance between groups and successful integration and assimilation of migrants into the host society (Kalmijn, 1993).

Societal and economic changes may have influenced patterns of intermarriage over time. Firstly, intermarriage based on geographical origin is contingent upon the population structure and group sizes within a society (Blau & Schwartz, 1984). Migration has been a significant driver of population change throughout history, bringing individuals with distinct social, economic, and demographic characteristics into the host societies.

On the one hand, changes in the ethnic composition of a society may increase intermarriage rates due to a more diverse population. On the other hand, social groups, especially migrants, often experience spatial and social segregation, which can hinder intermarriage (Danubio & Pettener, 1997; De Marco, 1980). Previous studies have demonstrated the extent to which intermarriage has increased during periods of high migration and how migration has heightened the likelihood of intermarriage at the individual level (Dribe & Lundh, 2009; Dribe et al., 2019; Puschmann et al., 2014; Van de Putte, 2003; Van de Putte & Oris, 2005).

An significant historical barrier to geographical intermarriage was the influence of families, as they often sought to maintain continuity and connections with the original group through their children's marriages. Families also played a significant role in shaping the social environment in which their children were raised and where they typically sought partners. Families were responsible for the primary socialization of children, instilling a sense of group solidarity that influenced their preference for endogamy. However, societal changes throughout history have weakened the influence of families on their children's' choices. Factors such as the development of educational systems (Klesment et al., 2020), the expansion of wage-based economic systems (Treiman, 1970), industrialization (Blau & Duncan, 1967), and the proliferation of mass communication and transportation (Ekamper et al., 2011; Maas & Zijdeman, 2010) have increased individuals' independence from their families and are often associated with a higher likelihood of geographical heterogamy.

2.2. Age similarity

Age differences between partners have traditionally served as an indicator of the balance between personal and sentimental factors versus instrumental considerations in partner choice (Shorter, 1975; Van de Putte et al., 2009; Van Poppel et al., 2001).

In pre-industrial societies, newly formed households needed to achieve economic independence without jeopardizing the family's overall economic situation. As a result, age hypergamy, where men were typically older and possessed greater economic security and power, was the prevailing couple arrangement (Ariès, 1983; Van de Putte et al., 2009). On the other hand, younger women, with their higher potential for reproduction, might have been preferred by families interested in lineage continuation. However, with modernization and industrialization, the economic imperatives associated with marriage gradually diminished, allowing more room for personal considerations in partner selection. Research has indicated a significant increase of age homogamy by the end of the 19th century, which has been interpreted as a reflection of the growing prominence of non-instrumental factors in choosing a partner.

2.3. *Assortative mating as a multidimensional process*

Most studies on assortative mating focus on specific dimensions, such as migration background or age, in isolation. However, in reality, individuals seek partners who possess multiple characteristics simultaneously (Kalmijn, 1998). In this paper, we approach assortative mating from a multidimensional perspective, specifically examining the interplay between migration background and age. We develop two competing hypotheses to explain this phenomenon. The first, known as the by-product hypothesis (Kennedy, 1944), suggests that if individuals choose partners with similar migration backgrounds, they are also likely to exhibit homogamy in terms of age. This could be attributed to the structure of local mating markets, which may exhibit both ethnic and age homogeneity. In contrast, the status exchange hypothesis (Davis, 1941; Merton, 1941) suggests that higher levels of age heterogamy may be observed when there is homogamy based on migration background. According to this hypothesis, individuals might be willing to trade similarities in age for similarities in migration background, particularly if they value maintaining strong connections with their community of origin.

Furthermore, we anticipate that there may be gender differences in these patterns (Sassler, 2005). Historical societies often restricted women's opportunities for education and employment outside their parental homes (Sassler, 2005, 2000), resulting in a less diverse social environment for women than men. Additionally, the transmission of ethnic identity primarily occurred within the home environment through practices such as food, religion, and traditions, with women often playing a central role in preserving ethnic identity (Foner & Dreby, 2011). Lastly, women typically faced greater pressure from their families of origin to marry within their ethnic group. Therefore, we expect homogamy based on migration background to be of greater importance for women. As a result, they may be more willing to exchange other characteristics, such as age, to achieve homogamy. We might think of migrant women as an exception to this pattern, as migration might be a way to gain independence and emancipation (Sharpe, 2002), and this could be reflected also in their marriage choices.

2.4. *The intergenerational persistence of mating behavior across generations*

Studying the degree of resemblance in demographic behaviors among individuals within the same family can provide valuable insights into population transformation processes (Mare, 2011). The parent-child link has been extensively examined concerning various economic (income, occupation) and social (education, class) outcomes, highlighting the strength of this association (Breen & Jonsson, 2005; Erikson & Goldthorpe, 1993). Additionally, there has been a growing interest in understanding the intergenerational transmission of demographic behaviors and the resemblance between generations in recent years (Mare, 2011; Song et al., 2015).

Parents influence children's behaviors through interconnected channels, including socialization, cultural factors, and genetic transmission. Children internalize preferences and attitudes through socialization and cultural influences, which can lead to replicating of their parents' demographic choices. Moreover, recent research has shed light on the heritability of certain demographic characteristics, indicating genetic factors at play (Barban et al., 2016). Families can also directly shape their children's choices, particularly in past societies where parental interference was more prevalent (Van Leeuwen et al., 2005).

Interestingly, there has been little focus on the intergenerational persistence of assortative mating between generations. However, a strong correlation between the mating patterns of parents and their children is one mechanism through which resources become concentrated within families across generations (Goñi, 2022; Marcassa et al., 2020). Moreover, the persistence of mating behavior between generations can be seen as an additional indicator of group isolation and polarization. Continuous reinforcement of group strength and cohesion can occur if endogamous marriages consistently renew and preserve group boundaries. Although research has shown that parents may actively influence their children's marital choices (Van Leeuwen et al., 2005), to the best of our knowledge, there are no explicit studies examining the intergenerational persistence of assortative mating.

3. Historical patterns of assortative mating in the United States

Our study investigates the evolution of mating patterns in the United States among birth cohorts from the 18th and 19th centuries. The United States presents an ideal context for our research due to the remarkable economic, political, social, and demographic changes during this period. Particularly noteworthy is the country's experience of multiple waves of migration throughout the 18th, 19th, and early 20th centuries (Fogleman, 1992; Martin, 2021; Potter, 1965). Immigration waves in the US followed some specific country patterns. Large-scale immigration in the 1830s and 1850s came from Britain, Ireland and Germany, followed by Catholics and Jewish migrants from Southern and Eastern Europe (Martin, 2021).

Previous empirical studies on intermarriage by migration background in the United States have predominantly focused on the Mass Migration period (1870–1920) (Abramitzky & Boustan, 2017; Angrist, 2002; Kalmijn, 1993; Meng & Gregory, 2005; Pagnini & Morgan, 1990; Sassler, 2005). Findings from these studies emphasize the persistent barriers to marriage between native-born individuals and migrants, despite the increasing proportion of migrants and their descendants in the overall population.

The first-generation migrants exhibited higher rates of endogamy, while the second-generation individuals demonstrated a greater inclination to marry within the native population, supporting the concept of assimilation (Kalmijn, 1993). Furthermore, variations emerged among ethnic groups, with more recent migrants, such as Italians and Poles, displaying a stronger inclination toward endogamy. Additionally, research suggests that gender plays a role, as women with a migration background exhibited a higher degree of homogamy in terms of ethnic origin, indicating potential differences in marriage market dynamics (Sassler, 2005).

Historical investigations into age homogamy in the United States have been limited. Atkinson and Glass (1985) explored age differences between spouses using Census data from 1900, 1960, and 1980, revealing a shift toward age homogamy. While there is some understanding of earlier periods and long-term trends, we acknowledge the existence of two notable studies. Haines (1996) examined the age of marriage from colonial times to the present, drawing from a range of pre-census sources and Census data. The marriage patterns in North America differed from the characteristic pattern of late marriage observed in Europe (Hajnal, 1953), with spouses in the United States marrying at younger ages. Similarly, Fitch and Ruggles (2000) investigated trends in median marital age between 1850 and 1990, revealing their sensitivity to economic cycles.

4. The potential of genealogical data for the study of assortative mating

To the best of our knowledge, no study has specifically investigated long-term trends in assortative mating by geographical origin and age in the United States, primarily due to limited data availability. We fill this gap using online crowd-sourced genealogical data, which suits our research questions for two main reasons. Firstly, they allow to investigate a broader period compared to other data sources, enabling us to trace individuals back to the 18th century. Secondly, genealogical data offer information on vertical relationships, such as parent-child connections over long periods, which is not always possible with official historical data.

Genealogical data have often suffered from issues of representativeness, because they often included very selective populations such as aristocracies or high-status families, with lower sample sizes and geographically and temporally located (Westendorp & Kirkwood, 1998). Compared to previously used genealogical data, FamiLinx provides a bigger sample with a larger geographical and temporal focus. Nevertheless, assessing how it resembles official statistics is crucial. Extensive data validation has been performed by Kaplanis et al. (2018) and more recently for Europe by Blanc (2023) showing it is consistent with official statistics. On the other hand, it has been documented that FamiLinx tends to underestimate women (Minardi et al., 2023), and mortality levels (Chong et al., 2022; Stelter & Alburez-Gutierrez, 2022). As for couples, given the genealogical design of the data, FamiLinx tends to underestimate childless couples. Moreover, some recent contributions (Minardi et al., 2023) have raised the attention of scholars toward the fact that individuals with more complete information might be selected in terms of socioeconomic status.

Keeping these limitations in mind, we conducted in Appendix D further data quality checks of our FamiLinx sample with the US Census data, when possible (see Appendix D). We compare trends in the population by migration background, and patterns of assortative mating by age and geographical origin to the Censuses for the years when it is possible. Overall, the Familinx estimates are consistent with the censuses.

5. Data, sample, variables, and methods

5.1. Data and sample

We use FamiLinx data, the publicly available dataset derived from the genealogical website Geni.com. This dataset encompasses comprehensive individual-level information and genealogical trees, encompassing 86 million individuals across various geographical locations and spanning over four centuries.

We started our sample selection process by keeping cases with valid information on the birth and death countries and the year of birth. Therefore, we selected individuals dead in the United States who were born between 1700 and 1910, with complete information on their dates and places of birth. We also restricted the sample to individuals and parents who reached at least 30 years old and not more than 110 years old. The upper limit is meant to exclude outliers and unreasonable values; the lower limit is because Familinx data are not acceptable representative for younger individuals, but become more accurate for middle-aged and older adults (Chong et al., 2022).

Leveraging the genealogical structure of the data, we were able to gather detailed information on the birthplaces of their parents. Since we do not have direct information on marriages, we identify as a partner the individual of the opposite with whom the subject shares at least one child. For this individual, we can retrieve information on his/her place and year of birth, and for his/her parents too. To visualize the relationships, refer to Figure 1.

The resulting dataset comprises 19,275 individuals who possess complete information regarding their birth and death dates, and their parents', partners', and parents-in-law's birthplaces. We ended up with a very strong reduced sample compared to the original FamiLinx data. This is the result of two processes. On the one hand, there is a selection directly coming from the completeness of the original data. For instance, of the original 86 million individuals, only around 8 million had complete information on the place of birth and death. On the other, the criteria that we impose of complete information for two different genealogical trees (the individual and his/her partner) further decreases our sample. Appendix C provides a more detailed explanation of the steps in the sample selection. Besides this selection, our sample is representative of the US census data of the same periods (Appendix D shows the comparison between US Census data and Familinx).

5.2. Variables

To examine patterns of assortative mating by geographical origin, we utilize the country of birth information to construct relevant variables. Firstly, we categorize individuals based on their migration histories. By considering the individual's country of birth and that of their parents, we can differentiate between three groups. If the

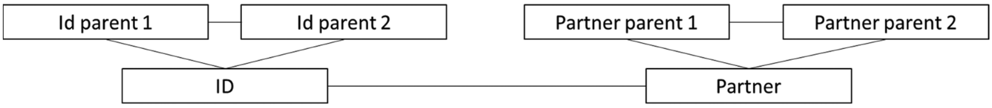

Figure 1. Id and relationships for the construction of the dataset.

Table 1. Variables.

Variable	Units	Scale/Categories	Information needed
Migration background	– Id – Partner – Id parents – Partner's parents	– Native – Migrant (1st or 2nd generation)	– Birth place of id – Birth place of parents
Assortative mating	– Id – Id partner	– Homogamy (same migration background) – Heterogamy (different migration background)	– Migration background of partners
Assortative mating by age (metric)	– Id	– Age difference between partners	– | male birth year – female birth year |
Assortative mating by age (categorical)	– Id	– Age homogamy (0–2 years of difference) – Age hypergamy (male 3+ years older) – Age hypogamy (woman 3+ years older)	– Id birth year – Partner birth year

individual and their parents are born in the United States, we classify them as native individuals with native parents. In cases where the individual is born in the United States but has at least one parent born outside the country,[1] we classify them as second-generation. To include an additional level of detail, we add in the models a variable accounting for the number of parents born inside or outside the United States. Individuals who were born outside the United States are classified as first-generation migrants.[2] We apply the same methodology to compute the corresponding variables for partners.

We constructed a measure of assortative mating based on geographical origin using the migration information. If both the individual and their partner share the same migration background, we consider them to be homogamous, while they are classified as heterogamous if their migration histories differ. We apply the same categorization to parents. We further build a variable indicating whether the partners were born in the same country.

As for age assortative mating, we developed two measures. As suggested by Kolk, age heterogeneity and age hypergamy are two theoretically different dimensions. The first indicates just the age gap between the partners, and it is used as an indicator of the egalitarian nature of the union (Kolk, 2015). Empirically, it can be calculated in our data as the absolute difference between the year of birth of the male partner and that of the female partner. Age hypergamy rather indicates the gendered dimension of age assortative mating, which can be grounded in gendered age preferences and can have gendered consequences for partners in the union (Kolk, 2015). We created a categorical variable that identifies whether an individual is in an age homogamous (with a difference of 0 ± 2 years), hypergamous (with the man at least 3 years older), or hypogamous (with the woman at least 3 years older) couple. Table 1 provides a summary of the characteristics of the main variables for our analyses.

We exploit a set of additional variables: the 50-years birth cohorts (1700–1749, 1750–1799, 1800–1849, 1850–1909), the state where the individual died, and the share of individuals with a migration background in the birth cohort calculated from FamiLinx data.

5.3. Methods

5.3.1. Mating trends description

We calculated crude rates of migration homogamy and heterogamy for moving birth cohorts of 10 years.[3] Additionally, we document the prevalence of age pairing categories across birth cohorts and track the trend in the absolute age difference within couple arrangements based on geographical origin (both natives, both migrants, mixed).

5.3.2. Association between partners' migration background

We employ log-linear analysis to examine how the association between partners' migration histories evolved, while accounting for historical changes in marginal distributions (Hout, 1983). Specifically, we utilize the log-multiplicative layer effects model (Xie, 1992), which is well-suited for investigating changes across groups, such as cohorts. The model is represented as follows in Equation 1:

$$\log F_{ijk} = \lambda + \lambda_i^{R} + \lambda_j^{C} + \lambda_k^{L} + +\lambda_{jk}^{RL} + \lambda_{ij}^{CL} + \exp(\psi_{ij}\varphi_k) \tag{1}$$

$logF_{ijk}$ is the natural logarithm of the expected frequency in cell (*I,j,k*), $\lambda_i^R, \lambda_j^C, \lambda_k^L$ the marginal effects of *R* (row), *C* (column) & *L* (layer), $\lambda_{ik}^{RL}, \lambda_{jk}^{CL}$ the two-way interactions *R*x*L* and *C*x*L*. The parameters of interest are ψ_{ij}, which expresses the origin-destination association, and φ_k, which indicates the origin-destination association levels for different layers being compared. It expresses in relative terms how much the association between R&C varies between layer *k* and layer *k**. We specify the model from a 2×2 marriage table in which the individual and his/her partner's migration history (R and C) are included (see Table 2), the layers (1700–1749, 1750–1799, 1800–1849, 1850–1909). The empirical marriage table can be found in Appendix A1. We show results for φ_k, that gives a measure of changes in the association between variables across time. Further estimates are shown in Appendix A1.

5.3.3. Association between parents and children's mating behavior

We apply Eq. 1 to a 2×2 intergenerational contingency table in which the individual mating (homogamy and heterogamy) corresponds to the row (R), and the parents' is the column (C) (see Table 3). The empirical table and further estimates are in Appendix A2.

Table 2. Marriage table for partners' migration histories.

		Partner's migration background	
		Native	*Migration background*
Id's migration background	*Native*	Homogamy	Heterogamy
	Migration background	Heterogamy	Homogamy

Table 3. Contingency table for individual's and parents' mating.

		Parents' mating	
		Homogamy	*Heterogamy*
Id's mating	*Homogamy*	Persistence	Difference
	Heterogamy	Difference	Persistence

5.3.4. *Assortative mating as a multidimensional process*

We use multinomial regression models to analyze the categorical variable of age difference (age homogamy, age hypergamy, and age hypogamy). This variable is modeled as a function of mating by migration background (homogamy/heterogamy) and migration background (native/1st gen/2nd gen). We include interaction terms to examine potential heterogeneities across groups. Our models also incorporate the birth cohort, the individual's death state to account for regional variations, and the share of migrants in the birth cohort to control – although indirectly – for the mating market structure. Additionally, we consider other couples' characteristics, such as similarity in country of origin and the number of parents born in the United States. We conduct separate models for men and women and present the results as predicted probabilities by migration background and birth cohorts.

6. Results

6.1. *Trends in mating patterns*

Figure 2 illustrates the trends in rates of homogamy and heterogamy based on migration history across different birth years. In this analysis, we grouped first and second-generation migrants into a broader category of migrants and examined mobile cohorts of 10 years. Notably, we observed distinct patterns in trends between individuals with a migration history in their families (1st or 2nd generation) and natives (individuals whose parents were born in the United States). Throughout the two centuries, natives consistently displayed higher rates of homogamy.

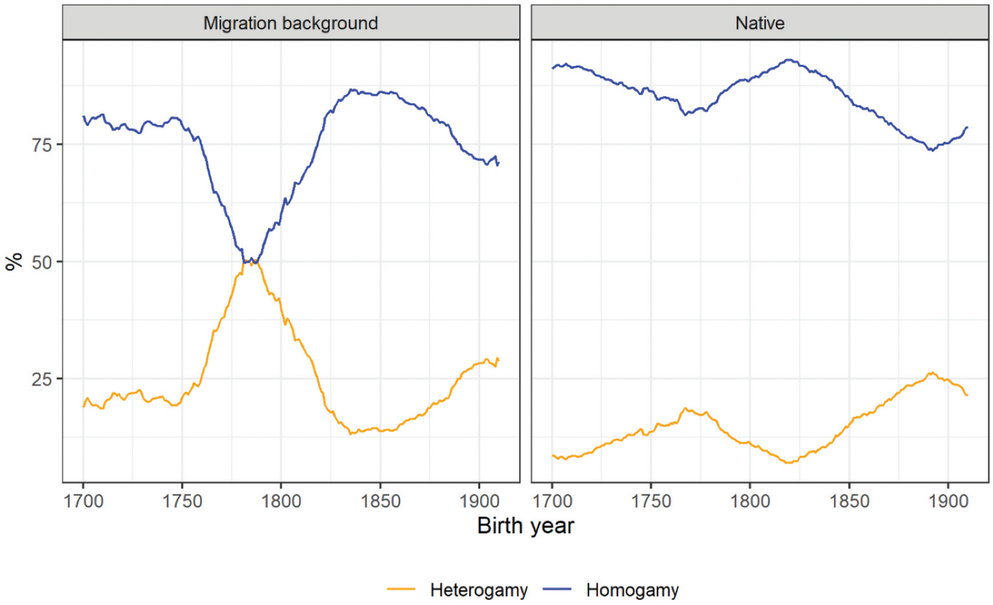

Figure 2. Rates of homogamy and heterogamy by birth cohort and migration histories, 1700–1910.

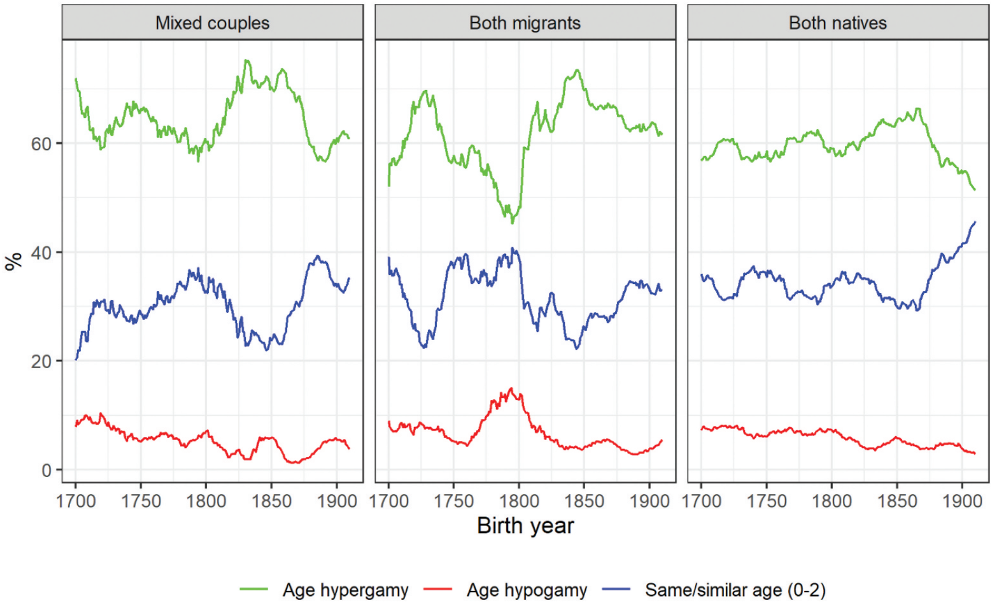

Figure 3. Trends in assortative mating by age, 1700–1910.

Another noteworthy aspect is the cyclic pattern observed in the trends, particularly among individuals with migration histories. We identified two significant drops in rates of homogamy, which coincided with two prominent migration waves in the history of the United States: the wave spanning 1820–1860 and the Mass Migration Era (1870–1920) (Martin, 2021).

Figure 3 presents the trends in assortative mating by age for individuals born between 1700 and 1910. The trends are depicted based on the type of couple, including both natives, both migrants, and mixed couples. Throughout the analyzed time period and across all couple types, male hypergamy (where the man is older by more than 3 years) is the predominant age arrangement. It remains consistent over time. Age homogamy follows as the second most prevalent arrangement, while female hypergamy represents approximately 10% of couples throughout the years.

In addition to these consistent patterns, there are noticeable differences and changes in trends. Couples in which both partners are migrants exhibit greater fluctuations in their age arrangements, particularly in birth cohorts from the late 18th and 19th centuries. Furthermore, there is an increasing trend towards age homogamy among individuals born in the late 19th century, particularly among native and mixed couples, as it has been documented in other Western countries (Van de Putte et al., 2009).

The trend of growing age homogamy at the end of the 19th century is further supported by examining the changes in the absolute age difference between partners, as illustrated in Figure 4. The average age difference is approximately 5 years, with an initial increase observed in cohorts from the first half of the 19th century. However, this is followed by a notable decrease in subsequent generations.

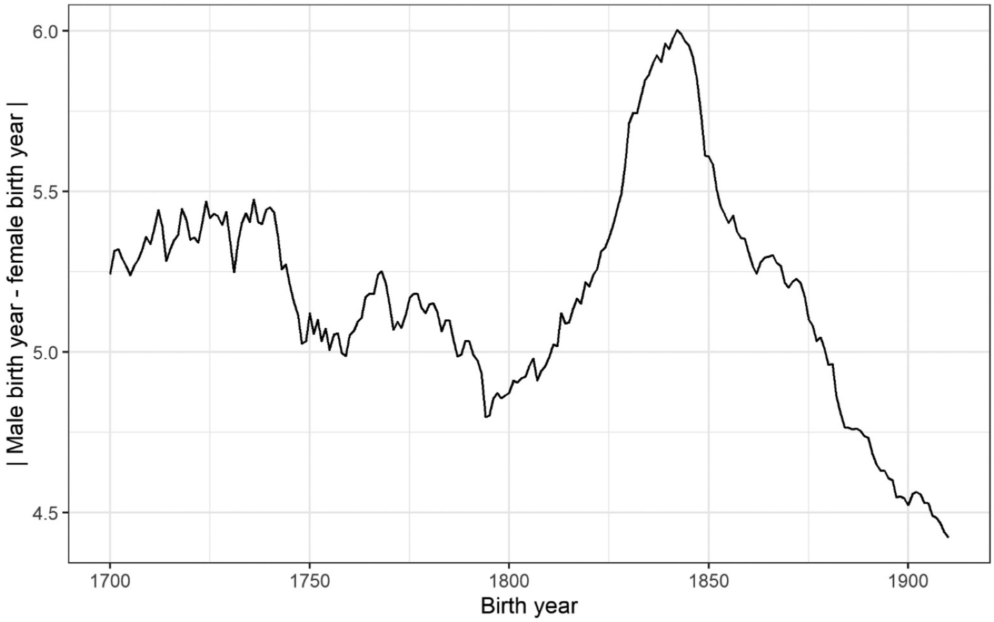

Figure 4. Trends in the absolute value of age difference between partners, 1700–1910.

6.2. Association between partners' migration background

Figure 2 reveals a cyclic pattern in the trends of assortative mating by migration, indicating lower rates of homogamy in specific birth cohorts. However, it is crucial to determine whether these trends result from changes in the population composition or actual shifts in partner choice criteria. To address this question, log-linear models are valuable as they enable control over marginal distributions. In our analysis, we apply these models to marriage tables, provided in Appendix A1, and examine them separately for each birth cohort.

Specifically, we model the association between an individual's migration profile (native or migration history) and their partner's migration profile across different birth cohorts. The log-multiplicative layer effect serves as the framework for our analysis, with birth cohorts acting as the layers. In Table 4, we present the φ_k parameters, which allow us to interpret the extent of changes in the association between partners' migration histories compared to the reference birth cohort (1700–1749). Additional model measures such as k coefficients and measures of fit can be found in Appendix A1 and A2.

Table 4. Layer coefficients, multiplicative-log effect layer model of partners' migration background association.

Birth cohorts	Exp (estimate)	Estimate	Std. Error	Quasi SE	Pr(>|z|)
1700–1749	1.00	0.00	0.00	0.02	NA
1750–1799	0.67	−0.40	0.04	0.04	***
1800–1849	1.06	0.06	0.03	0.03	0.1
1850–1910	0.74	−0.29	0.03	0.02	***

*** 0.00 ** 0.01 × 0.05

Table 4 provides insights into the relative changes in the φ_k parameters across different birth cohorts. Consistent with the observed trends in Figure 2, we observe significant decreases in the association between partners' migration histories in the cohorts of 1750–1799 and 1850–1910 compared to the cohorts of 1700–1749 and 1800–1849. This confirms that, even when controlling for changing marginal distributions, the cyclic pattern of partner choice remains evident. It suggests that partner choice criteria, including personal preferences and the influence of third parties, may undergo transformations within a context characterized by substantial changes in the population structure.

6.3. Association between parents and children's mating behavior

We explore the intergenerational persistency of mating behavior across birth cohorts using log-linear modeling. To analyze this, we apply the model to the intergenerational contingency tables provided in Appendix A2. In these tables, the rows represent the mating behavior of children, while the columns represent the mating behavior of their parents.

Table 5 presents the φ_k parameters across various birth cohorts. Surprisingly, we observe a remarkable stability in the association between parents' and children's mating behavior, despite significant changes in the population structure over time. However, there is a notable reduction in the intergenerational persistency of mating behavior in the 1850–1910 cohort. This cohort demonstrates a lower degree of persistence than the previous cohorts, suggesting a shift in mating patterns during this period.

6.4. Assortative mating as a multidimensional process

We delve into assortative mating as a multidimensional process, specifically examining the dimensions of migration background and age. We explore two different scenarios based on prevailing theories: the by-product hypothesis and the status exchange theory. To present our findings, we utilize predicted probabilities for various age pairing outcomes (homogamy, hypergamy, or hypogamy) stratified by sex and migration background.

Figure 5 focuses on natives and provides valuable insights. Firstly, we observe that the trends in age homogamy outcomes align with what we observed in the descriptive section. There is an increasing trend of age homogamy across birth cohorts, accompanied by a decrease in age hypergamy. Notably, we identify differences between women and men in these outcomes. Among women, those in homogamous partnerships (indicated by the orange dot) exhibit higher levels of age homogamy

Table 5. Layer coefficients, multiplicative-log effect layer model of parents' and children's mating behavior association.

Birth cohorts	Exp (estimate)	Estimate	Std. Error	Quasi SE	Pr(>|z|)
1700–1749	1.00	0.00	0.00	0.06	NA
1750–1799	0.85	−0.16	0.09	0.07	0.1
1800–1849	1.05	0.04	0.09	0.07	0.59
1850–1910	0.39	−0.95	0.12	0.11	***

*** 0.00 ** 0.01 × 0.05

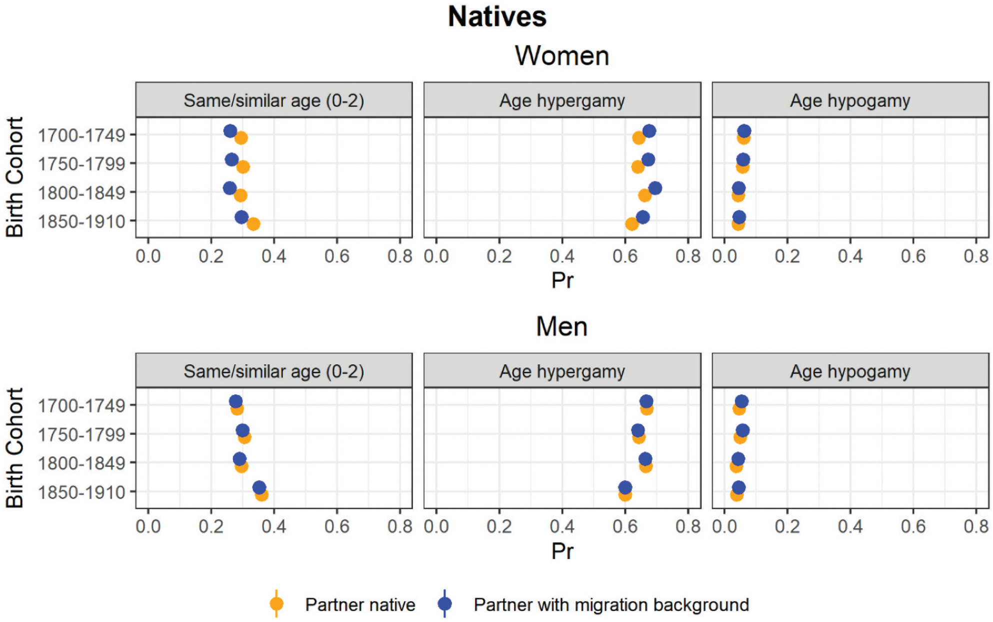

Figure 5. Predicted probabilities of age homogamy, male hypergamy and hypogamy conditional to mating and migration background. Natives, women and men.

(left panel) and lower levels of age hypergamy (middle panel) compared to women in heterogamous partnerships (represented by the blue dot). However, no significant differences are found for age hypogamy. In contrast, among men, we do not find such evidence, as there are no notable differences in age homogamy outcomes based on mating by migration. This finding supports the by-product hypothesis and suggests a gendered dynamic in the mating market. Women may have had access to a more homogeneous mating market in terms of geographical and age composition, possibly due to their relatively limited access to diverse environments like the labor market.

The picture interestingly changes when we look at first-generation migrants (Figure 6). First, they display lower levels of age homogamy than natives across all birth cohorts, and higher rates of age hypogamy.

Surprisingly, we observe that migration homogamy (represented by the orange dot) is associated with higher levels of age hypogamy than marriages where one partner has a migration background (indicated by the blue dot), regardless of gender. This result suggests the presence of sex-biased dynamics within the mating market. Given that women constituted a smaller proportion of the migrant population (Martin, 2021), they may have been exposed to an excess of young men, creating room for non-traditional age pairings.

Turning our attention to second-generation individuals (Figure 7), we observe a shift in the pattern. They exhibit levels of age homogamy comparable to those of natives, indicating a potential assimilation process. When considering age homogamy outcomes, we once again detect a gendered pattern. Among women, homogamy by migration background (i.e. partnering with a migrant with a migration

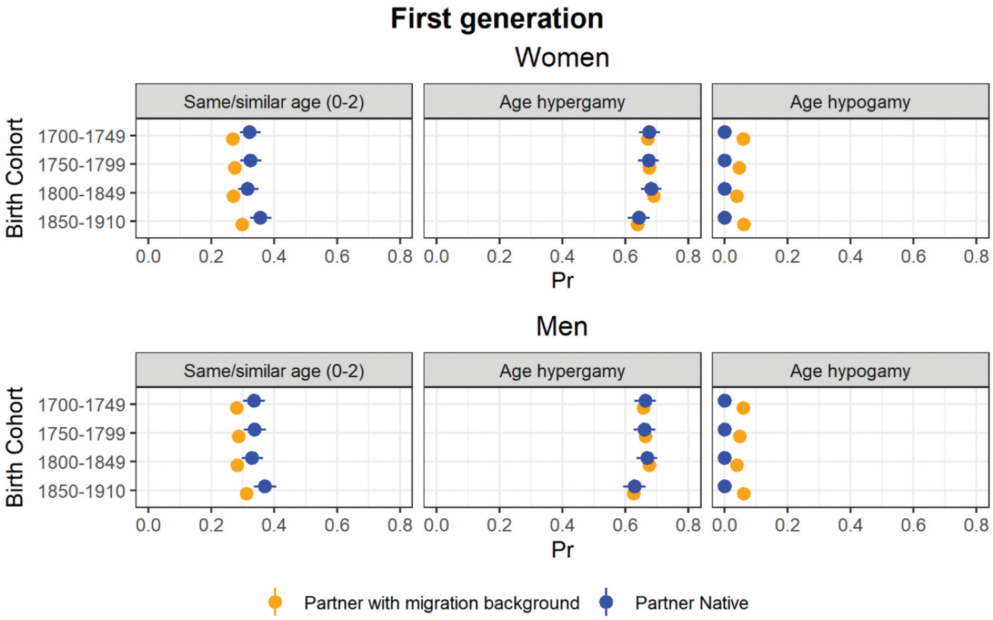

Figure 6. Predicted probabilities of age homogamy, male hypergamy and hypogamy conditional to mating and migration background. First generation migrants, men and women.

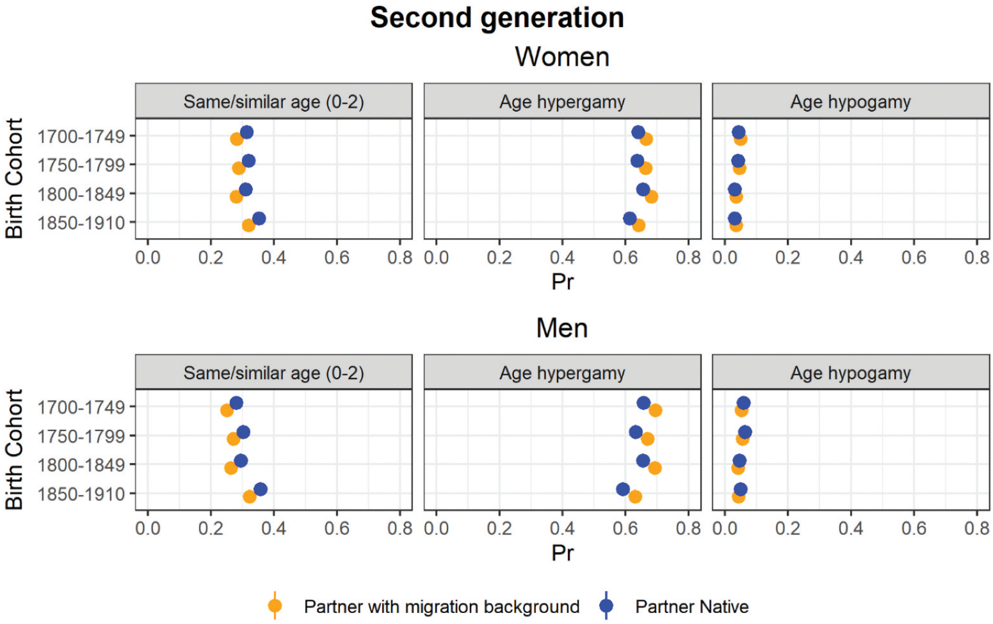

Figure 7. Predicted probabilities of age homogamy, male hypergamy and hypogamy conditional to mating and migration background. Second generation, men and women.

history) is associated with lower age homogamy than intermarriages. Conversely, homogamy by migration history is linked to higher levels of age hypergamy. This finding supports to the exchange hypothesis, suggesting that when individuals partner within the migrant group, there is evidence of a potential trade-off involving age as a trait.

7. Discussion and conclusion

Family networks are complex social structures influenced by various factors, including individual choices related to fertility, marriage, and migration. These decisions, made across generations, shape the dynamics of families and have long-lasting effects on society. Among these decisions, marriage and assortative mating play a particularly significant role in how families reproduce themselves, both in terms of biological reproduction (through fertility) and social reproduction (through the transmission of resources and social advantages). Consequently, exploring and understanding long-term patterns of assortative mating is a crucial area of study in the social sciences. By examining how individuals select their partners based on various characteristics, such as socioeconomic background, education, and cultural factors, we can gain valuable insights into the evolution of societies over time and the mechanisms that contribute to the reproduction of social inequalities.

Online platforms have provided unprecedented access to vast amounts of data. One area that has benefited from these developments is the study of historical societies. Online genealogical data, in particular, has emerged as a valuable resource for investigating patterns of longevity, fertility, and population dynamics in the past (Blanc, 2021; Hsu et al., 2021; Kaplanis et al., 2018). In this study, we take advantage of the FamiLinx dataset, a rich source of genealogical information that offers extensive coverage across different time periods and geographical locations. Using this dataset, we documented assortative mating in the United States, focusing on individuals born between 1700 and 1910.

Our study uncovers three significant findings regarding assortative mating. Firstly, we reveal that the trends in partner selection, specifically concerning geographical origins, do not follow a consistent trajectory over time. Instead of a linear progression towards increased heterogamy, we observe fluctuations concentrated within specific birth cohorts. This pattern aligns with previous research by Haines (1996) and Fitch and Ruggles (2000), which highlight the sensitivity of mating behaviors to shifts in the social and economic landscape, such as migration waves. These findings emphasize the dynamic nature of mate selection and its responsiveness to broader societal changes, that should be pursued as a future venue for research in the long-term trends of assortative mating.

Second, our study uncovers significant variations among different groups, shedding light on the complexities of assortative mating. We find that migrants' mating behavior is more responsive to changes than natives, and this could be due also to the differences in group sizes. Additionally, we observe that women are particularly sensitive to the interplay between age and geographical origin, whereas men exhibit less pronounced patterns. These findings underscore the multidimensional nature of mate selection, where various dimensions interact and vary depending on individual characteristics. The observed differences between men and women in mating dynamics may be attributed to their distinct societal positions throughout history (Sassler, 2005).

Third, an intriguing finding of our study is the notable slowdown in processes when shifting the focus from the individual to the family level. Intergenerational reproduction of mating behavior proves to be remarkably persistent and consistent across time, highlighting the significance of carefully considering the unit of analysis in investigations of long-term social trends.

It should be acknowledged that in this paper we aimed to document long-term trends of assortative mating. The exploration of the underlying mechanisms and the association with historical events and developments are beyond our scope. We find indications that changes in marriage choices coincide with major migrant waves, that notably changed the American marriage market and society (Martin, 2021), but we are not able to further investigate these aspects; an interesting venue for future research would be the integration of online crowdsourced genealogical data with other sources that allow measuring historical processes and events.

Nevertheless, it is crucial to acknowledge the limitations of our work. The reliance on reconstructed individual and family background information introduces a strong selection bias to our sample. As demonstrated in Appendix C, data availability constraints result in sample restrictions. Individuals who provide detailed and complete information are likely a subset of the population that is positively selected based on various characteristics. For instance, missing information tends to be more prevalent in earlier periods and diminishes gradually over time. Those with comprehensive information on individual traits and family networks are more likely to belong to groups that exhibit positive selection based on factors such as socioeconomic background, geographic location, and educational attainment (Minardi et al., 2023).

Moreover, genealogies of ascendant types, like FamiLinx, may be susceptible to additional sources of bias (Hollingsworth, 1976). It should be noted that childless individuals are unlikely to be represented in the data, which can be relevant as childless couples may display selectivity in terms of individual and couple characteristics. These considerations emphasize the importance of carefully acknowledging potential biases when utilizing crowdsourced genealogical data (Chong et al., 2022; Minardi et al., 2023; Stelter & Alburez-Gutierrez, 2022).

Notes

1. Because of the limited sample size, we are not able to further distinguish geographical areas.
2. Among first-generation migrants, we exclude individuals whose first child was born in the country of origin. This selection allows us to indirectly include individuals in our sample who formed a couple in the United States.
3. We calculate estimates on a sample defined as the reference year from 1700 to 1900 plus and minus ten years – i.e. 1690 (1700) 1710, 1691 (1701) 1711, 1692 (1702) 1712 . . . 1890 (1900) 1910. This allows us to avoid a strict separation between cohorts and maximize sample size.

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