

Fertility and Modernity*

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Abstract

We investigate the historical dynamics of the decline in fertility in Europe and its relation to measures of cultural and ancestral distance. We test the hypothesis that the decline of fertility was associated with the diffusion of social and behavioral changes from France, in contrast with the spread of the Industrial Revolution, where England played a leading role. We argue that the diffusion of the fertility decline and the spread of industrialization followed different patterns because societies at different relative distances from the respective innovators (the French and the English) faced different barriers to imitation and adoption, and such barriers were lower for societies that were historically and culturally closer to the innovators. We provide a model of fertility choices in which the transition from higher to lower levels of fertility is the outcome of a process of social innovation and social influence, whereby late adopters observe and learn about the novel behaviors, norms and practices introduced by early adopters at the frontier. In the empirical analysis we study the determinants of marital fertility in a sample of European populations and regions from 1830 to 1970, and successfully test our theoretical predictions using measures of genetic distance between European populations and a novel data set of ancestral linguistic distances between European regions.

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1 Introduction

The transition from high to low fertility has been a central feature of the process of modernization over the last two hundred years. However, what explains the fertility transition remains a theoretical and empirical puzzle.¹ At one extreme is the view, which comes naturally to economists, that fertility decline and modern economic development are two sides of the same coin. As societies increase their productivity and income per capita through industrialization and technological progress, fertility rates decline. A causal mechanism going from higher income to lower fertility is at the center of Becker's (1960) classic argument that industrialization led to lower fertility, by increasing the opportunity cost of raising children. Conversely, the standard Solow model predicts that lower population growth will be associated with higher income per capita in steady state. At the other extreme is the view, more popular among some demographers and anthropologists, that the decline in fertility is not the outcome of economic calculation and adaptation to a changing economic and social environment. For instance, supporters of a non-economic view of fertility decline, such as the contributors to the landmark Princeton European Fertility Project (Coale and Watkins, 1986), argued that the pattern of fertility transition in Europe during the 19th and 20th centuries is not consistent with simple stories linking industrialization and lower fertility. According to the Princeton project data, European societies at relatively lower levels of economic development and industrialization experienced a decline in fertility at the same time, or even before, economically more advanced societies.² In sum, the determinants of the fertility decline in Europe and its relation with other economic and social variables remain a mystery.

In this paper we provide a new empirical analysis of the determinants of marital fertility in a sample of European populations and regions from 1830 to 1970, using a novel data set of ancestral and linguistic distances between European regions. Our key hypothesis is that the fertility decline can best be understood as a process of diffusion of new social norms and behavioral changes, spreading from early adaptors to imitators. In this respect, the fertility transition was similar to the spread of productivity-enhancing innovations associated with the diffusion of the Industrial Revolution from England to other societies, which we studied in previous work (Spolaore and

¹For recent in-depth discussions of the literature, see Galor (2011, chapter 4) and Guinnane (2011).

²Coale and Watkins (1986). See also Galor (2011, chapter 4, p. 118). For a critical discussion of the Princeton project's methodology and conclusions see Guinnane, Okun and Trussel (1994), Brown and Guinnane (2007) and Wetherell (2001).

Wacziarg, 2009, 2011, 2013, 2014). However, a key difference between the diffusion of fertility decline and the diffusion of industrialization is that the two processes started at *different frontiers*. In this paper, we formulate and successfully test the hypothesis that the decline of fertility was associated with the diffusion of social and behavioral changes from France, in contrast with the spread of the Industrial Revolution, where England played a leading role. We argue that the diffusion of fertility decline and the spread of industrialization followed different patterns because societies at different relative distances from the respective innovators (the French and the English) faced different barriers to social learning, imitation, and adoption. In particular, we test empirically the hypothesis that barriers to the diffusion of the fertility transition were lower for societies that were historically and culturally closer to the innovators (the French), finding considerable empirical support for this hypothesis.

Our findings help assess and partly reconcile conflicting views about the spread of fertility decline in Europe. On the one hand, these results show that the historical fertility transition and the spread of the industrial revolution were indeed separate processes, with different early adopters and different patterns of diffusion and imitation. At the same time, however, once cultural and linguistic barriers are factored in, both the spread of industrialization and the fertility transition can be understood theoretically and empirically as processes of choice by individuals and groups faced with new information about behaviors, outcomes, and norms in related societies. In particular, our empirical findings are consistent with a theoretical framework where marital fertility is the outcome of rational household choices that take into account both intrinsic costs and benefits from fertility and social norms regarding fertility control.

Our analysis builds on the recent literature on the economics of social distance, social influence and social interactions.³ In our model, the transition from higher to lower levels of fertility is the outcome of a process of social innovation and social influence, where late adopters observe and learn about the novel behaviors, norms and practices introduced by earlier adopters at the innovation frontier. In the empirical analysis we successfully test the implications of the theoretical framework, including predictions about the timing of the fertility transition in different societies, and about the dynamics of the relationship between average fertility levels and relative social distance from

³For example, see Akerlof (1997) for an analysis of choice with social preferences and social distance, Young (2009) for a study of the diffusion of innovations in models of social influence and social learning, Fogli and Veldkamp (2011) for the diffusion of female labor force participation in the United States, and Ioannides (2013) for an in-depth general overview and discussion of the growing literature on the economics of social interactions.

the earlier adopters.

Section 2 presents a theoretical framework to guide the empirical analysis in the rest of the paper. Section 3 studies the spread of marital fertility decline across a sample of 37 European populations. Section 4 extends the empirical analysis of marital fertility transition to a sample of 775 European regions, using a new dataset of linguistic distances which we constructed based on the distribution of 275 ancestral regional languages in Europe. Section 5 concludes.

2 Fertility Decline: A Conceptual Framework

2.1 Context and Literature

The transition from high fertility to low fertility, occurring in society after society since the 19th century, is one of the most important and consequential phenomena in modern human history, and has spurred an enormous theoretical and empirical literature across multiple disciplines. Within this literature, an ongoing debate concerns the role played by economic mechanisms and choices. At one extreme is the view that the fertility decline is the direct outcome of economic forces and rational household decisions. Followers of this economic approach have mostly focused on changes in production, human capital and labor markets that directly or indirectly affect the trade-off between the benefits and costs from having children.⁴ At the other extreme is the view, held for instance by some anthropologists and sociologists, that economic forces and rational choices are not responsible for the demographic transition. Support for this non-economic view came from the already mentioned Princeton Project on the Decline of Fertility in Europe (Coale and Watkins, 1986). According to the leading authors of the Princeton Project, the decline in fertility could not be explained as the result of adaptation to different economic and social forces in different societies because, according to these authors, almost all European societies - even though they differed in economic and social traits - transitioned to lower levels of fertility roughly simultaneously. The authors of the Princeton Project interpreted this evidence as supportive of a *diffusion* interpretation of the fertility transition, which they viewed as an alternative to explanations based on a rational adaptation to changing economic forces.

In the subsequent debate, critics (Guinnane, Okun and Trussell, 1994; Brown and Guinnane,

⁴For an excellent overview, see for instance Galor, 2011, chapter 4. For a recent study arguing that human capital was the driving force behind the demographic transition in a worldwide sample of countries, see Murin (2013).

2007) pointed out several conceptual and methodological issues with the Princeton Project's non-economic conclusions. For instance, the Princeton Project non-economic interpretation was based on the presumption of a simultaneous adoption of the new fertility behavior by all households across heterogeneous societies. Instead, critics of the Princeton Project noted that the data are not inconsistent with a more gradual transition, in which minorities of households within different societies may have significantly increased their use of fertility control methods, before such behavior spread to most other households in their society (Guinnane, Okun and Trussell, 1994, p. 3).

In spite of its methodological limitations, the Princeton Project provided a wealth of regional data that are still unmatched for the comparative study of fertility decline across European regions in the past two hundred years. In particular, the evidence collected at the regional level by scholars associated with the Princeton Project strongly suggested that cultural variables played an important role in the spread of fertility controls. For instance, in Belgium during the 19th century "the early adoption of fertility control [...] stopped at the language border. Not only did Flemings and Walloons who lived as neighbors in this very narrow strip along the language border fail to intermarry to a considerable extent, but they also did not take each other's attitude toward fertility. As a result, two separate diffusion patterns developed in Flanders and Wallonia" (Lesthaeghe, 1977, p. 227). However, to our knowledge, no systematic attempt has been made by either economists or non-economists to formally quantify social and cultural barriers to the diffusion of fertility controls across different European regions and to relate them explicitly to the dynamics of the fertility transition.

Our goal is to help close that gap, while providing a theoretical and empirical analysis of fertility decline that partly reconciles the conflicting views in the literature. On the one hand, we pursue an economic approach where fertility is the outcome of social and economic forces that affect household choices and behavior. However, as part of those forces, we explicitly model mechanisms - such as social influence and cultural distances - that are not typically included in economic studies of fertility. In this respect, this paper is part of a recent but growing economic literature on the theory and empirics of social and cultural variables and interactions.⁵ We do interpret the process of fertility decline in Europe as a process of diffusion, in which social and cultural barriers have played a central role. However, as detailed in the rest of this section, we model this diffusion process

⁵On the economics of social interactions see for instance Akerlof (1997), Durlauf and Ioannides (2010) and Ioannides (2013). On economics and culture see for example Bisin and Verdier (2001, 2010), Spolaore and Wacziarg (2013), Alesina and Giuliano (2013) and Spolaore (2014).

within an economic framework in which households adopt novel social norms and behavior as part of conscious decisions, in response to a changing social and economic environment.

2.2 A Model of Fertility Choice

2.2.1 The Basic Framework

Consider a household i that chooses marital fertility f_i to maximize the following indirect utility:

$$U_i = bf_i - \frac{c}{2}f_i^2 - \sigma(f_n - f_i) \quad (1)$$

where $f_i \leq f_n$. The first two terms capture standard intrinsic benefits and costs from fertility, such as the utility associated with children and the opportunity costs, in terms of foregone consumption, from raising them.⁶ The third term captures the costs of reducing fertility below a natural or normal level f_n : In order to reduce fertility below the natural level, agents must incur costs, measured by the parameter σ . A possible interpretation of this parameter could be technological, as a function of the availability of fertility-control technologies (i.e., contraceptive devices). In this case, a high σ would mean costly contraception, while the introduction of innovations that allow more effective and less costly fertility controls would be captured by a lower σ . f_n can be interpreted as the maximum level of fertility that is typically achieved biologically by a household when no fertility control is exercised. At the limit, if fertility controls were completely costless ($\sigma = 0$), the household would just choose the intrinsically optimal level of fertility b/c . A broader interpretation of the parameter σ , which we prefer, is in terms of social norms: Agents pay a marginal social cost σ when choosing fertility below the normal level f_n .⁷ By the same token, the natural level f_n can be interpreted not just as a biological outcome, but also as a socially and culturally determined level - that is, as the

⁶This reduced-form specification is chosen for analytical convenience, along the lines of Akerlof's (1997) simple model of social interactions. The term "intrinsic" utility for the first two terms is also borrowed from Akerlof (1997). Specific models of fertility choice stemming from trade-offs between benefits from having children and costs to raise them are provided for instance in Galor (2011, chapter 4). In Galor's model (2011, p. 120), a household's optimal number of children is given by the ratio between a parameter capturing the direct utility of children and a parameter capturing the opportunity cost of raising a child as a fraction of the parental unit-time endowment. Such models could be extended to include the social costs from fertility control, analogous to those introduced in our basic reduced-form specification.

⁷In this respect σ , when interpreted in terms of social norms and social preferences, plays an analogous role to parameter d in Akerlof's (1997) analysis of social interactions.

normal level of fertility that would occur in a society when households decide not to adopt fertility control practices that are socially stigmatized.

The equilibrium choice of fertility in this model is:

$$f^* = \min\left\{ \frac{b + \sigma}{c}, f_n \right\} \quad (2)$$

It will prove useful to distinguish between traditional societies, where households choose $f^* = f_n < (b + \sigma)/c$, and modern societies, where households choose $f^* = (b + \sigma)/c < f_n$. A few observations are in order:

First, whether a society has traditional levels of fertility close to the natural level f_n or a lower level $f^* < f_n$ will depend, in general, on both intrinsic costs (c) and benefits (b) *and* on social norms (σ). A society may have very high levels of fertility ($f^* = f_n$) because of very high intrinsic benefits from fertility, very low intrinsic costs, and/or high social stigma associated with fertility control.

Second, in societies with very high intrinsic benefits from fertility relative to individual costs ($b/c > f_n$), households will always choose the maximum level of fertility, independent of the costs of fertility controls σ . In such a world, therefore, social norms that limit fertility controls ($\sigma > 0$) do not have an effect on actual fertility choices, and do not reduce indirect utility below what it would have been in the absence of social norms. In contrast, in societies where $b/c < f_n$, households would choose a level of fertility below f_n in the absence of social costs associated with fertility control ($\sigma = 0$). In such societies, a change in σ does matter for choices, and does affect indirect utility.

Third, the effects of intrinsic costs and benefits on observed fertility choices differs depending on social costs. In a traditional society that attaches high social costs to fertility controls (formally, as long as $\sigma > cf_n - b$), relatively small changes in b or c will not be reflected in fertility choices. In such a society, only a major shock to the parameters, in particular a dramatic fall in σ , would produce a reduction in fertility and a transition to a modern equilibrium where $f^* = (b + \sigma)/c < f_n$. Conversely, once a society has transitioned to a lower-fertility equilibrium, and as long as $\sigma < cf_n - b$, changes in b and/or c would indeed be reflected in immediate changes in fertility. In sum, traditional societies with very high social stigma associated with fertility control would not respond much to changes in the intrinsic benefits and costs of fertility, while fertility would tend to be much more sensitive to those intrinsic costs and benefits in modern societies with lower (or even zero) values of σ .

Overall, fertility choice can be in one of three possible equilibria, depending on the value of the parameters:

1) *Intrinsically optimal traditional equilibrium*: $f^* = f_n < b/c$ for all $\sigma \geq 0$. In this case, a high natural fertility is intrinsically optimal, and households have no private incentives to lower their fertility even in the absence of social costs ($\sigma = 0$). In other terms, when intrinsic benefits from fertility are very high relative to intrinsic costs, social norms that impose additional social costs on lower fertility can emerge without reducing households' indirect utility. This can help explain how such social norms can emerge in equilibrium, and why in such a setting there are weak incentives for social change leading to lower σ 's.

2) *Intrinsically suboptimal traditional equilibrium*: $b/c < f^* = f_n \leq (b + \sigma)/c$. In this equilibrium, fertility is above the intrinsic optimum and social norms against fertility control are binding. Clearly, this equilibrium can hold only if parameter σ is strictly positive and large enough (formally, only for $\sigma \geq cf_n - b$). In this setting, a reduction in σ has positive effects on indirect utility.

3) *Modern equilibrium*: $f^* = (b + \sigma)/c < f_n$. In this equilibrium, fertility is below the natural level f_n . Fertility is at the intrinsic optimum for $\sigma = 0$ and above the intrinsic optimum for $\sigma > 0$.

This simple model captures both the effects of intrinsic costs and benefits and social norms. A prediction of the model is that a significant fall in the intrinsic benefits of fertility relative to its costs, while a precondition to make a decline in fertility intrinsically optimal, would not be sufficient to produce an actual fertility decline *unless* it is also accompanied by a significant change in the social norms associated with fertility control. Only when the social costs of fertility control become small enough, can the intrinsic benefits and costs of fertility take the driving seat. This stylized framework can therefore reconcile two conflicting views of fertility decline: the economic view that focuses on intrinsic costs and benefits and the social view that stresses social norms. Both sets of forces matter, but in different ways and at different points along the transition from traditional high fertility societies to modern low-fertility societies. In what follows we extend the model in order to derive explicitly the dynamics of the fertility transition within and across societies.

2.2.2 The Diffusion of the Fertility Decline

In the basic framework, household decisions are determined by their intrinsic benefits and costs from fertility and their perceptions of the social costs associated with fertility control. But where do those social costs come from, and how do they change over time? In this section we extend the

model to account for the possibility of social change, from traditional equilibria where $f^* = f_n$ to modern equilibria where $f^* < f_n$. As already mentioned, a reduction in social costs could lead to a shift from a traditional to a modern equilibrium only if intrinsic benefits over costs are already low enough. In other words, relatively low intrinsic benefits over costs are a precondition for a switch from a traditional equilibrium to a modern equilibrium, but they may not be sufficient in the absence of a significant reduction in σ . Therefore, in the rest of the analysis we only consider societies that are ripe for change, that is, societies where, for all households, $b/c < f_n$.

To fix ideas, consider three societies: X , Y and Z , each inhabited by a continuum of households with mass normalized to 1. At time $t < 0$, all households in the three societies are at an intrinsically suboptimal traditional equilibrium, where $b/c < f^* = f_n \leq (b + \sigma_0)/c$. At time 0 the innovator society X experiences a shock to its social norms, so that σ for all its household becomes $\sigma_1 < cf_n - b < \sigma_0$. Consequently, at time 0 society X goes to the new modern equilibrium $f^* = f_m \equiv (b + \sigma_1)/c < f_n$.⁸

The Dynamics of Social Influence. The change in social norms in society X will affect decisions in societies Y and Z through a mechanism of *social influence*.⁹ At each time $t > 0$, each household in society Y and Z considers whether to adopt the new social-norm parameter σ_1 (that is, to imitate the social innovator) or to stick to the old value σ_0 . While all households would gain from the switch in terms of intrinsic benefits net of intrinsic costs, each agent is willing to abandon the old social norms only if a *sufficiently large* number of other households have already adopted the new social norms. Consistent with the literature on social interactions and social distance (e.g., Akerlof, 1997), we assume that, when deciding whether to conform to the new or to the old social norms, each household in societies Y and Z will weigh the influence of other households based on their respective social distance. In general, social distance between two agents captures the extent to which the agents are likely to have socially valuable interactions, and therefore to care about each other's preferences and behavior and to learn from each other. In particular, we assume

⁸For simplicity, we assume that all households in society X experience the shift to the new modern equilibrium simultaneously. The model could be easily generalized to allow for a gradual diffusion of the new social norms *within* society X , starting from a subset of innovators, along the lines of the diffusion process from society X to societies Y and Z , discussed next. The qualitative results of the analysis would not be affected by this extension.

⁹For a general discussion of models of social influence and social learning, see Young (2009). For a recent application in the context of female labor force participation, see Fogli and Veldkamp (2011).

that the impact of a social innovator on a household will depend on what Akerlof (1997, p. 1010) calls "inherited" social distance between the two agents. In our empirical analysis, building on our previous work (Spolaore and Wacziarg, 2009, 2011, 2013, 2014), we measure such social distance in terms of distances in a set of intergenerationally transmitted traits - such as linguistic distances between ancestral dialects across different European regions.¹⁰

Let $d(i, j) = d(j, i)$ denote the social distance between agent i and agent j . For simplicity, we assume that all household within society Y are at a social distance $d(Y, Y) = 0$ from each other. By the same token, all households within society Z are at a social distance $d(Z, Z) = 0$ from each other. In contrast, each household in society Y is at a distance $d(X, Y) = d(Y, X) > 0$ from each household in society X , while each household in society Z is at a (larger) distance from each household in X . That is, $d(X, Z) = d(Z, X) > d(X, Y)$. Finally, households in societies Y and Z are at distance $d(Y, Z) = d(Z, Y) > 0$ from each other.

At time $t > 0$, a household i in society Y will adopt social norms σ_1 if and only if the mass of households that have already adopted these social norms, weighed by their social distance to i , is at least as large as household i 's critical threshold μ_i . Formally, household i in society Y will adopt the new social norms at time t if and only if:

$$\sum_{k=X,Y,Z} [1 - \beta d(Y, k)] M_{kt-1} \geq \mu_i \quad (3)$$

where M_{kt} denotes the mass of households in society k which have already adopted social norms σ_1 by time $t - 1$. By the same token, each household i in society Z will adopt the new social norms at time t if and only if:

$$\sum_{k=X,Y,Z} [[1 - \beta d(Z, k)] M_{kt-1} \geq \mu_i \quad (4)$$

The parameter β captures the impact of social distance on social influence, where $\beta \leq 1/d(k, j)$ for all $k \neq j$.¹¹ Moreover, to simplify the analysis we assume prohibitive barriers between society Y

¹⁰Interestingly, the relation between dialects and social distance has been explicitly discussed in the literature on social interactions. For instance, Akerlof (1997, p. 1015) wrote : "the existence of stable dialects for subgroups of a population can only be interpreted as due to the clustering of social interactions. [...] Thus dialects act as a diagnostic for social interaction."

¹¹More generally, the conditions could be written as: $\sum_{k=X,Y,Z} \max\{0, [1 - \beta d(Y, k)]\} M_{kt-1} \geq \mu_i$ and $\sum_{k=X,Y,Z} \max\{0, [1 - \beta d(Z, k)]\} M_{kt-1} \geq \mu_i$.

and Z . That is, $1 - \beta d(Y, Z) = 0$.¹²

We assume that households are heterogeneous with respect to their critical thresholds μ_i . That is, some households are willing to adopt the new social norms as long as those norms have been adopted by a relatively small number of other households, while other households will need to observe a much larger mass of modern households before changing their own social attitudes. An interpretation of such thresholds is that they measure the extent to which different households are conformist in their adoption of social norms and social innovations. Formally, we assume that, in each society critical thresholds μ_i 's are distributed uniformly over the continuum of households, between a minimum threshold $\mu_L \geq 0$ and a maximum threshold $\mu_H > \mu_L$.¹³

We are now ready to derive the dynamics of diffusion of new social norms within and across societies. In order to allow for *any* spread of innovations across societies, we assume that the minimum threshold μ_L is not too high:¹⁴

$$\mu_L < 1 - \beta d(X, Y) \tag{5}$$

At time 0, only the innovator society has adopted the new social norms, and therefore $M_{X0} = 1$, $M_{Y0} = M_{Z0} = 0$. At time 1, the new social norms are adopted by all households in society Y for whom the social threshold μ_i is smaller or equal to the mass of households who have already adopted the innovation in society X , weighed by their social distance. That is, all households such that:¹⁵

$$\mu_i \leq [1 - \beta d(X, Y)]M_{X0} = 1 - \beta d(X, Y) \tag{6}$$

Consequently, at time 1 the new social norms are adopted by the following fraction of households in society Y :

$$M_{Y1} = \min \left\{ \frac{1 - \beta d(X, Y)}{\mu_H - \mu_L}, 1 \right\} \tag{7}$$

¹²The derivation for the case $1 - \beta d(Y, Z) > 0$ is available upon request. Relaxing the simplifying assumption of prohibitive barriers between Y and Z significantly complicate the analysis without changing the fundamental results.

¹³For simplicity, we assume that such threshold distributions are identical in society Y and Z .

¹⁴If the case $\mu_L \geq 1 - \beta d(X, Y)$, no (positive mass of) households in society Y (and, a fortiori, in society Z) would ever adopt the new social norms introduced in society X , and, therefore, the social innovation would never spread across societies.

¹⁵In order to allow for *any* spread of innovations across societies, we assume that $\mu_L < 1 - \beta d(X, Y)$. In contrast, if we had $\mu_L \geq 1 - \beta d(X, Y)$, societies Y and Z would be so conformist that no positive mass of households in society Y (and, a fortiori, in society Z) would ever adopt the new social norms introduced in society X , and, therefore, the social innovation would never spread across different societies.

In society Z two cases are possible. For $\mu_L \geq 1 - \beta d(X, Z)$ (i.e., relatively high levels of societal conformism and/or high levels of inter-societal barriers $\beta d(X, Z)$), no household in society Z adopts the new social innovation at time 1. For $\mu_L < 1 - \beta d(X, Z)$, in contrast, a positive fraction of households in society Z will also adopt the new social norms introduced in society X . In that case, the mass of households adopting the new social norm will be given by:

$$M_{Z1} = \min \left\{ \frac{1 - \beta d(X, Z)}{\mu_H - \mu_L}, 1 \right\} \quad (8)$$

The number of adopters of new social norms is lower in society Z than in society Y - that is, $M_{Z1} \leq M_{Y1}$, because of the larger relative social distance from the innovator $d(X, Z) > d(X, Y)$. The only instance when $M_{Z1} = M_{Y1}$ is in the extreme case when all households in both societies adopt the new social norms immediately, which would occur at very low levels of barriers and/or conformism, that is, for $\mu_H \leq 1 - \beta d(X, Z)$.

At time 1, the average level of fertility in society Y is:

$$f_{Y1} = M_{Y1}f_m + (1 - M_{Y1})f_n \quad (9)$$

while the average level in society Z is:

$$f_{Z1} = M_{Z1}f_m + (1 - M_{Z1})f_n \quad (10)$$

In general, $f_{Z1} \geq f_{Y1}$, with the highest gap between f_{Z1} and f_{Y1} occurring when $f_{Z1} = f_n$, i.e. for $\mu_L \geq 1 - \beta d(X, Z)$. In contrast, there will be no gap ($f_{Z1} = f_{Y1}$) in the extreme case $M_{Y1} = M_{Z1} = 1$, i.e. for $\mu_H \leq 1 - \beta d(X, Z)$. In the rest of this analysis, we abstract from polar cases, and focus on the intermediate range of parameters in which a positive number of households, but not all households, adopt the novel behavior in society Z at time 1, that is, the case $\mu_L < 1 - \beta d(X, Z) < \mu_H$.

At time 2, in society Y the new social norms are adopted by all households with critical threshold μ_i such that:

$$\mu_i \leq 1 - \beta d(X, Y) + \frac{1 - \beta d(X, Y)}{\mu_H - \mu_L} \quad (11)$$

which implies the following number of modern households in society Y at time 2:

$$M_{Y2} = \min \left\{ \frac{1}{\mu_H - \mu_L} \left[1 - \beta d(X, Y) + \frac{1 - \beta d(X, Y)}{\mu_H - \mu_L} \right], 1 \right\} \quad (12)$$

By the same token, at time 2 in society Z the new social norms are adopted by all households with critical threshold μ_i such that:

$$\mu_i \leq 1 - \beta d(X, Z) + \frac{1 - \beta d(X, Z)}{\mu_H - \mu_L} \quad (13)$$

which implies the following number of modern households in society Z :

$$M_{Z2} = \min \left\{ \frac{1}{\mu_H - \mu_L} \left[(1 - \beta d(X, Z) + \frac{1 - \beta d(X, Z)}{\mu_H - \mu_L}) \right], 1 \right\} \quad (14)$$

and so on as t increases.

To further simplify notation and without much loss of generality, in the rest of the analysis we will assume $\mu_H - \mu_L = 1$. The general levels of M_{Yt} and M_{Zt} at time t can then be written as:

$$M_{kt} = \min\{t[1 - \beta d(X, k)], 1\} \quad (15)$$

where $k = Y, Z$.

The Relations between Timing of Transition, Fertility Levels, and Social Distances.

We can now study the relationship between social distance and the dynamics of the diffusion of novel norms of fertility. An immediate implication of the model is that, in a society at a lower social distance from the innovator, a given fraction of households will adopt modern norms, and therefore a lower level of fertility, *earlier* than in a society at a higher social distance. Formally, let $M^\#$ denote the fraction of modern households such that average fertility is given by a given level $f^\# < f_n$, that is:

$$f^\# = M^\# f_m + (1 - M^\#) f_n \quad (16)$$

Let $T(f^\#)$ denote the *earliest* time at which such a level $f^\#$ is achieved. It is immediate to see that $T(f^\#)$ occurs earlier for society Y at distance $d(X, Y)$ than for society Z at distance $d(X, Z) > d(X, Y)$:

$$T_Y(f^\#) < T_z(f^\#) \quad (17)$$

An important special case is when the society has completely transitioned to the new lower level of fertility, i.e. $M^\# = 1$ and $f^\# = f_m = \frac{b + \sigma_1}{c}$. Formally, and abstracting from the fact that T must be an integer, we can write the following general closed-form solution for the time when a society at social distance $d(k, X)$ will reach a level of modernization equal to $M^\#$ with fertility equal to $f^\#$:

$$T_k(f^\#) = \frac{M^\#}{1 - \beta d(k, X)} \quad (18)$$

As an important special case, the time at which a given society at distance $d(k, X)$ will achieved full modernization ($M^\# = 1$ and average fertility equal to f_m) is given by:

$$T_k(f_m) = \frac{1}{1 - \beta d(k, X)} \quad (19)$$

Therefore, the model has a straightfoward empirical implication, linking fertility transition time to social distance from the innovator:

Proposition 1: *Societies at a smaller social distance from the social innovator experience an earlier transition to lower fertility*

In the empirical section, we will directly test this prediction.

The model also implies direct and testable predictions with respect to the patterns of fertility in different societies, and the dynamics of their relations with relative social distance from the innovator. A numerical example will help illustrate such predictions. Assume that $\beta d(X, Y) = 2/3$ and $\beta d(X, Z) = 4/5$. Then, the two societies will experience transitions to lower fertility as detailed in the following table:

Time	M_{Yt}	f_{Yt}	M_{Zt}	f_{Zt}
1	1/3	$\frac{1}{3}f_m + \frac{2}{3}f_n$	1/5	$\frac{1}{5}f_m + \frac{4}{5}f_n$
2	2/3	$\frac{2}{3}f_m + \frac{1}{3}f_n$	2/5	$\frac{2}{5}f_m + \frac{3}{5}f_n$
3	1	f_m	3/5	$\frac{3}{5}f_m + \frac{2}{5}f_n$
4	1	f_m	4/5	$\frac{4}{5}f_m + \frac{1}{5}f_n$
5	1	f_m	1	f_m

In this example, society Y will achieve full modernity before society Z , at time 3 rather than at time 5 (empirically, we can interpret each period as a generation). Eventually, both societies transition to the full modern equilibrium in which fertility is equal to f_m . Overall, fertility levels are inversely related to distance from the innovator in the earlier phases of the transition to lower fertility, but the relation between fertility and distance from the innovator across societies eventually fades as households in the more distant society catch up and adopt the new social norms.

A useful way to capture this change in the relation between fertility levels and social distance over time is by looking at the correlation between levels of fertility and distances from the innovator at different points in time. To fix ideas, assume that $f_m = 1$, $f_n = 3$ and $\beta = 1$. Then, at time 1 there is a perfect correlation ($\rho = 1$) between levels of fertility in societies X , Y and Z - which are 1, 7/3, and 13/5, respectively - and relative distances from the innovator, which are $d(X, X) = 0$,

$d(X, Y) = 2/3$ and $d(X, Z) = 4/5$. At time 2 the correlation, while still very high, will have decreased to $\rho = 0.95$, as fertility rates in societies Y and Z move, respectively, to $5/3$ and $11/5$. At times 3 and 4 the correlation between fertility and relative distance goes down to $\rho = 0.63$ as society Y converges to full modern fertility $f_m = 1$ at time 3, while society Z 's fertility decreases first to $9/5$ at time 3 and then to $7/5$ at time 4. Finally, at time 5 there is no longer a positive covariance between fertility levels and distance from the innovator, as all three societies now have the same levels of fertility $f_m = 1$.¹⁶

This pattern of decreasing correlation between fertility levels and social distance from the innovator, illustrated in the above example, is a general feature of the dynamics predicted by our model of social influence. Over time, all societies that are adopting the new norms will eventually converge to the same level of fertility f_m , provided that they have similar individual costs and benefits.¹⁷ This is because, as t increases, M will increase, and hit 1 in finite time. Therefore, over time fertility levels will become more similar among societies at different distances from the innovator. Formally, for any pair of societies Y and Z such that $d(Y, X) < d(Z, X) \ll 1/\beta$ there will be a time T^e such that $f_{Yt} < f_{Zt}$ for $t < T^e$, but $f_{Yt} = f_{Zt}$ for $t \geq T^e$, implying:

Proposition 2: *In the earlier phases of the diffusion of the fertility decline, there is a strong positive relationship between fertility levels and distance from the innovator, but this relationship becomes weaker as more societies adopt modern social norms over time. Consequently, measured correlations between fertility levels and relative social distance from the innovator are high and positive during the earlier phases of the transition, and decline over time as more societies decrease their fertility levels.*

This second proposition will also be brought to the data.

¹⁶ At time 5 the correlation between fertility levels and distances is technically undefined because the fertility rate is constant across societies, and therefore its standard deviation is zero. The correlation could be defined, for instance, if we slightly extend the model to allow for some (small) variation in (modern) fertility - that is, if $f_m = 1 + \varepsilon$, where ε is a random variable with zero mean and a very small but positive variance. In that case, the correlation would be defined, and equal to 0, at time 5.

¹⁷ Formally, these are the societies that are at a sufficiently close social distance $d(X, k) < 1/\beta$ from the innovator.

3 The Decline of Marital Fertility across European Populations

This section provides an overview of the decline of marital fertility in Europe in the 19th and 20th century and an exploratory analysis of the relation between the timing of the decline in fertility and measures of human and cultural distance across European populations. We use aggregate data that are available for broad populations (the French, the Italians, the Germans, and so on), mostly coinciding with national populations within modern political borders (France, Italy, Germany, etc.). We supplement this nation level data with a limited number of additional subnational populations for which we have separate data on genetic or linguistic distance (these include the Basques, the Lapps, the Sardinians, the Scots, etc.). This high level of aggregation limits the number of observations to 37 populations. Due to the paucity of observations the analysis here is mostly descriptive, although the results are informative regarding the validity of our theoretical predictions. We leave a deeper analysis of the dynamics of the fertility transition to the next section, where we exploit a richer regional dataset to more formally test our model.

3.1 Marital Fertility Limitations

The starting point for our analysis is the data about marital fertility in Europe over the past two centuries collected in the landmark Princeton European Fertility Project (Coale and Watkins, 1986, henceforth PEFP). The study was the final outcome of a massive interdisciplinary research project started in 1963, and remains the most comprehensive source of historical data on fertility in Europe in the 19th and early 20th century. We focus on the index of marital fertility, I_g , rather than total fertility, because that was the reproductive outcome for which European populations experienced the most novel and dramatic changes during the demographic transition (Coale, 1986). More precisely, European populations underwent an unprecedented reduction in marital fertility.¹⁸ The authors of the PEFP have interpreted such changes as stemming from what demographers call "parity-specific limitation" (Coale, 1986, p. 9). Parity-specific limitation refers to changes in behavior by married couples - e.g., by using withdrawal, other forms of contraception, or abortion - to avoid having more children after the desired number of children has been born. In contrast,

¹⁸European societies had experienced fluctuations in overall fertility before (Livi-Bacci, 2001). However, in pre-modern times fertility control and decline took place mostly through marriage postponement and other ways to reduce fertility irrespectively of one's number of children. See Voigtländer and Voth (2012) for a discussion of marriage postponement in Europe starting in medieval times, as a means to reduce total fertility.

nonparity-specific limitation is a pattern of behavior that affects the probability of conception irrespective of the number of children already produced. Critics of the PEFP have questioned this parity-specific interpretation, and argued that marital fertility might also have been reduced through changes in behavior that are typically considered non-parity specific, such as changes in breastfeeding (Guinnane, Okun and Trussell, 1994). Our interpretation of the reduction of marital fertility in Europe as stemming from a major change in social norms associated with fertility controls below a maximum natural rate, while consistent with the use of parity-specific limitations emphasized in the PEFP, also holds in a more general setting where both parity-specific and non-parity specific controls become socially more acceptable within marriage.

The PEFP provides data on fertility for a large number of European regions, also aggregated to the level of nation states. As already mentioned we focus on I_g , the index of marital fertility. For each region or country, I_g is equal to the total number of children born to married women divided by the maximum conceivable number of children, obtained from data on the Hutterites, an anabaptist sect that does not practice any form of fertility limitations.¹⁹ For any society i :

$$I_{gi} = \frac{B_i^m}{\sum_{j=1}^N M_{ij} G_j} \quad (20)$$

where B_i^M is the total number of children born to married women, j denotes an age cohort defined at 5-year intervals, M_{ij} is the number of married women in age cohort j and G_j is the Hutterite rate of fertility for age cohort j . The denominator therefore represents the total number of children that could conceivably be generated in society i if it had the age-specific schedule of fertility of the Hutterites.

From periodic observations of the resulting I_g index, PEFP provides an estimate of a fertility transition date for 19 countries or nations (Table 2.1, page 39).²⁰ This date represents the first instance when a 10% decline in marital fertility I_g is detected for a population (so, for instance, if for a given population the first recorded level of I_g is 0.7, the transition date is the first date for which I_g falls below 0.63). PEFP provides specific dates for some nation-states, which we supplement here with additional dates for some specific populations, also defined as the date when I_g has fallen by at least 10%.²¹ In total, we have I_g data and marital fertility transition dates for a set of 37

¹⁹See Coale and Treadway (1986), chapter 2, Appendix B, p. 153 in Coale and Watkins (1986).

²⁰These countries are Austria, Belgium, Denmark, England and Wales, Finland, France, Germany, Greece, Hungary, Ireland, Italy, The Netherlands, Norway, Portugal, European Russia, Scotland, Spain, Sweden and Switzerland.

²¹PEFP also provides maps, at the regional level, displaying color-coded dates of the marital fertility transition at

aggregated geographic areas, which for simplicity we refer to as "populations" in what follows.

Figure 1 plots changes in marital fertility levels for a selected group of European countries. According to Coale (1986, p.10), the large decline in fertility was a change from relatively high or moderate fertility, kept under control by late marriage, permanent celibacy, and nonparity-specific limitation, to low fertility due to the novel introduction of extensive parity-specific limitation of marital fertility. The idea that a couple would "marry, have a couple of kids, and then stop," is a relatively novel and modern idea, which thoroughly spread across European populations only during the 19th and early 20th centuries, with significant variation in both the timing and extent of the decline, apparent from Figure 1.

A key fact about the modern marital fertility decline is the pioneering role played by France. Table 1 shows estimated dates for the transition to permanently lower marital fertility in our baseline sample of 37 European populations. Clearly, France was at the frontier of this process, with an estimated transition date of 1827, and regions closer to France followed before more distant regions. Moreover, there is anecdotal evidence in Table 1 of a linguistic and cultural channel: a region linguistically and culturally very close to France such as Walloon Belgium experienced the transition to lower marital fertility about 30 years earlier than Flemish Belgium, even though the two regions were part of the same country and geographically close to France. Sardinia, a genetic and linguistic isolate, came last in 1934. Transitions also occurred in clusters that are aligned with linguistic cleavages: Countries speaking Germanic and Scandinavian languages tended to transition between 1887 and 1905, while many Romance language countries of Southern Europe featured a later transition: Italy, Portugal, Spain have transition dates between 1913 and 1920.

An open question, which we do not address in this paper, is why the transition to lower marital fertility through parity-specific control started in France. Several factors may have contributed to the onset of the marital fertility transition in France. One is the cultural development towards secular and modern norms and values, which had already spread among elites and other groups in France during the Enlightenment (or even earlier) and accelerated with the French Revolution. A

10 year intervals. For these regions, the dates we obtained from looking directly at the I_g data always fall within the 10-year interval seen on the map. The 20 additional regions / populations under consideration are: Latvia, Catalonia, Walloon Belgium, Flemish Belgium, England, Wales, Freisland, Bretagne, Provence, the Czech Republic, Lithuania, Ukraine, Poland, Lapland, Slovakia, Yugoslavia, Belarus, the Basque Country, Iceland and Sardinia. The choice of these additional regions was dictated strictly by the availability of separate genetic and linguistic data, as further explained below.

parallel mechanism points to political and institutional changes that affected the traditional power structure - in particular, the Church and other traditional centers of political and cultural influence - therefore determining or facilitating changes in social norms and behavior.²² Microeconomic evidence about the diffusion of the fertility transition within France through internal migration in the 19th century, analyzed and discussed in Daudin, Franck and Rapoport (2013), is consistent with a change in cultural norms taking place via social interactions and social influence. Irrespective of the specific factors behind the onset of the fertility decline in France, we hypothesize that such novel behavior would spread along human and cultural lines, with populations closer to the French being more likely to learn about the new behavior, and more willing to adopt it: we focus on the diffusion process, not on the factors that generated the onset.

3.2 Genealogical and Linguistic Distances

A systematic test of the hypothesis that human distance from France predicts the timing of the fertility transition requires measuring genealogical distance. We use two classes of measures to capture ancestral distance, based either on genetic or linguistic data.

Genetic distance captures the degree of genealogical relatedness between populations, and is now widely used for such a purpose in the economics literature (see for instance Spolaore and Wacziarg, 2009, 2012, 2013, 2014). Genetic distance is a summary measure of differences in gene frequencies between populations, constructed using neutral genes that are not subject to selective pressure (Cavalli-Sforza, Menozzi and Piazza, 1994). When two populations split apart, random genetic changes result in increasing genetic differentiation from one generation to the next. The longer the separation time, the greater the genetic distance computed from a set of neutral genes. The specific measure we use, F_{ST} , correlates strongly with historical separation times by construction. In sum, genetic distance is a summary measure of relatedness between populations, capturing the time since two populations have shared common ancestors (i.e., since they were the same population).

It is important to stress that we are not arguing that populations at a higher genetic distance from the innovator would have a genetic endowment that makes them permanently less likely to adopt the new behavior. On the contrary, in our model such barriers are temporary: We expect that they are mainly of a historical and cultural nature, and that barriers can be overcome with

²²For the effects of the French Revolution on modern institutional reform see Acemoglu, Cantoni, Johnson and Robinson (2011).

time, as the novel behavior spreads gradually to regions with culture and ancestry closer to one's own. The test of our hypothesis is not whether a population will or will not adopt the innovation at all, but about how long it will take for a population at a given distance from the innovator to finally adopt the innovation.

Figure 2 presents the phylogenetic tree of European populations, showing how the different populations in our sample split over time. The data is available for 26 European populations, which were matched to each of the 37 geographic units. These 26 populations are mostly overlapping with nation states and, in a few cases, with subnational units (Scottish, Basque, Sardinian, Lapp). To exploit the latter variation, we consider Scotland, the Basque Country, Sardinia and Lapland as separate data points of our baseline sample of 37 populations. In other cases, such as Walloon Belgium and Flemish Belgium, there is no separate genetic data, so both are matched to the genetic population labeled "Belgian".

As an alternative measure of cultural distance we also use linguistic data. Because languages are transmitted from parents to children and because linguistic innovations also arise in a regular fashion, linguistic distance also captures separation times between populations speaking different languages. It is important not to interpret the effect of linguistic distance narrowly as reflecting the ability to communicate, but to interpret it as an indicator of broader cultural distance: the barriers captured by linguistic distance include both communication, trust, differences in norms, values and attitudes, i.e. ancestral distance more generally.

The main source of linguistic distance data consists of linguistic trees provided in Ethnologue, for 37 European languages. The availability of additional data on languages guided a further expansion of our sample of European populations. For instance, we have separate linguistic data on Lithuanian, Latvian, Belarusian, Ukrainian, Frisian, Walloon, Flemish, Czech and Slovak, Occitan, Catalan, Breton, and to exploit this linguistic variation we consider the corresponding regions as separate data points (for instance the availability of linguistic data guided considering Walloon Belgium and Flemish Belgium as separate data points). For each language, we can count the number of common nodes it shares with a reference language, say French. The measure of linguistic distance is then the maximum number of shared nodes (in the case of French, 10) minus the number of common nodes. This is the number of different linguistic nodes between two populations (see Fearon, 2003, p. 211, and Desmet et al. 2012 for examples using the structure of linguistic trees to measure linguistic distance). As with genetic distance, we were able to match every population in

our sample to a linguistic group, so our sample using this source is again 37 data points.²³

Finally, as an alternative measure of linguistic distance, we use data from the field of lexicostatistics, or quantitative linguistics (Dyen et al., 1992). The data are based on basic meanings shared by most cultures (concepts such as "mother" and "blood"). Consider a list of 200 meanings. Each language uses a word to convey each of these meanings. For a given meaning, two words are designated as "cognates" if linguists determine that they stem from a common root in a proto-language. For instance "table" in English and "tavolo" in Italian both stem from the Latin root "tabula" and are therefore cognates. For two languages, the percentage of cognate words then is a measure of the closeness between these languages. We use one minus the percentage of cognate words as a measure of linguistic distance. This measure is available for all 37 populations.²⁴ The correlation between the lexicostatistical measure of linguistic distance and that based on language trees is 0.939 (Table 2, Panel B). On the other hand, the linguistic distance measures are more weakly correlated with genetic distance, with correlations of 0.26 – 0.27.²⁵ This motivates the use of genetic and linguistic distance as alternative measures of genealogical relatedness.

²³For populations with more than one language, such as Switzerland, we matched to the language used by the majority of the population, in this case Swiss German. Our analysis at the regional level in Section 4 is not subject to this problem, since regions are sufficiently small so that, in the context of Europe, each region can only be matched to one ancestral language.

²⁴For non-Indoeuropean languages, which are not covered in Dyen et al. (1992) we coded the percentage of cognate words with French as zero. This was the case for Finland, Hungary, Lapland, and the Basque Country where either Uralic languages or language isolate are spoken.

²⁵While linguistic trees and phylogenetic trees look a lot like each other (Cavalli Sforza et al., 1994), various reasons explain why the distance measures themselves are only moderately positively correlated. First, language replacement can weaken the link. For instance, the genetic admixture from the Magyar (Finno-Ugric) conquest of the current Hungarian territory in the 9th and 10th centuries AD only added very little to the gene pool of Hungary. The original language was completely replaced, but Hungarians remain genetically close to other Eastern European populations. Second, there can be gene replacement through migration, with the incoming population adopting the hosts' language. Finally, genetic distance is a continuous measure based on multiple neutral genes, while linguistic distance is a discrete measure that is based on linguistic trees. A split between two languages may have occurred far in the past but only once, of successive splits may have occurred in close succession but more recently, weakening the link between linguistic distance based on common nodes and genealogical distance.

3.3 Specification and Results

3.3.1 Genetic Distance and the Transition Date

To test whether the diffusion of fertility behavior followed lines of genealogical relatedness, we first explore the determinants of the marital fertility transition date:

$$MTD_i = \beta_0 + \beta_1 FST_i^f + X_i' \beta_2 + \varepsilon_i \quad (21)$$

where MTD_i refers to the marital transition date of population i , FST_i^f denotes its F_{ST} genetic distance from the French population and X_i is a vector of controls, mostly geographic distance measures that are potentially correlated with both genetic distance and the transition date.

The results are presented in Table 3. Across columns we successively add more controls. The univariate regression of column (1) reveals a strongly positive effect of genetic distance to France on the date of the fertility transition. The relationship captured by this regression is depicted graphically in Figure 3. From this figure, Lapland and Sardinia appear to be outliers, but excluding these two regions actually leads to an increase in the standardized effect of genetic distance (from 44.8% to 52.4%). Excluding France also leads to a slight increase in the standardized effect of genetic distance.²⁶ In column (2), adding geodesic distance to France as a control weakens the effect only modestly. This conditional relationship is depicted in Figure 4, where the same outliers as before can be identified. In the same way, however, excluding these outliers actually strengthens the relationship.

In the preferred specification of column (3), adding a wide range of geographic controls actually leads to a slightly larger effect than in column (2). In this specification the standardized beta coefficient on FST_i^f is 38.3%, a large effect. To put this number in context, a one standard deviation increase in genetic distance (equal to 69.48) delays the marital fertility transition by almost 8 years. Finally in column (4) we add per capita income in 1820 as an explanatory variable. If indeed the demographic and industrial transitions went hand in hand we would expect income per capita at the beginning of the period to be negatively associated with the date of the fertility transition. We lose 11 data points for which Maddison data on per capita income in 1820 are not available. The latter does not enter significantly, while genetic distance to France continues to have a large magnitude and remains significant at the 10% level despite the much smaller sample. This

²⁶Excluding at once France, Lapland and Sardinia leads to a yet larger standardized effect of genetic distance, equal now to 47.7%.

finding suggests the primary driving force behind the fertility transition was not elevated initial per capita income that might have come from early industrialization, but rather how distant a population happened to be from the population that first adopted the new fertility behavior - the French.

In Table 4 we run the same specification as in equation (21), augmented with genetic and geographic distance from England. The idea is to run a horserace between genetic distance from France and genetic distance from England (the correlation between the two genetic distances is 0.515). England was the birthplace of the Industrial Revolution and France that of the fertility transition. If the fertility transition stemmed mostly from economic modernization we would expect the main axis of diffusion to stem from England. If instead it arose from a process of imitation and diffusion from the first country to undergo the transition, then genetic distance from France should win out in a horse race. This is indeed what we find in Table 4. Column (1) runs a univariate regression of the fertility transition date on genetic distance from England, which comes out with a positive coefficient. Adding geodesic distance from England (column 2) weakens the effect to almost zero, while adding genetic distance from France flips the sign to negative and insignificant (column 3). Genetic distance from France itself comes out highly significant and with a magnitude roughly similar to that found in Table 3. This picture does not change when adding our long list of geographic controls (column 4): Genetic distance from France wins in a horserace against genetic distance from England.²⁷

Overall, these results regarding the determinants of the fertility transition date of lower marital fertility in Europe are consistent with diffusion from France. Societies that are ancestrally closer to the French face lower initial barriers to the adoption of the novel behavior, even through eventually all European populations adopted the new behavior.

²⁷Basso and Cuberes (2012) find a positive effect of genetic distance from the UK on the fertility transition date in a worldwide sample of countries. However, in this broader sample, much of the variation in genetic distance comes from the distance between non-European and European populations, trumping variation between Europeans. This fact opens up the possibility that the frontier for fertility limitations was not the English but another European population. We show that this population was in fact the first adopter of the new fertility behavior, France, where economic modernization came late relative to the UK, the birthplace of the modern Industrial Revolution. Hence, in contrast with the conclusions in Basso and Cuberes (2012), our results suggest that economic development was not the sole or principal force in the spread of fertility limitations in Europe, but that a process of cultural and social diffusion from France was an important force.

3.3.2 Genetic Distance and the Marital Fertility Rate (I_g)

Examining the determinants of the fertility transition date is informative but has limitations. The transition starts before the date specified (without the decline in I_g reaching 10%, a somewhat arbitrary threshold) and continues after the date is reached. An alternative is to directly examine the determinants of the level of I_g . For a cross-section of populations at a point in time corresponding to the main period of the fertility transition, we can hypothesize that I_g itself may be related to genealogical distance from the frontier, according to the following specification:

$$I_{gi} = \gamma_0 + \gamma_1 FST_i + X_i' \gamma_2 + \varepsilon_i \quad (22)$$

The baseline time period over which we measure I_g in this equation (22) is 1911-1940. The choice of this period is motivated by the availability of I_g data for all 37 populations.²⁸ This is also a period when the fertility transition was still in full-swing in many countries, as seen in Figure 1.

The results are presented in Table 5. Focusing on the baseline specification of column 3, with all the geographic distance controls, we find a positive effect of genetic distance to France on the level of I_g . The magnitude is large as a one standard deviation increase in genetic distance raises I_g by 57% of its standard deviation. Few of the controls are significant at conventional levels of significance. This finding still holds when controlling for per capita income in 1913, to account for the possible impact of economic modernization on fertility behavior (we find no impact of per capita income itself on marital fertility). These results are reassuring in that the effect of genealogical distance extend from transition dates to I_g itself. Since the multiple observations through time for I_g open up the possibility of panel analysis, we investigate the dynamics of the effect of genealogical distance on I_g when turning to the analysis of the regional data.

3.3.3 Linguistic Distance and the Fertility Transition

In addition to genetic distance we now consider the effects of linguistic distance on either the transition dates or I_g . We use the same specifications as in equations (21) and (22), replacing genetic distance to France alternately with the number of different linguistic nodes with the French language ("Français") or the percentage of words not cognate with French.

²⁸Earlier periods feature fewer observations. If more than one observation on I_g was available for a given population during this time interval, all observations were averaged. On average, there were 2.25 observations on I_g for each population between 1911 and 1940.

Results are presented in Table 6 and are consistent with the hypothesis that genealogical distance to the frontier is positively associated with the transition date and the level of I_g . In column (1), with the transition date as the dependent variable, the number of different linguistic nodes with the French language enters significantly (at the 5% level), positively and strongly, with a standardized magnitude of 56.7%, a bit larger than the previously documented effect of genetic distance. In column (2) we consider the lexicostatistical measure of linguistic distance, finding a positive effect that is significant at the 10% level and a standardized magnitude around 45%. The last two columns explore the determinants of I_g averaged over 1911-1940, finding results in line with the previous findings. The effect of the measure based on linguistic trees is still significant at the 5% level, while the effect of the lexicostatistical measure is significant at the 13% level (one should not overemphasize these differences in significance levels given the paucity of observations in the population-level dataset of 37 data points).

In sum, approaching the issue with different dependent variables reflecting the fertility transition and different measures of genealogical distance, we document a strong pattern of a positive association between ancestral distance to France and the adoption of marital fertility limitations, consistent with a model of behavioral adoption from the innovator. Moreover, distance to France trumps distance to England, the birthplace of the Industrial Revolution, suggesting that the diffusion of marital fertility limitations followed a diffusion process very different from that of industrialization.

4 The Dynamics of The Decline in Marital Fertility across the Regions of Europe

While the analysis at the level of 37 populations is informative, the underlying database of marital fertility rate is much richer as it includes information on various measures of fertility across subnational regions of Europe from 1831 to 1970. This opens up the possibility of a much larger and richer sample of regions, as well as the ability to control for country fixed-effects and to more thoroughly explore the dynamics of the diffusion of marital fertility limitations. In this section, we turn to this task, assembling a panel dataset on fertility, geographic distance and ancestral distance for a sample of 775 European regions.

4.1 The Regional Dataset

The regional dataset opens up new possibilities, but it is not without challenges. Firstly, during the period under scrutiny, the borders of European countries changed sometimes drastically, so that a region that was located in one country at one point in time may be part of another later on. For example, this is the case for many regions of Poland, variously in Germany or Russia at different times in the sample period. Similar cases abound. In the source data on fertility these regions are alternately included in one country or another, sometimes with different region names and borders. We redefined a single identifier for each region, with consistent borders throughout, and separately coded the country to which each region belongs at different points in time, at 20-year intervals between 1846 and 1946. This opens up the possibility of controlling for country fixed effects, using country borders defined for different periods.

Secondly, we lack data on genetic distance at the level of disaggregation that we now use. Instead, we painstakingly constructed a database of ancestral European languages at a disaggregated geographic level corresponding to the regional boundaries in the fertility data. Using a detailed map of the ancestral languages and dialects of Europe (including extinct dialects), delineating the areas where languages and dialects were spoken in the 18th and 19th centuries, we matched every language in the source map to a subnational region in the fertility dataset from Coale and Watkins (1986).²⁹ We ended up with 275 languages and dialects matched as primary languages of each of the 775 regions.³⁰ It is important to note that these languages are no longer necessarily spoken in the corresponding regions, as the 19th and 20th centuries saw the virtual elimination of many subnational dialects in several European countries through nation building (Alesina and Reich, 2013). For instance regions of Southern France are variously matched to Langue d’Oc, Provençal,

²⁹The source for the language data was the map provided at <http://www.muturzikin.com/carteurope.htm>. To our knowledge this is the most comprehensive and detailed maps of historical European languages. Moreover language headings used in this map closely track those in Ethnologue, on which we rely to derive linguistic distance.

³⁰In a minority of cases where a region straddles two linguistic areas we matched the region to two languages - a primary and a secondary one. 108 of the 775 regions are matched to a secondary language. In most of the case the match was to a language that is otherwise the primary language of some region, but for 26 regions the secondary language is unique to that region. For instance, Kerneveg (a sub-dialect of Breton) is nowhere the primary language but is matched as the secondary language of 3 subdivisions of Brittany (each of which is matched to a different sub-dialect of Breton as primary language). We only made use of the primary language in our analysis. A region’s secondary language is usually very closely related to its primary language, as the example of the regions of Brittany suggests.

or Savoyard, spoken nowadays by very few. Next, for each ancestral language we found its linguistic classification from Ethnologue.³¹ This allowed us to calculate the linguistic distance of each language to any other (our main focus will be distance to French and English) by counting the number of different linguistic nodes separating any pair of languages.³² Thus, we obtained a series describing the linguistic distance of each region in our regional dataset to French and to English. Of particular note, the series on the number of different linguistic nodes to French (Français) ranges from 1 to 10, with a mean of 7.5 (Table 7). This is the main variable used to assess the role of genealogical distance to the birthplace of the fertility transition as a determinant of its diffusion to the rest of Europe.

Thirdly, we also assembled a comprehensive database of geographic characteristics for each of the 775 regions. In particular, we determined the coordinates of the centroid of each region, and calculated their geodesic, longitudinal and latitudinal distance to France and England. We also coded whether a region is on an island, whether a region is landlocked, the sea or ocean to which a coastal region is located, whether it is contiguous to France and whether a region is separated from France by a mountain range (the Alps and the Pyrenees). These serve to construct the geographic controls included in the regressions that follow.

A final challenge was to define the temporal unit of analysis. While the right-hand side variables are time invariant, the rate of marital fertility I_g as provided by PEFP is an unbalanced panel. Some countries like France have vast amounts of data through time. Others, chiefly in Eastern Europe have fewer years of data available in the interval 1831 to 1970. To ensure that enough observations are available in any period we defined 12 overlapping periods of 30 years centered at 10-year intervals, so that period 1 is 1831 to 1860, period 2 is 1841 to 1870, etc.³³ The analysis will be conducted on these 30-year periods, with marital fertility averaged over all available years within these periods. In the tables for the sake of brevity we report only results for the odd-numbered

³¹For instance, French (Français) is classified as follows: Indo-European - Italic - Romance - Italo-Western - Western - Gallo-Iberian - Gallo-Romance - Gallo-Rhaetian - Oil - Français.

³²For instance, the linguistic classification of Italian is Indo-European - Italic - Romance - Italo-Western - Italo-Dalmatian. Thus, Italian shares 4 nodes in common with French out of a possible 10 nodes, and it's linguistic distance to French is equal to 6.

³³For the first period data was available only for 184 regions from 5 countries (defined by their 1946 borders). By period 3 we have 531 regions from 20 countries, and by 1911-1940 (period 9) we have 766 regions from 25 countries, i.e. most of the regions in the sample have available data on fertility in the early decades of the 20th century.

periods.

Summary statistics for the regional dataset are presented in Table 7. Here we see the marital fertility transition at work: the average level of I_g declines from 0.623 in 1831-1860 to 0.336 in the 1951-1970 period. Across regions, the average date of the transition is 1899, with a standard deviation of about 25 years. Turning to correlations in Panel B of Table 7, we see that I_g is highly correlated with linguistic distance to France early in the period, but that this correlation declines as time goes by and more and more regions undergo the transition, consistent with our diffusion model.

4.2 Specification and Results

4.2.1 Determinants of the Transition Date

Our first specification, similar to equation (21) seeks to explain the transition date, but adding country fixed effects to control for any country-specific time invariant characteristics:

$$MTD_{jc} = \delta_1 LD_{jc}^f + X'_{jc} \delta_2 + \alpha_c + \varepsilon_{jc} \quad (23)$$

where j denotes the region, c denotes the country, LD_{jc}^f is the linguistic distance of region j to French, and α_c is a country fixed effect. Country borders used to define the country dummies are obtained from 1846 borders, but it matters little for our results whether countries are defined by later borders.³⁴

The transition dates MTD_{jc} are available from PEFP at the regional level at 10-year intervals in map form (map 2.1 annexed to Coale and Watkins, 1986). For each region we assigned a date equal to the midpoint of each 10-year interval. We verified that these dates indeed correspond to the earliest 10% decline in I_g . For transition dates before 1830 and after 1930, we referred to the data on I_g to determine the date of a 10% decline in the index of marital fertility. We ended up with data for 771 regions, from 25 European countries.³⁵

Table 8 presents the baseline results considering distance to the French language (for linguistic distance) and to Paris (for geographic distance). We again find a positive and highly significant effect of linguistic distance on the marital fertility transition date - whether or not we control for

³⁴Results using alternative dates to define country borders are available upon request.

³⁵4 regions in the Balkans did not have enough I_g data to ascertain a date and were not coded on the source map.

geographic distance. In the baseline specification of column 4, with the broadest set of geographic controls, we find a standardized effect of linguistic distance equal to about 26.78%. This is smaller than in the cross-population regressions, but still large in magnitude, and the effect is highly significant statistically. The regression overall does a good job at accounting for variation in transition dates, with an overall R^2 of 72% (dropping the country dummies, the R^2 only falls to 60%). This alleviates concerns that transition dates may be estimated with too much error to allow for meaningful estimates of their determinants. Both the R^2 and the coefficient on linguistic distance to French remain very stable across specifications as we add controls, alleviating concerns that there may be an important omitted variable (Oster, 2014).

Table 9 runs a horserace between distance to English/London and distance to French/Paris, again with country fixed-effects. When entered on its own linguistic distance to English has essentially no effect on the timing of the fertility transition. When adding geographic distance to London the effect actually turns weakly negative. When adding linguistic distance to French and geographic distance to French (column 4), linguistic distance to French enters with a positive and highly significant effect while the effect of distance to English is only significant at the 10% level and small in magnitude (the correlation between linguistic distance to French and to English is equal to -0.485 explaining why the inclusion of linguistic distance to France flips the sign of linguistic distance to the English). A similar conclusion holds when including the whole battery of geographic controls (column 5). Now distance to English becomes statistically significant at the 5% level, but its magnitude is one third that of distance to French.

In sum, distance to French wins in a horse race with distance to English. These results are consistent with a diffusion process for marital fertility behavior stemming from France, and cast doubt on the view that the marital fertility transition was primarily a byproduct of industrialization. These results are particularly noteworthy in light of the inclusion of country fixed effects, a stringent test of our hypothesis since it requires identification from within-country, cross-regional variation in the data.

4.2.2 Determinants of Transition Status

We now seek to better understand the dynamics of the fertility transition. In this subsection we define a simple dichotomous indicator taking on a value of 1 if, in a given period t , a region j from country c has undergone the transition, and regress this indicator, separately at each date t , on

linguistic distance to France and the usual set of geographic controls:

$$T_{jct} = \gamma_0 + \gamma_1 LD_{jc}^f + X_{jc}'\gamma_2 + \varepsilon_{jct} \quad (24)$$

We start by displaying graphically the cumulative share of regions, among the 771 for which transition date data is available, for which T_{jct} takes on a value of 1 (Figure 5). The process follows a logistic distribution. The earliest transition dates signalling the first 10% decline in I_g are in 46 French regions; regions with the latest dates are located mostly in Ireland and Spain in the late 1920s, 1930s and early 1940s. The last regions to begin the marital fertility transition in this dataset are Salamanca (1941), Zamora (1941), Avila (1942), Dublin County (1943) and Las Palmas/Canary Islands (1945).

Interestingly, this logistic pattern could not be generated by a mechanical process due to simple delays and inertia (Young, 2009, p. 1902). Moreover, since the hazard rate (the rate at which nonadopters become adopters) in the above process is partly increasing relative to the number of adopters, the diffusion cannot be the outcome of contagion, in which nonadopters become adopters by simple contact with other adopters (Young, 2009, pp. 1903-04). Instead, as discussed in Young (2009), this pattern is consistent with a more complex diffusion process in which an innovation is gradually adopted by different agents through mechanisms of social influence and social learning, as discussed in our conceptual framework.

The analysis has two limitations: 1) We no longer include country fixed effects: since at a given date all or none the regions of certain countries have $T_{jct} = 1$, the corresponding country dummy perfectly determines the outcome, resulting in far fewer observations from which to estimate the within country-effects of the other covariates. However, on this smaller subset of regions, controlling for country fixed effects, we still find that linguistic distance from France in the early sample periods reduces the probability of having undergone the onset of the marital fertility transition (these results are available upon request). 2) We include a smaller set of covariates, excluding the geographic dummy variables but maintaining the geographic distance metrics. The reason is the same as the preceding: for some periods, some dummy variables perfectly predict the outcome, and the corresponding observations must be dropped. Since we wish to compare the magnitude of the effect of linguistic distance at various periods, we maintain the same set of controls at all dates, and drop the geographic dummies. Once again, however, the results (available upon request) are robust to including the dummies for the periods where this is possible.

Results from estimating equation (24) using probit are presented in Table 10, at 20 year-intervals from 1841 to 1941, a period that covers the bulk of the transition period. We display graphically the standardized effect of linguistic distance in Figure 6, where a standardized effect is estimated at every date between 1831 and 1941 for which a transition occurs in some regions. At the beginning of the period, only regions in France have transitioned. The effect of linguistic distance from France on the probability of having begun the transition is therefore essentially zero. As we enter the diffusion period the effect of linguistic distance from France progressively becomes strongly negative (i.e. being linguistically distant is associated with a lower probability of starting the marital fertility transition), with the standardized effect peaking at -61.45% in 1891. As more and more regions at greater distances from France begin their transitions, the effect then diminishes back to zero. The U-shaped time profile of the effect of linguistic distance on the probability of experiencing the onset of the marital fertility transition is therefore strongly suggestive of a diffusion process that goes in great measure through ancestral distance.

4.2.3 Determinants of I_g

We now conclude our analysis of the dynamics of the fertility transition by estimating directly the determinants of I_g . The advantage of this approach is that we can once again control for country fixed effects and the full set of geographic controls. I_g is also a continuous rather than a dichotomous indicator, so we avoid the arbitrariness of having to define a transition as the earliest occurrence of a 10% drop in I_g . Our specification is:

$$I_{g_{jct}} = \eta_1 LD_{jc}^f + X'_{jc} \eta_2 + \alpha_c + \varepsilon_{jct} \quad (25)$$

where the regression is run separately for each 30-year period τ .

Results are presented in regression form in Table 11 and in graphical form in Figure 7.³⁶ We find a large, positive and statistically significant effect of linguistic distance to France on the level of I_g , throughout the sample period. Moreover, focusing on a common sample of regions, the last row of Table 11 displays the standardized magnitude of the effect of linguistic distance to French going back to 1871, showing that this effect declines as more and more regions at progressively greater linguistic distances from France adopt new fertility behavior, consistent with Proposition 2 from our model. Figure 7 displays the same effect through time for a smaller set of 519 regions,

³⁶The same estimates obtained without using country fixed-effects, with substantive results very similar to those discussed here, are available upon request.

estimated from the same specification (equation (25)), but going back farther back in time to 1861. The standardized effect is slower to decay to zero than in the probit regressions of the preceding subsection because these explored the determinants of the *onset* of the fertility transition. This transition presumably continues for a while past the date of its onset. Hence countries continue to converge to the frontier behavior past their transition dates, and linguistic distance to French continues to predict how far these regions are from the frontier.

Overall, using a variety of empirical approaches, these results show that ancestral distance from France strongly predicts the fertility transition; that ancestral distance acts as a powerful barrier to the transmission of fertility behavior; that the generalization of marital fertility restrictions throughout Europe is best understood as a process of gradual diffusion of novel fertility behaviors first adopted in France; and that this diffusion process occurred first in regions that were linguistically, culturally and genealogically close to France, and spread later to more distant cultures.

5 Conclusion

In this paper we studied the dramatic decline in fertility in Europe over the 19th and 20th century. We provided a model of fertility choice that reconciles an economic approach to fertility decisions with a central role for the diffusion of new social norms along cultural lines. In our framework, the transition from higher traditional fertility to lower modern fertility is the outcome of a process of social innovation and social influence, whereby the late adopters observe and learn about the novel behaviors, norms and practices introduced by early adopters. We argued that the diffusion of the fertility decline and the spread of industrialization followed different patterns because societies at different relative distances from the respective innovators - the French and the English - faced different barriers to imitation and adoption, and such barriers were lower for societies that were historically and culturally closer to the innovators. Thus, our model reconciles an explicitly optimizing view of fertility choices with an important role for social norms as determinants of fertility choices.

Empirically, we successfully tested the hypothesis that the decline of fertility was associated with the diffusion of social and behavioral changes from France, in contrast with the spread of the Industrial Revolution, where England played a leading role. In the empirical analysis we studied the determinants of marital fertility in a sample of European populations and regions from 1831 to 1970, and tested our theoretical model using measures of genetic distance between European

populations and a novel data set of ancestral linguistic distances between European regions. We found that ancestral distance from the innovator (France), captured using genetic and linguistic distance, is positively related with the date of onset of the fertility transition across populations and regions. We also found that the dynamics of the fertility transition match the prediction of the model: linguistic distance to France matters early and at the peak of the transition period, but fades as more and more regions adopt the modern behavior. These findings highlight the importance of taking into account social norms and social influence in any economic explanation for the decline of fertility in Europe.

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Table 1 - Dates of the Fertility Transition in a Sample of 37 European Populations

Country name	Date	Country name	Date
France	1827	Austria	1907
Latvia	1865	Hungary	1910
Catalonia	1875	Ukraine	1910
Walloon Belgium	1875	Finland	1912
Switzerland	1887	Poland	1912
Germany	1888	Greece	1913
England	1892	Italy	1913
Scotland	1894	Lapland	1915
Freisland	1897	Slovakia	1915
Netherlands	1897	Yugoslavia	1915
Denmark	1898	Portugal	1916
Sweden	1902	Spain	1920
Norway	1903	Ireland	1922
Bretagne	1905	Russia	1922
Czech Republic	1905	Belarus	1925
Flemish Belgium	1905	Basque Country	1930
Lithuania	1905	Iceland	1930
Wales	1905	Sardinia	1934
Provence	1906		

Table 2 – Summary Statistics for the Main Population-level Variables

Panel A – Means and Standard Deviations

Variable	# Obs.	Mean	Std. Dev.	Min	Max
Marital Fertility Transition Date	37	1904	20.099	1827	1934
Marital Fertility Index (Ig) (1911-1940 average)	37	0.461	0.098	0.284	0.670
Genetic distance to France*	37	69.324	69.475	0.000	350
Geodesic distance to France (1000 km)	37	1.176	0.800	0.000	2.494
# of different linguistic nodes with Français	37	7.946	2.571	0.000	10
% not cognate with Français, lexicostatistical measure	37	674.378	268.810	0.000	999

(* Genetic distance was multiplied by 10,000 to facilitate readability of the regression tables)

Panel B – Simple Correlations

	Marital Fertility Transition Date	Marital Fertility Index (Ig)	Genetic distance to France	Geodesic distance to France	# of different linguistic nodes with Français
Marital Fertility Index (Ig) (1911-1940 average)	0.708	1			
Genetic distance to France	0.448	0.521	1		
Geodesic distance to France (1000 km)	0.358	0.422	0.478	1	
# of different linguistic nodes with Français	0.493	0.310	0.270	0.355	1
% not cognate with Français, lexicostatistical measure	0.376	0.231	0.261	0.362	0.939

Summary statistics based on 37 observations: Austria, Basque Country, Belarus, Bretagne, Catalonia, Czech Republic, Denmark, England, Finland, Flemish Belgium, France, Freisland, Germany, Greece, Hungary, Iceland, Ireland, Italy, Lapland, Latvia, Lithuania, Netherlands, Norway, Poland, Portugal, Provence, Russia, Sardinia, Scotland, Slovakia, Spain, Sweden, Switzerland, Ukraine, Wales, Walloon Belgium, Yugoslavia.

Table 3 - Population-level Regressions for the Transition Date
(Dependent variable: Marital Fertility Transition Date)

	(1)	(2)	(3)	(4)
	Univariate	Control for distance	Control for geography	Control for initial income 1820
Genetic distance from France	0.130 (2.45)**	0.104 (1.93)*	0.111 (2.26)**	0.107 (2.05)*
Geodesic distance from France (1000s of km)		4.666 (0.88)	4.316 (0.40)	-12.222 (0.55)
Absolute difference in latitudes, from France			-69.611 (0.88)	-52.858 (0.46)
Absolute difference in longitudes, from France			4.782 (0.21)	124.772 (0.54)
1 for contiguity with France			-11.320 (1.09)	-13.818 (1.57)
=1 if an island			1.167 (0.10)	2.738 (0.20)
=1 if shares at least one sea or ocean with France			7.862 (1.00)	12.035 (0.57)
Average elevation between countries to France			28.236 (0.70)	45.242 (0.94)
=1 if landlocked			-1.599 (0.22)	-13.797 (0.53)
Per capita income, 1820, from Maddison				-0.007 (0.39)
Constant	1,895.115 (361.65)***	1,891.406 (256.60)***	1,885.426 (131.40)***	1,889.543 (35.65)***
R ²	0.20	0.23	0.30	0.36
Number of populations	37	37	37	26
Standardized Beta (%)	44.842	35.969	38.298	41.187

(Robust t-statistics in parentheses: * p<0.1; ** p<0.05; *** p<0.01)

Table 4 - Horserace with Distance to England, Population-level Regressions
(Dependent variable: Marital Fertility Transition Date)

	(1)	(2)	(3)	(4)
	Univariate	Control for distance	Horserace, simple	Horserace, geographic controls
Genetic distance from England	0.152 (2.67)**	0.062 (0.89)	-0.036 (0.67)	-0.125 (1.35)
Geodesic Distance from England (1000s of km)		6.520 (0.93)	9.776 (0.90)	76.939 (3.08)***
Genetic distance from France			0.117 (2.54)**	0.160 (3.49)***
Geodesic distance from France (1000s of km)			-3.472 (0.30)	-59.688 (1.96)*
Constant	1,895.918 (377.11)***	1,892.873 (279.48)***	1,890.223 (275.00)***	1,893.256 (140.95)***
R ²	0.10	0.13	0.24	0.40
Number of populations	37	37	37	37
Standardized Beta on genetic distance from England (%)	32.147	13.079	-7.708	-26.406
Standardized Beta on genetic distance from France (%)			40.302	55.217

(Robust t-statistics in parentheses: * p<0.1; ** p<0.05; *** p<0.01)

All regressions are based on a sample of 37 populations.

Additional geographic controls in column 4 (estimates not reported) include all those in column 3 of Table 3, i.e. absolute difference in latitudes, absolute difference in longitudes, contiguity dummy, island dummy, landlocked dummy, shared sea/ocean dummy, average elevation along the path to France / England, entered both relative to France and relative to England where applicable.

**Table 5 - Population-level Regressions for Marital Fertility, 1911-1941 period
(Dependent variable: Index of Marital Fertility, Ig)**

	(1)	(2)	(3)	(4)
	Univariate	Distance control	All Geography Controls	All Geography Controls
Genetic distance from France	0.733 (3.55)***	0.582 (2.39)**	0.802 (3.66)***	0.961 (3.24)***
Geodesic distance to France (1000s of km)		27.360 (1.49)	-17.484 (0.33)	-65.110 (0.43)
Absolute difference in latitudes, from France			-832.471 (1.89)*	-413.682 (0.64)
Absolute difference in longitudes, from France			135.769 (1.33)	-373.766 (0.32)
1 for contiguity with France			-86.143 (1.83)*	-109.189 (1.96)*
=1 if an island			61.349 (1.34)	98.192 (0.92)
=1 if shares at least one sea or ocean with France			28.761 (0.57)	12.274 (0.13)
Average elevation between countries to France			225.541 (2.05)*	221.951 (1.76)*
=1 if landlocked			-133.433 (1.93)*	-93.008 (0.81)
Per capita income, 1913, from Maddison				-0.040 (1.27)
Constant	410.528 (20.13)***	388.782 (15.46)***	412.678 (5.95)***	603.407 (3.71)***
R ²	0.27	0.31	0.51	0.55
# of populations	37	37	37	29
Standardized Beta on genetic distance (%)	52.141	41.429	57.066	72.114

(Robust t-statistics in parentheses: * p<0.1; ** p<0.05; *** p<0.01)

The data on marital fertility is for the 1911-1941 period; if more than one observation was available on Ig for a given country in that period, the available observations were averaged.

Table 6 - Population-level Regressions Using Linguistic Distance
(Dependent variable: As in the second row)

	(1)	(2)	(3)	(4)
	Transition Date	Transition Date	Ig 1911-1940	Ig 1911-1940
# of different nodes with Français	4.432 (2.43)**		13.739 (2.16)**	
% not cognate with French, lexicostatistical measure		0.034 (1.81)*		0.113 (1.58)
Geodesic distance to France (1000s of km)	22.318 (2.39)**	22.365 (2.10)**	91.735 (1.94)*	93.127 (1.77)*
Absolute difference in latitudes, from France	-139.423 (1.82)*	-146.493 (1.67)	-1,040.387 (2.10)**	-1,081.450 (2.00)*
Absolute difference in longitudes, from France	-22.115 (1.28)	-19.797 (1.12)	-57.001 (0.73)	-49.367 (0.63)
1 for contiguity with France	3.961 (0.55)	1.754 (0.27)	-20.579 (0.41)	-25.314 (0.53)
=1 if an island	-3.678 (0.29)	-2.289 (0.18)	30.500 (0.58)	34.897 (0.68)
=1 if shares at least one sea or ocean with France	9.775 (1.11)	10.800 (1.04)	15.612 (0.27)	20.622 (0.34)
Average elevation between countries to France	6.577 (0.25)	10.842 (0.35)	124.769 (1.31)	135.742 (1.45)
=1 if landlocked	-3.933 (0.52)	-3.304 (0.41)	-147.410 (2.04)*	-145.477 (2.00)*
Constant	1,849.404 (79.45)***	1,860.408 (73.14)***	311.517 (3.57)***	338.945 (3.87)***
R-squared	0.43	0.34	0.44	0.41
Standardized Beta (%)	56.684	45.080	36.174	31.020

(Robust t-statistics in parentheses; * p<0.1; ** p<0.05; *** p<0.01)

Ig was multiplied by 1000 to make the numbers more readable.

All regressions are based on a sample of 37 populations.

Results do not change materially with the addition of per capita income in 1820 to columns (1) and (2) or the addition of per capita income in 1913 to columns (3) or (4).

Table 7 – Summary Statistics for the Region-Level Dataset

Panel A. Means and Standard Deviations for the main variables of interest

Variable	# Obs	Mean	Std. Dev.	Min	Max
Marital Fertility Transition date	771	1899.096	24.989	1830	1945
Difference in linguistic nodes to Français	775	7.495	2.827	1	10
Geodesic distance to Paris (km)	775	1109.641	714.633	0.000	3977.143
Ig (1831-1860)	184	0.623	0.136	0.321	0.972
Ig (1861-1890)	609	0.664	0.123	0.271	1.001
Ig (1891-1920)	675	0.594	0.129	0.225	0.914
Ig (1921-1950)	766	0.421	0.121	0.086	0.763
Ig (1950-1970)	706	0.336	0.097	0.129	0.714

Panel B. Simple Correlations among the Main Variables of Interest

	Ig 1831-1860	Ig 1861-1890	Ig 1891-1920	Ig 1921-1950	Ig 1950-1970	Marital Fertility Transition date	Difference in linguistic nodes to Français
Difference in linguistic nodes to Français	0.729	0.514	0.511	0.197	-0.080	0.521	1
Geodesic distance to Paris (km)	0.366	0.089	0.399	0.491	-0.042	0.541	0.373
# of obs.	184	609	675	766	706	771	775

Note: There are 4 regions with Ig data but no fertility transition dates. These regions, in the Balkans, have too little data to ascertain when the transition occurred. These regions are Bosnia and Herzegovina, Kosovo in Serbia, Podrinje (a small region of Bosnia) and Zetska (Montenegro).

Table 8 - Cross-Regional Regressions for the Marital Fertility Transition Date, with country fixed-effects
(Dependent variable: Marital Fertility Transition Date)

	(1)	(2)	(3)	(4)
	Univariate	Control for geodesic distance	Control for all distances	Control for micro-geography
# of different nodes with Français	2.409 (5.30)***	2.248 (4.94)***	2.289 (5.05)***	2.363 (5.11)***
Geodesic distance to Paris, km		0.011 (7.14)***	-0.0002 (0.03)	0.001 (0.16)
Absolute difference in longitudes, to Paris			0.795 (2.16)**	0.744 (1.96)*
Absolute difference in latitudes, to Paris			0.341 (0.99)	0.233 (0.66)
=1 if area is barred by a mountain range from France				11.761 (2.19)**
=1 if area is contiguous with France				-4.653 (1.30)
=1 if area shares at least one sea or ocean with France				1.196 (0.52)
=1 if area is landlocked				1.975 (0.93)
=1 if area is an island				0.887 (0.16)
Constant	1,889.677 (408.72)***	1,880.531 (378.89)***	1,879.800 (365.08)***	1,872.125 (345.88)***
R ² overall	0.70	0.71	0.71	0.72
Standardized Beta (%) on linguistic distance	27.298	25.471	25.938	26.775

Robust t-statistics in parentheses: * p<0.1; ** p<0.05; *** p<0.01.

The sample is comprised of 771 regions from the following 25 countries: Austria, Belgium, Bulgaria, Czechoslovakia, Denmark, England and Wales, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Luxembourg, Netherlands, Norway, Poland, Portugal, Romania, Russia, Scotland, Spain, Sweden, Switzerland, Yugoslavia.

Country fixed effects are based on 1846 borders.

Table 9 - Cross-Regional Regressions, English-French Horserace, with country fixed-effects
(Dependent variable: Marital Fertility Transition Date)

	(1)	(2)	(3)	(4)	(5)
	Univariate	Control for geodesic distance	Horserace with geodesic distance	Horserace with all distance controls	Horserace with all geography controls
# of different nodes with English	-0.070 (0.09)	-0.959 (1.15)	1.354 (1.75)*	1.336 (1.67)*	1.847 (2.26)**
# of different nodes with Français			2.234 (4.87)***	2.274 (4.96)***	2.410 (5.21)***
Geodesic distance to London, km		0.011 (5.74)***	-0.025 (2.01)**	-0.043 (2.58)**	-0.050 (2.90)***
Geodesic distance to Paris, km			0.033 (2.94)***	0.043 (2.41)**	0.053 (2.84)***
Constant	1,909.021 (723.81)***	1,898.308 (602.79)***	1,884.775 (285.71)***	1,882.509 (268.31)***	1,871.968 (266.92)***
R ² overall	0.68	0.69	0.72	0.72	0.72
Standardized Beta on linguistic distance to English (%)	-0.341	-4.642	6.558	6.472	8.944
Standardized Beta on linguistic distance to Français (%)			25.321	25.771	27.305

Robust t-statistics in parentheses: * p<0.1; ** p<0.05; *** p<0.01

All regressions estimated on a sample of 771 European regions.

Column (4) includes controls for: absolute difference in longitudes to London, absolute difference in latitudes to London, absolute difference in longitudes to Paris.

Column (5) includes all the controls in column (4) plus: dummy for contiguity to England, dummy for regions that share at least one sea or ocean with England, dummy for contiguity to France, dummy for landlocked region, dummy for regions located on an island.

The sample is comprised of the regions of the following 25 countries: Austria, Belgium, Bulgaria, Czechoslovakia, Denmark, England and Wales, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Luxembourg, Netherlands, Norway, Poland, Portugal, Romania, Russia, Scotland, Spain, Sweden, Switzerland, Yugoslavia.

Table 10 - Probit Regressions for Fertility Transition

	(1)	(2)	(3)	(4)	(5)	(6)
	1841	1861	1881	1901	1921	1941
# of different nodes with Français	-0.00002 (0.93)	-0.008 (2.76)***	-0.025 (5.44)***	-0.022 (2.86)***	0.019 (3.87)***	0.001 (1.07)
Geodesic distance to Paris, 1000 km	0.0001 (0.33)	0.079 (1.95)*	-0.048 (0.46)	-1.036 (4.80)***	0.197 (1.93)*	0.004 (0.42)
Absolute difference in longitudes, to Paris	-0.032 (0.83)	-6.623 (2.55)**	-1.823 (0.28)	27.183 (2.05)**	-22.857 (3.51)***	-0.120 (0.24)
Absolute difference in latitudes, to Paris	-0.016 (0.40)	-9.104 (2.42)**	-11.418 (1.43)	48.128 (3.02)***	-30.036 (4.26)***	-0.969 (1.22)
Pseudo R ²	0.61	0.47	0.41	0.32	0.21	0.18
Standardized Effect (%)	-0.077	-26.495	-52.331	-16.097	6.549	0.204

(t-statistics in parentheses; * p<0.1; ** p<0.05; *** p<0.01)

The dependent variable for year t is defined as 1 is a region has undergone the fertility transition by year t (defined as having attained a 10% decline in I_g by date t), zero otherwise.

The table reports probit marginal effect. The standardized effect is equal to the probit marginal effect multiplied by the standard deviation of linguistic distance to Français, divided by the mean of the dependent variable.

Regressions are based on a balanced sample of 771 regions from 25 countries: Austria, Belgium, Bulgaria, Czechoslovakia, Denmark, England and Wales, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Luxembourg, Netherlands, Norway, Poland, Portugal, Romania, Russia, Scotland, Spain, Sweden, Switzerland, Yugoslavia.

Table 11 – Cross-regional Regressions for Ig through Time, with Country Fixed-Effects
(Dependent variable: Index of Marital Fertility, Ig)

	(1)	(2)	(3)	(4)	(5)	(6)
	Period 1 ^a (1831-1860)	Period 3 ^b (1851-1880)	Period 5 ^c (1871-1900)	Period 7 ^d (1891-1920)	Period 9 ^e (1911-1940)	Period 11 ^f (1931-1960)
# of different nodes with Français	16.299 (4.24)***	23.346 (12.53)***	22.183 (11.57)***	20.105 (9.66)***	12.858 (6.68)***	7.601 (4.74)***
Geodesic distance to Paris, km	0.142 (0.55)	0.068 (1.02)	0.006 (0.10)	0.018 (0.28)	-0.008 (0.25)	-0.022 (0.77)
Constant	578.165 (5.46)***	494.478 (12.08)***	468.778 (11.66)***	375.595 (8.78)***	55.956 (1.04)	191.099 (4.59)***
R-squared	0.69	0.69	0.61	0.59	0.65	0.64
# of regions	184	531	659	675	766	748
# of nations	5	20	24	25	25	24
Standardized Beta (%)	41.074	54.865	49.900	43.141	26.431	18.354
Standardized Beta (%), common sample of 630 regions ^g	-	-	49.548	43.218	26.978	17.980

Notes: t-statistics in parentheses: * $p < 0.1$; ** $p < 0.05$; *** $p < 0.01$

All regressions include additional controls for: Absolute difference in longitudes to Paris, absolute difference in latitudes to Paris, dummy = 1 if region is barred from France by a mountain range, dummy for contiguity to France, dummy if region shares at least one sea or ocean with France, dummy for landlocked region, dummy for region being on an island.

Ig was multiplied by 1000 for readability of the estimates.

In terms of their 1946 borders, countries to which regions belong are as follows:

(a): 5 countries as follows: Denmark, England and Wales, France, Netherlands, Switzerland.

(b): 20 countries as follows: as in (a) plus: Austria, Belgium, Finland, Germany, Ireland, Italy, Norway, Poland, Russia, Scotland, Sweden, Czechoslovakia, Hungary, Romania, Yugoslavia.

(c): 24 countries as follows: as in (b) plus Greece, Luxembourg, Portugal and Spain.

(d): 25 countries as follows: as in (c) plus Bulgaria.

(e): 25 countries as follows: as in (d).

(f): 24 countries as follows: as in (e) minus Czechoslovakia.

(g): Common sample of 630 regions comprises the following 23 countries: Austria, Luxembourg, Belgium, Denmark, England and Wales, Finland, France, Germany, Greece, Ireland, Italy, Netherlands, Norway, Poland, Portugal, Russia, Scotland, Spain, Sweden, Switzerland, Hungary, Romania, Yugoslavia.

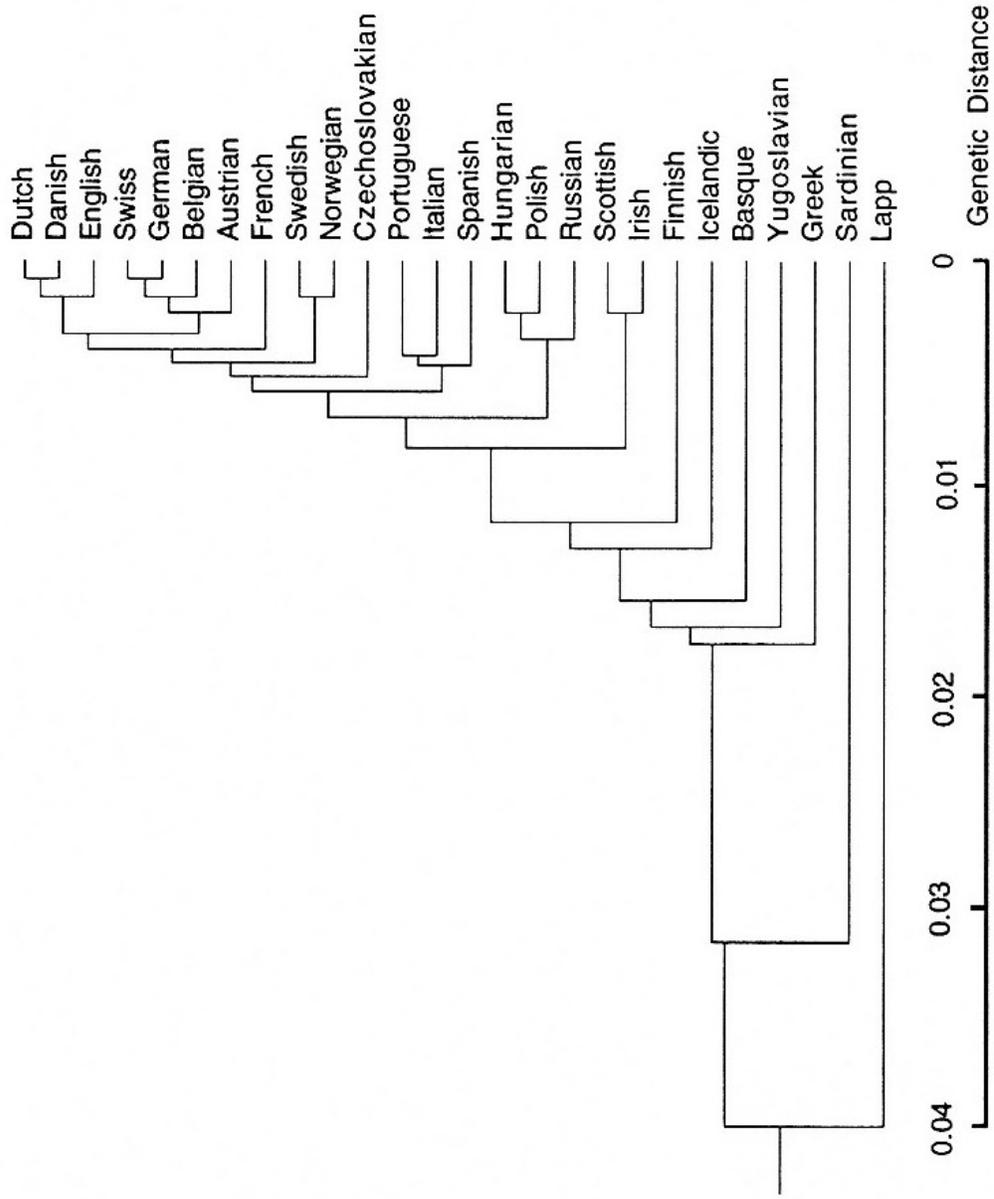


Figure 2 – Phylogenetic Tree of 26 European Populations
 (Source: Cavalli Sforza et al., 1994)

Figure 3 - Genetic Distance to France and the Fertility Transition

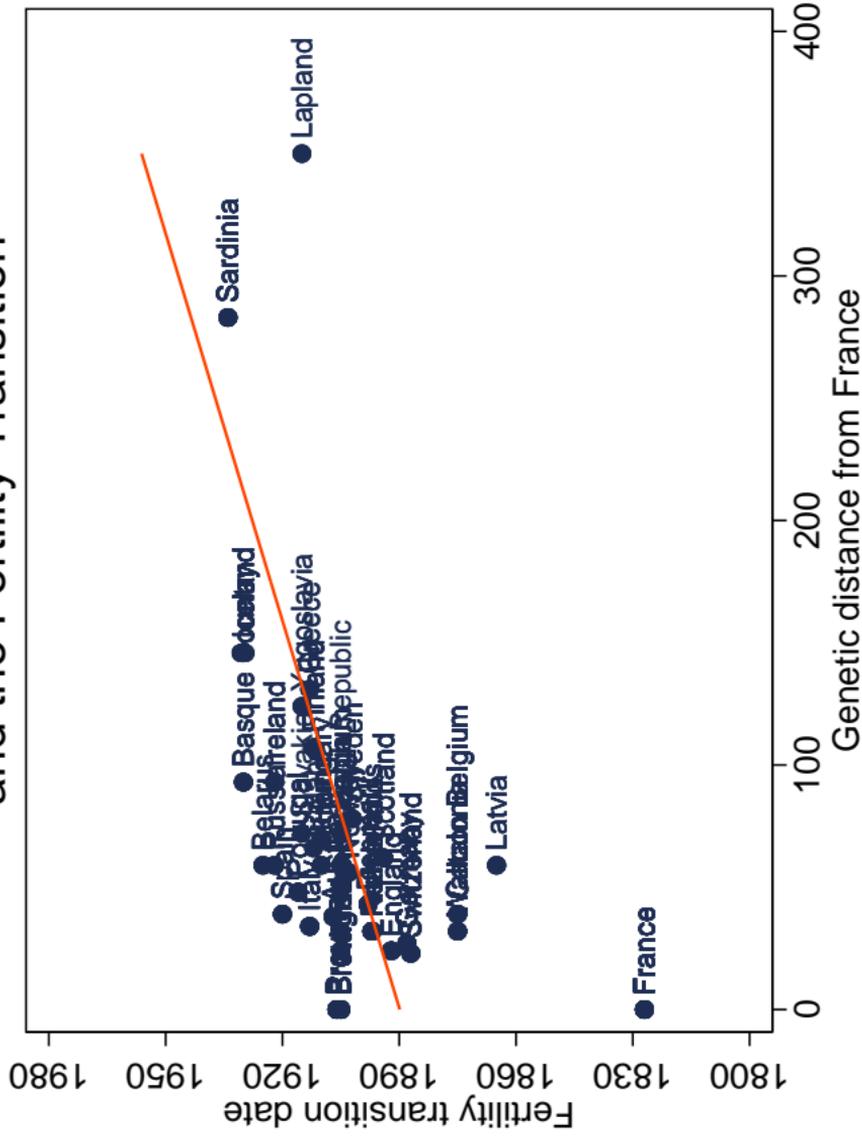


Figure 4 - Genetic Distance to France and the Fertility Transition, controlling for geodesic distance

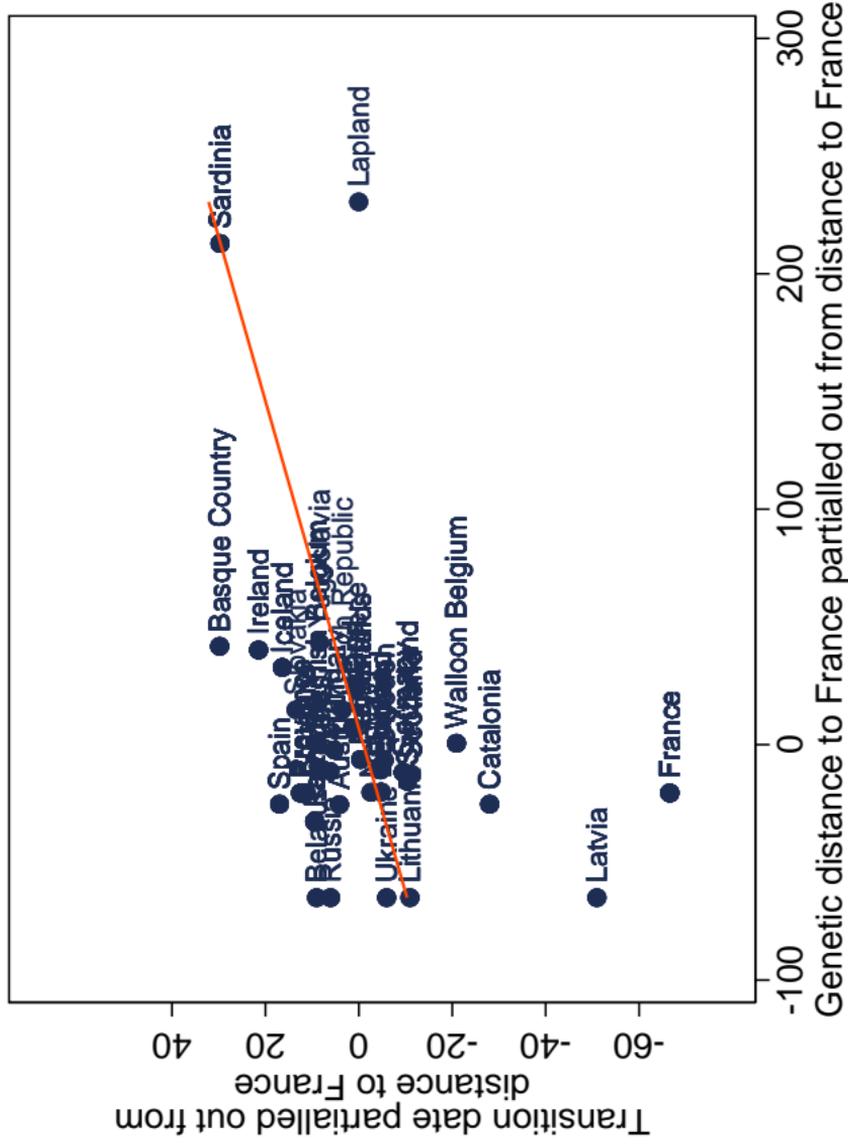


Figure 5 - Cumulative Distribution of Fertility Transition Dates

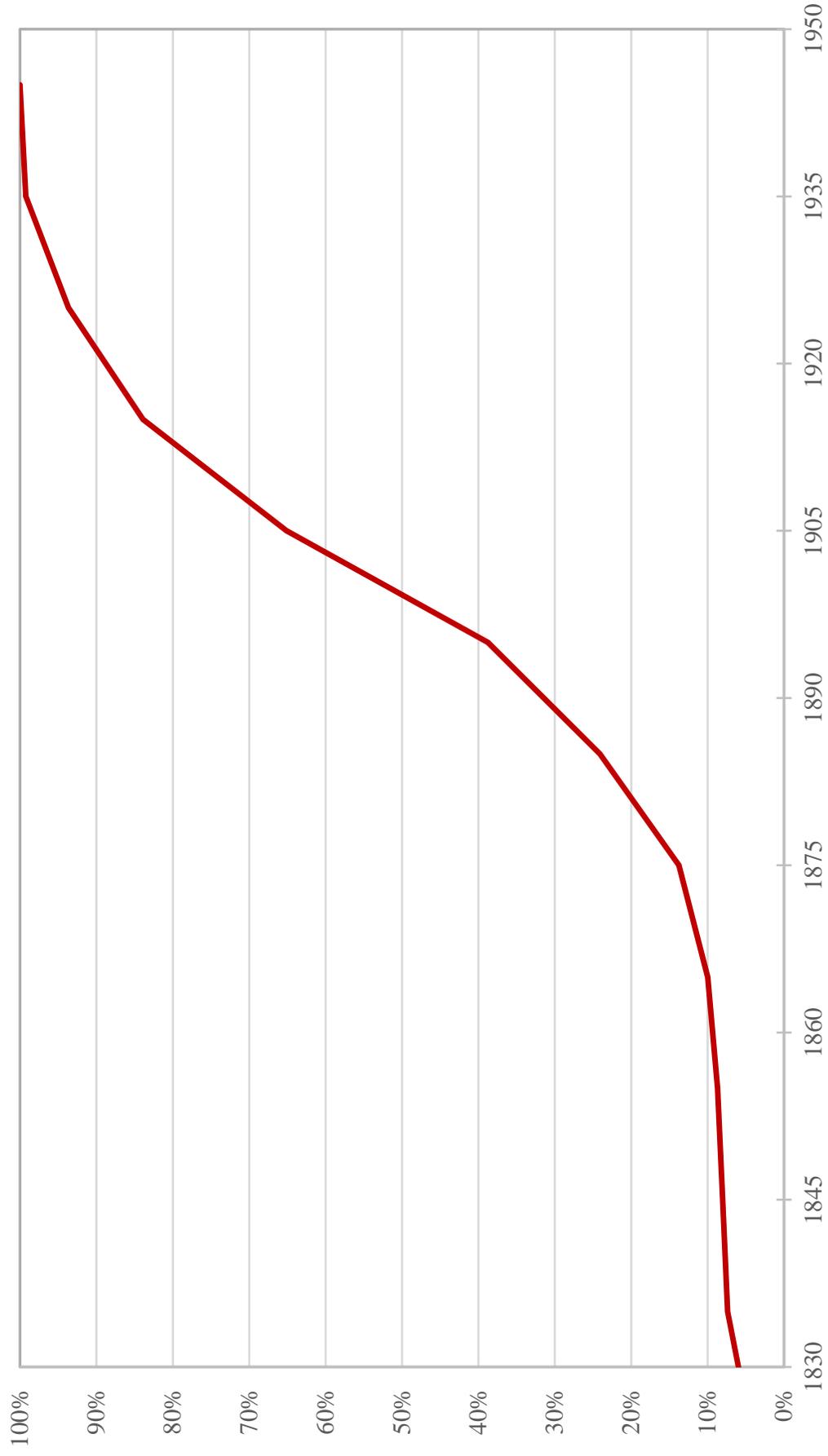
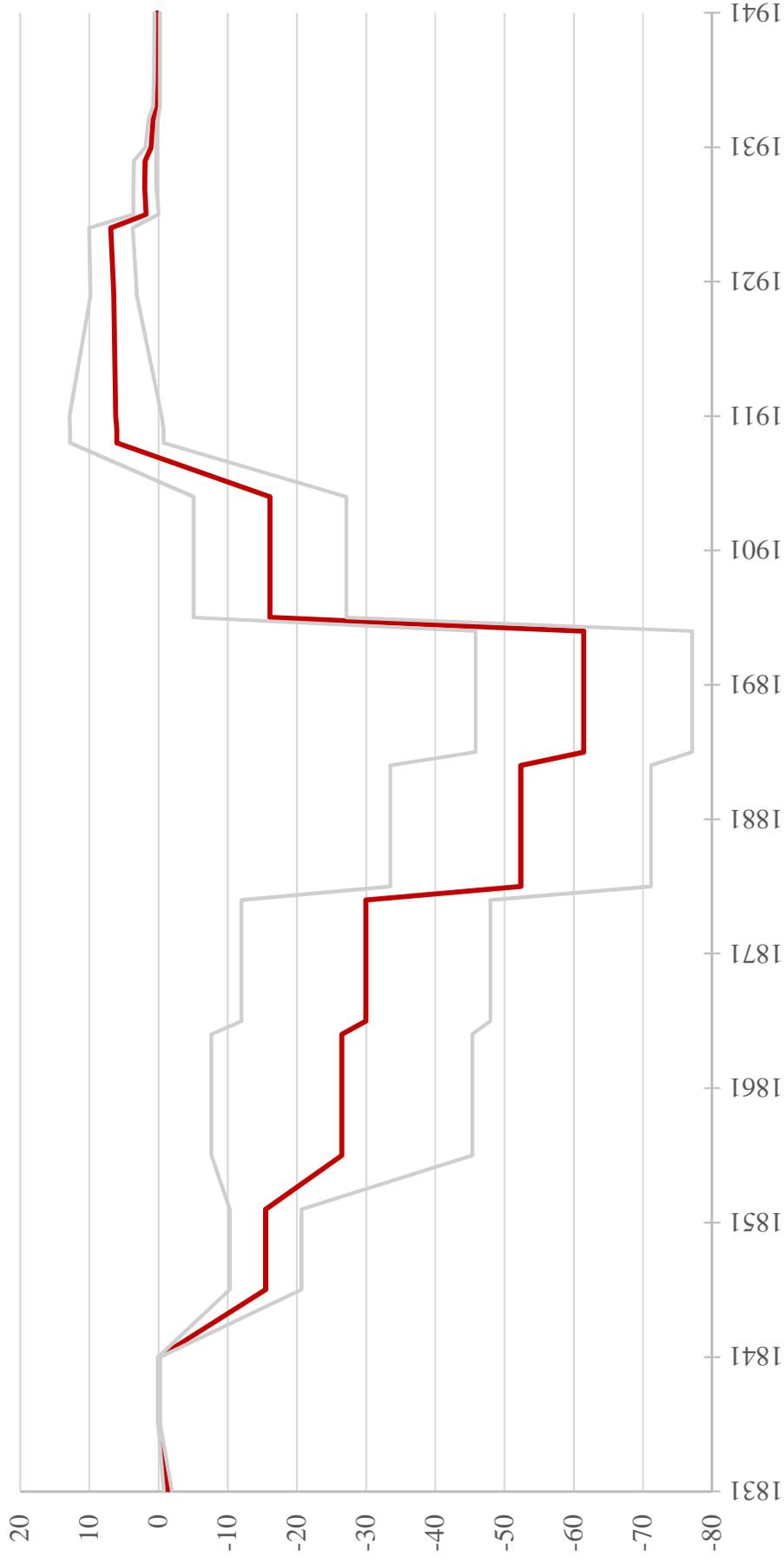
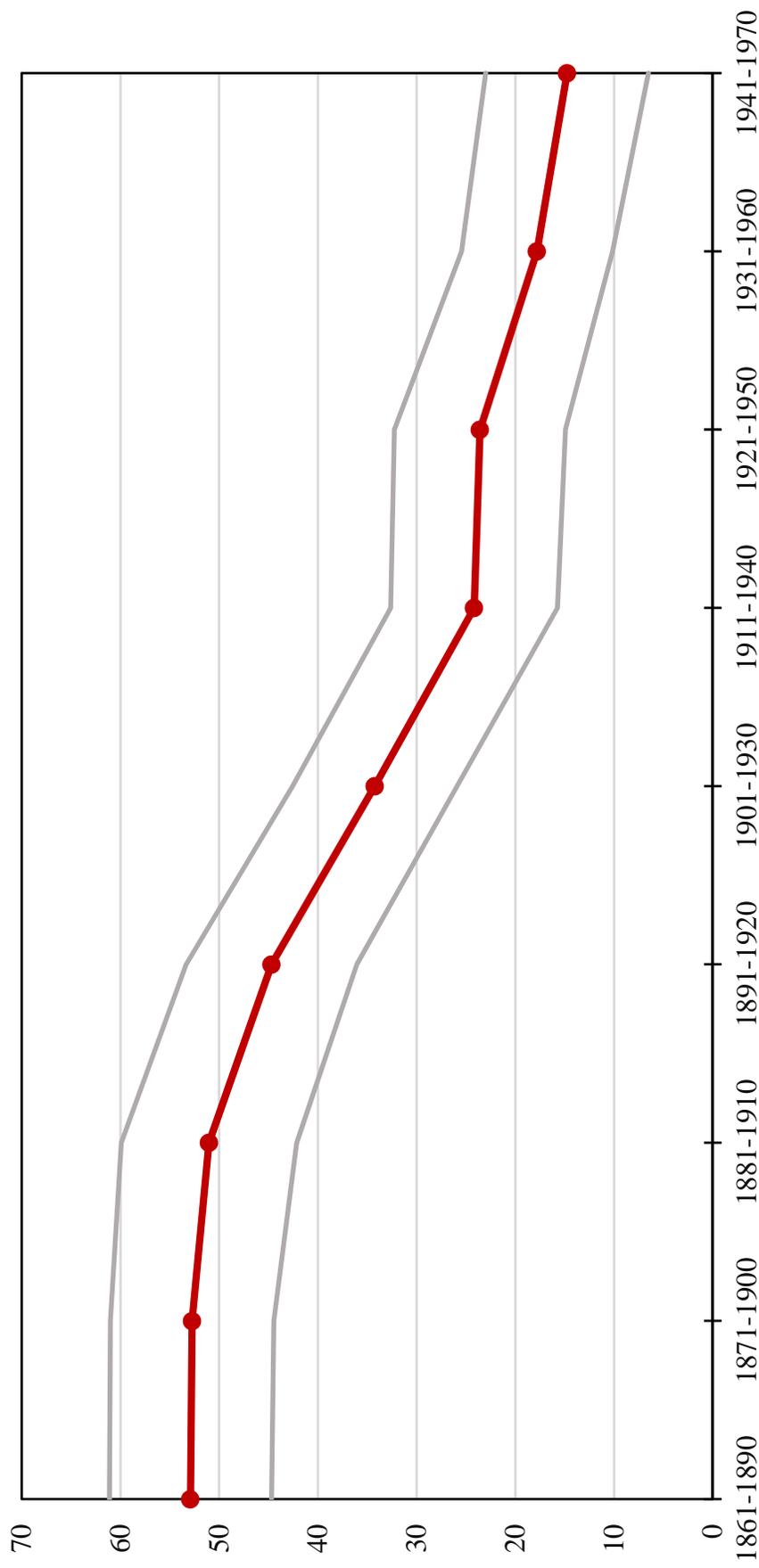


Figure 6 - Standardized Effect of Linguistic Distance to Français on the Probability of Having Experienced the Fertility Transition (95% CI in grey)



This chart depicts the standardized effect of linguistic distance to Français on the probability of having experienced the fertility transition, defined by a 10% decline in Ig, prior to the date on the x-axis. Estimates are obtained from cross-sectional probit specifications run at periodic dates between 1831 and 1941 in a balanced sample of 771 European regions.

Figure 7: Standardized Effect of Linguistic Distance to Français on I_g , common sample (95% CI in grey; 30 year bandwidth)



This chart depicts the standardized effect of linguistic distance to Français on marital fertility (I_g) through time, in overlapping samples of 30 years depicted on the x-axis. The sample is a balanced sample of 519 European regions.