The Diffusion of Development

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Abstract

This paper studies the barriers to the diffusion of development across countries from a very long-term perspective. We find that genetic distance, a measure associated with the amount of time elapsed since two populations' last common ancestors, bears a statistically and economically significant relationship with pairwise income differences, even when controlling for various other measures of geographical, climatic, cultural and historical differences. We provide an economic interpretation of these findings, within a framework in which (a) genetic distance captures divergence in characteristics that are transmitted vertically across generations within populations over the long term, including cultural traits, and (b) such differences in vertically-transmitted characteristics act as barriers to the horizontal diffusion of innovations from the world technological frontier. The empirical evidence over time and space is consistent with this "barriers" interpretation.

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1 Introduction

What explains the vast differences in income per capita that are observed across countries?[1] In this paper, we argue that barriers to the diffusion of development prevent poor countries from adopting economic practices, institutions and technologies that make countries rich. We argue that these barriers are not only geographic, but also human. We propose a way to measure overall differences in human characteristics that have been transmitted with variations across generations over the very long run, including culturally-transmitted traits, using genetic distance. We then test the hypothesis that these long-term differences have created barriers to the diffusion of innovations from the world technological frontier in modern times.[2]

At the center of our analysis is an important measure of distance between populations: genetic distance. For the first time, we document and discuss the relationship between genetic distance and differences in income per capita across countries. We find that measures of genetic distance have a statistically and economically significant effect on differences in income per capita, even when controlling for various measures of geographical isolation, and measures of cultural, climatic and historical differences.[3] The effect of genetic distance holds not only for contemporary income

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[1] Recent contributions to the literature on the determinants of income per capita using cross-country regressions include Hall and Jones (1999), Acemoglu, Johnson and Robinson (2001), Easterly and Levine (2003), Alcalá and Ciccone (2004), Rodrik, Subramanian and Trebbi (2004), Glaeser, La Porta, Lopez-de-Silanes and Shleifer (2004), among many others.

[2] There is a voluminous literature on cross-country income convergence, dating back to Baumol (1986). In the neoclassical literature, convergence occurs because the marginal return to capital is higher in countries farther from their steady-state, which depends, among other things, on the level of technology. In contrast, we seek to shed light on the factors that prevent or facilitate the diffusion of productivity-enhancing innovations across countries. In this respect, our paper is closer to the approach in Barro and Sala-i-Martin (1997), where technological diffusion drives convergence. Policy-induced constraints on the diffusion of technology are analyzed by Parente and Prescott (1994, 2002). Policy experimentation and imitation across neighbors are studied by Mukand and Rodrik (2005). Unlike these contributions, we consider more broadly the barriers to the diffusion of economic development from a very long-term perspective.

[3] In principle, this correlation could just reflect the impact of variables affecting both genetic distance and income differences. If that were the case, controlling for those variables would eliminate the effect of genetic distance on income difference. We control for a large number of reasonable suspects. In particular, we control for geography and region-specific differences that may impede the diffusion of development, as emphasized by Jared Diamond in his influential book *Guns, Germs and Steel* (1997) (see also Olsson and Hibbs, 2005 and Chandra and Putterman, 2006), and for measures of microgeography and transportation costs (Giuliano, Spilimbergo and Tonon, 2006). We find that

differences, but also for income differences measured since 1500. Moreover, the effect of genetic distance holds not only for contemporary and historical worldwide income differences, but also for income differences within Europe. In fact, the magnitude of the effect of genetic distance is larger for a sample of European countries than across countries from all continents.

These empirical findings motivate two key questions: 1) What does genetic distance between human populations actually measure, and 2) Why is genetic distance positively correlated with economic distance? In this paper we provide an economic model of technological and institutional diffusion to shed light on these questions.

Measures of genetic distance between populations are based on aggregated differences in allele frequencies for various *loci* on a chromosome. We use measures of F_{ST} distance, also known as coancestor coefficients.[4] Since most genetic differences tend to accumulate at a regular pace over time, as in a kind of molecular clock, genetic distance is closely linked to the time elapsed since two populations' last common ancestors (that is, the time since the two populations were in fact the same population), and can be used to determine paths of genealogical relatedness of different populations over time. On average, populations that are more genetically distant have had more time to diverge in a broad variety of characteristics transmitted intergenerationally. These include characteristics that are passed on through DNA, but also traits that are passed on not through biological reproduction but through cultural transmission.[5] As long as these cultural characteristics are transmitted to younger generations from genetically related individuals within their population, they will be correlated with genetic distance.

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these geographical and regional variables often do have an effect on income differences, but that their inclusion does not eliminate the effect of genetic distance as an independent explanatory variable. Moreover, the effect of genetic distance on income differences holds within Europe, where geographic differences are much smaller.

[4] Our main source for genetic distances between human populations is Cavalli-Sforza, Menozzi and Piazza (1994). Recent textbook references on human evolution are Boyd and Silk (2003) and Jobling, Hurles and Tyler-Smith (2004). For a nontechnical discussion of these concepts see Dawkins (2004).

[5] Evolutionary models of cultural transmission have been developed by Cavalli-Sforza and Feldman (1981) and Boyd and Richerson (1985). For a nontechnical discussion see Cavalli-Sforza and Cavalli-Sforza (1995, chapter 8). Economic models of cultural transmission from parents to children have been provided by Bisin and Verdier (2000, 2001). Galor and Moav (2003) present an innovative theory of long-term economic growth in which a key role is played by evolutionary changes in preference parameters that are genetically transmitted across generations. For an in-depth discussion of these issues, see also Galor (2005).

Therefore, one should not view genetic distance as an exclusive measure of distance in DNA-transmitted characteristics, and should not assume that the mechanisms linking genetic distance to economic distance are necessarily genetic.[6] It is more appropriate to interpret genetic distance as a general metric for genealogical distance between populations, capturing overall differences not only in genetically transmitted features but also in culturally transmitted human characteristics. The literature on cultural transmission and evolution distinguishes between *vertical* transmission (across different generations within the same group) and *horizontal* transmission (within the same generation, across possibly unrelated groups).[7] We define as "vertically-transmitted characteristics" (or vertical characteristics, for short) all traits passed across generations within populations, whether genetically or culturally. If we take this broader perspective, we can interpret the effect of genetic distance on income differences as evidence of an important role for vertical characteristics transmitted with variations across generations over the very long run.

How do these long-term vertical characteristics affect current income differences? What are the economic mechanisms that link genetic distance to economic distance? Our key hypothesis is that differences in *vertical* characteristics act as barriers to the *horizontal* diffusion of innovations from the world technological frontier. The idea is quite intuitive: societies that are more similar to the innovator in terms of vertically-transmitted habits, customs and other traits such as language face lower current costs to imitate and adapt productivity-enhancing innovations. In contrast, societies that are historically more distant face higher imitation costs, stemming from a variety of possible obstacles to communication and adaptation (different rules and conventions, different norms and values, etc.). If this hypothesis is correct, the relevant measure of genetic distance associated with economic distance between two societies should not be the absolute pairwise genetic distance between the two societies, but their *relative* distance from the world technological frontier. In our empirical analysis we test this central implication using Britain and the United States as the world technological frontier in modern times. Consistent with our hypothesis, we find that the effect of relative genetic distance on economic distance is (a) positive, and (b) larger than the effect of absolute genetic distance, an imperfect proxy for the relative genetic distance from the frontier.

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[6] Moreover, as we discuss in Section 2, any sharp distinction between genetic and cultural characteristics may be misleading, since the economic impact of genetic and cultural characteristics is likely to depend on their combination and interaction.

[7] See Cavalli-Sforza and Feldman, 1981; Boyd and Richerson, 1985; Shennan, 2004. We will discuss this terminology in more detail in Section 3.

The variation over time of the effect of genetic distance on income differences provides additional important clues about the economic mechanisms underlying our results. The effect, while always large, positive and significant, has varied in magnitude since 1500 in interesting ways. The effect slightly declined from 1500 to 1820, spiked up and peaked in 1870, and steadily declined again afterwards. This is consistent with the interpretation of genetic distance as related to barriers to the diffusion of technological and institutional changes from the world technological frontier. The effect of barriers should increase right after a major improvement in the technology for the production of innovations and imitation (namely, the introduction of modern R&D at the onset of the Industrial Revolution), when only the innovator and its closest followers have adopted the new R&D technology. We show theoretically that the effect should eventually peak and then decline over time, as the regime change in R&D gradually spreads to more distant populations, improving their ability to imitate the continuous flow of innovations from the frontier Eventually, the effect of genetic distance on income differences returns to its long-term (positive) level. In summary, the pattern of the effect of genetic distance over time and space is consistent with our theoretical model: genetic distance captures long-term differences in vertically-transmitted characteristics that constitute barriers to the horizontal diffusion of innovations from the world technological frontier.

Our paper is organized as follows. Section 2 presents an analytical framework in which genetic distance captures divergence in characteristics that are transmitted vertically across generations within populations over the long run, and those differences act as barriers to the horizontal diffusion of innovations from the world technological frontier. In Section 3, we discuss our data on genetic distance and what it measures. In Section 4 we test the predictions of our theoretical model. Section 5 concludes.

2 The Long-Term Diffusion of Development

In this section we argue that differences in vertically transmitted characteristics create barriers to the long-term diffusion of development. We present a theoretical framework linking genetic distance, vertical characteristics, and the horizontal diffusion of economic development from the technological frontier. This section has three parts. First, we illustrate our key ideas within a simplified stylized setting. Second, we present a microfounded dynamic model of innovation and technological diffusion that confirms the basic insights from the simplified model, and generates additional testable implications. Third, we briefly provide a general discussion of the different possible channels linking genealogical relatedness and economic outcomes. The analytical framework presented in this section leads to testable predictions about the relationship between measures of genetic distance and differences in income per capita across time and space.

2.1 The Basic Ideas

Genetic distance between populations captures the time elapsed since two populations were in fact the same population and can be used to determine paths of genealogical relatedness of different populations over time. Therefore, genetic distance can be interpreted as a general metric for average differences in those characteristics. Typically, such traits include not only features that are directly transmitted from parents to children via DNA, but also characteristics that are culturally transmitted across generations within a population (customs, habits, etc.). While the mechanism of transmission itself is not genetic, these cultural traits are also linked to genealogical relatedness, insofar as the characteristics are passed on vertically by individuals who are genetically related. In fact. it has been noted that "the measured heritability between parents and offspring is as great for traits passed on culturally as for those passed on genetically by biological reproduction" (Shennan, 2002, p. 43; see also Boyd and Richerson, 1985, p. 55)[8] In this paper we define *vertically transmitted characteristics* (or vertical characteristics) as the set of characteristics passed on across generations within a population, biologically and/or culturally, over the very long run - i.e., over the time horizon along which populations have phylogenetically diverged (thousands or tens of thousands of years).[9] Consequently, the first step of our analytical framework is based on the following key idea:

Hypothesis 1. *Genetic distance between populations measures their average distance in the overall set of characteristics that are vertically transmitted across generations in the very long run.*

As already mentioned, this meaning of the term "vertical" is borrowed from the evolutionary

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[8] It is important to stress that such "vertical" transmission takes place across generations within a given population, and that "oblique" transmission from other (older) genetically-related people within the group is also part of our definition. Hence "vertical" in our context is not limited to parent-to-child transmission *stricto sensu*, but has a broader meaning. This broader connotation is slightly different from the use of the term often found in the anthropological literature and related fields. We thank Robert Boyd for pointing this out to us.

[9] The central importance of vertical transmission of cultural characteristics to account for differences among societies has been well documented in cross-cultural studies. For example, Guglielmino et al. (1995) show that vertical transmission has a paramount role in accounting for variation of cultural traits in a group of African societies. See also Shennan (2002, chapter 3).

literature on cultural transmission (Cavalli-Sforza and Feldman, 1981; Boyd and Richerson, 1985; Shennan, 2002; Richerson and Boyd, 2004). This literature distinguishes between *vertical* transmission (across different generations within the same group) and *horizontal* transmission (within the same generation, possibly across different groups). Our central hypothesis is that vertical and horizontal transmission are closely linked:

Hypothesis 2 *Distance in vertical characteristics acts as a barrier to the horizontal diffusion of innovations.*

In other words we assume that populations that share a more recent common history, and are therefore closer in terms of vertically transmitted characteristics (habits, customs, etc.), face lower costs and obstacles to adopt each other's innovations. In particular, we are interested in the horizontal diffusion of economic development in historical times, and especially after the Industrial Revolution. Thus, we will focus on differences in vertical characteristics as barriers to the diffusion of innovations from the modern technological frontier.[10]

A highly stylized model can illustrate our key ideas in the simplest possible way. Consider three periods (o for "origin," p for "prehistory," and h for "history"). In period o there exists only one population (population 0). In period p the original population splits in two populations (population 1 and population 2). In period h each of the two populations split in two separate populations again (population 1 into populations 1.1 and 1.2, and population 2 into populations 2.1 and 2.2), as in Figure 1. In this setting the genetic distance $d_g(i, j)$ between population i and population j can be simply measured by the number of periods since they were one population:

$$d_g(1.1, 1.2) = d_g(2.1, 2.2) = 1 \tag{1}$$

and:

$$d_g(1.1\ ,\ 2.1) = d_g(1.1\ ,\ 2.2) = d_g(1.2\ ,\ 2.1) = d_g(1.2\ ,\ 2.2) = 2 \tag{2}$$

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[10] World technological leadership since the British Industrial Revolution (1700s) has been predominantly associated with Britain and, by the late 1800s, the United States (Brezis, Krugman, and Tsiddon, 1993). In the years before the Industrial Revolution, the technological frontier was probably held by the the Dutch. According to Maddison (2003), in previous times the regions with the highest levels of income per capita were in Italy (around 1500) and China (around 1000). We will return to this issue in Section 4.

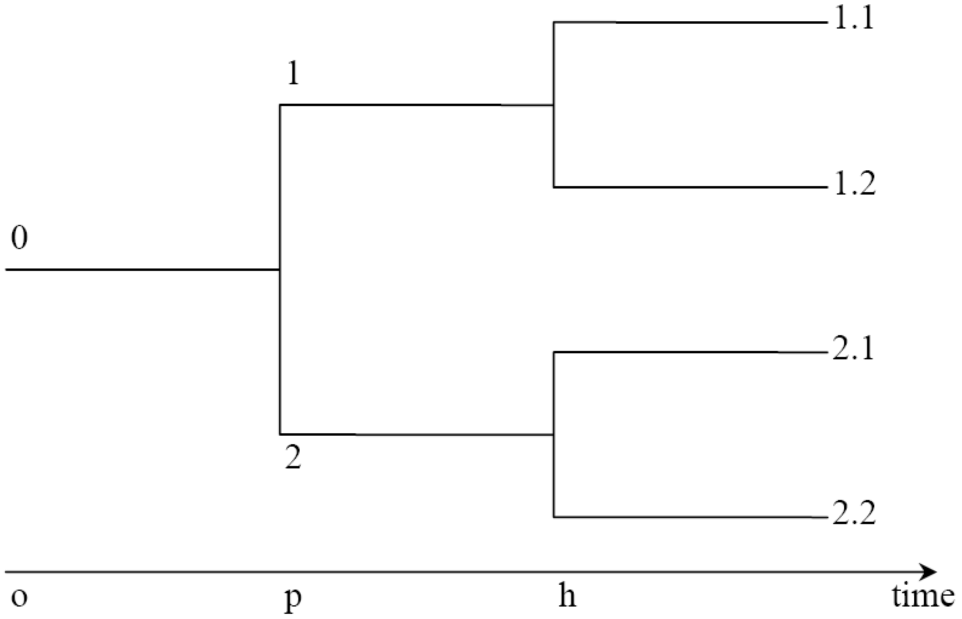

Figure 1 - Population Tree

For simplicity and without much loss of generality, we summarize all vertical characteristics of a population as a point on the real line That is, we say that a population i has vertical characteristics v_i, where v_i is a real number. These characteristics are transmitted vertically, with variations, over the long run (i.e., from one period to the next). Hence, populations inherit characteristics from their ancestor populations with changes. For example, in period p population 1 will have characteristics given by:

$$v_1 = v_0 + \eta_1 \tag{3}$$

where v_0 are the characteristics inherited from the previous generations, while η_1 denotes the change that has taken place between period o and period p. In general, a population i' descending from a population i will have characteristics:

$$v_{i'} = v_i + \eta_{i'} \tag{4}$$

In this analysis we are going to focus on the simplest possible mechanism for variation: vertical change as a random walk. In particular, we assume that for every population i', $\eta_{i'}$ takes value $\eta > 0$ with probability 1/2 and $-\eta$ with probability 1/2. That is, we model changes in vertically transmitted characteristics as neutral and due to random drift. This view is consistent with the interpretation of genetic distance itself as a molecular clock. While one could consider more complex processes, this formalization has two inherent advantages: (a) it is simple ("Occam's razor"), and

(b) it allows us to illustrate how neutral random changes can be *sufficient* to generate our theoretical predictions.[11]

When vertical transmission follows the above process, the distance in vertical characteristics between two populations $d_v(i, j) \equiv |v_j - v_i|$ is on average increasing in their genetic distance $d_g(i, j)$. Specifically, in period h the expected difference in vertical characteristics between populations at a genetic distance equal to 2 and populations at a genetic distance equal to 1 is given by:

$$E\{d_v(i,j) \mid d_g(i,j) = 2\} - E\{d_v(i,j) \mid d_g(i,j) = 1\} = \frac{\eta}{2} > 0 \tag{5}$$

That this is not a deterministic relationship. In principle, it is possible that two populations that are genealogically more distant may end up with *more similar vertical characteristics* than two populations that are more closely related. But that outcome is less likely to be observed than the opposite. On average, genetic distance and distance in vertically-transmitted characteristics go hand in hand. This is a specific illustration of our general Hypothesis 1.

Our main idea (Hypothesis 2) can also be illustrated within this highly simplified setting. Assume that in periods o and p all populations produce output using the basic technology $Y = A_0 L$, so that all populations have the same income per capita $y_0 = A_0$. In period h a population happens to find a more productive technology $A_1 = A_0 + \Delta$ where $\Delta > 0$.[12] Denote this population at the technological frontier with f. Consistent with Hypothesis 2, we assume that populations that are farther from population f in terms of vertical characteristics face higher barriers to adopt the new technology. To fix ideas, assume that a society i at a vertical distance from the frontier equal to $d_v(i, f)$ can improve its technology only by:

$$\Delta_i = [1 - \beta d_v(i, f)]\Delta \tag{6}$$

where the parameter $\beta > 0$ captures the barriers to the horizontal diffusion of innovations due to distance in vertical characteristics.[13] Hence, income per capita in society i is given by:

$$y_i = A_0 + [1 - \beta d_v(i, f)]\Delta \tag{7}$$

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[11] In Subsection 3.3 we will return to this issue more generally.

[12] We abstract from the possibility that the likelihood of finding the innovation may itself be a function of a society's vertical characteristics. Such direct effects of vertical characteristics may strengthen the links between genetic distance and economic outcomes, but are not necessary for our results.

[13] Without loss of generality, we assume that β is lower than 1/2. Alternatively, the formula could be re-written as $\Delta_i = \max\{[1 - \beta d_v(i, f)]\Delta, 0\}$

This immediately implies that the economic distance between population i and population j, measured by their income difference $d_e(i,j) \equiv |y_i - y_j|$, is a function of their *relative* vertical distance from the frontier $|d_v(i,f) - d_v(j,f)|$:

$$d_e(i,j) \equiv |y_j - y_i| = \beta\Delta|d_v(i,f) - d_v(j,f)| \tag{8}$$

As we have shown, vertical difference $d_v(i,j)$ and genetic distance $d_g(i,j)$ go hand in hand on average. Therefore, the above relationship implies that, on average, the income difference across societies is increasing in their *relative genetic distance* from the frontier society. Formally, we have:

$$\begin{aligned} E\{d_e(i,j)||d_g(i,f) - d_g(j,f)| &= 2\} - \\ E\{d_e(i,j)||d_g(i,f) - d_g(j,f)| &= 1\} = \frac{\eta\beta\Delta}{3} \end{aligned} \tag{9}$$

This result is intuitive. As we increase relative genetic distance from the frontier, the expected income gap increases. The size of the effect is a function of (a) the extent of divergence in vertically transmitted characteristics (η) as societies follow separate paths over time, (b) the extent to which this divergence in vertical characteristics constitutes a barrier to the horizontal diffusion of productivity-enhancing innovations (β), and (c) the size of the improvement in productivity at the frontier (Δ).

Thus, our framework predicts a positive correlation between *economic distance* $|y_j - y_i|$ and *relative genetic distance from the frontier* $|d_g(i,f) - d_g(j,f)|$. Our model can also account for a positive correlation between economic distance and simple genetic distance $d_g(i,j)$ as long as $|d_g(i,f) - d_g(j,f)|$ and $d_g(i,j)$ are positively correlated. In fact, it is easy to verify that the two measures are positively correlated in our theoretical framework. More importantly, as we will see in Section 4, relative genetic distance from the frontier and simple genetic distance are also positively correlated in the actual data. Our framework then provides an economic explanation for the observed positive correlation between economic distance and genetic distance. At the same time, our theory predicts that *relative* genetic distance from the frontier should have a *stronger* impact on economic distance than simple genetic distance, because it is a more accurate proxy for the true variable (relative distance from the frontier in terms of vertically transmitted characteristics). This point can be illustrated within our stylized framework. For example, the expected economic distance associated with an absolute genetic distance $d_g(i,j) = 1$ in our model is

$$E\{d_e(i,j)|d_g(i,j) = 1\} = \eta\beta\Delta \tag{10}$$

while the expected economic distance associated with an equivalent level of *relative* genetic distance $|d_g(i,f) - d_g(j,f)| = 1$ is *higher*:[14]

$$E\{d_e(i,j)||d_g(i,f) - d_g(j,f)| = 1\} = \frac{7\eta\beta\Delta}{6} > E\{d_e(i,j)||d_g(i,j) = 1\} \tag{11}$$

In summary, our theory has the following testable implications:

Implication 1. *Relative genetic distance from the frontier is positively correlated with economic distance.*

and:

Implication 2. *The effect on economic distance associated with relative genetic distance from the frontier is larger than the effect associated with absolute genetic distance.*

In Section 4 we will test these two implications empirically. Before we go to the data, we are going to extend our theoretical analysis in order to provide a formalization of the diffusion of innovations within a microfounded setup, yielding additional testable implications.

2.2 A Model of the Historical Period

Above we have presented a highly stylized model in which the horizontal diffusion of modern development has been collapsed into one big exogenous innovation of size Δ. In this subsection we will extend our analysis to a dynamic setting in which the processes of innovation and imitation are endogenous and take place over time. The purpose of this analysis is to illustrate our hypotheses within a model that closely builds on the existing literature on the endogenous diffusion of technology. Specifically, we build closely on Barro and Sala-i-Martin (1997, and 2004, chapter 8), with the additional assumption that imitation costs are a function of distance in vertical characteristics between the imitating society and the technological leader. Our analysis will now be focused on the more recent historical period in which horizontal diffusion of modern development takes place, rather than on the very long term in which populations split and vertical characteristics (slowly) change over time. Therefore, for simplicity, we will now abstract from long-term changes in populations and vertical characteristics, and assume a constant number of societies with given vertical characteristics.[15]

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[14] An analogous relationship exists between $E\{d_e(i,j) \mid |d_g(i,f) - d_g(j,f)| = 2\}$ and $E\{d_e(i,j) \mid |d_g(i,j) = 2\}$.

[15] In other words, the implicit assumption, quite realistically, is that convergence to the economic steady-state takes place faster than the long-term process of population splits and vertical cultural change. An extension of this model of diffusion to allow for changes in vertical characteristics over time is left for further research.

Consider a world in which each society i $(i = 1, 2, ...M)$ is inhabited by a population of size $L_i = 1$ with vertical characteristics v_i, where v_i is a point on the real line, and $d_v(i,j) \equiv |v_i - v_j|$ is the distance between society i and society j in the space of vertical characteristics. Time t is continuous. At each time t consumers in each economy i maximize:

$$U_i(t) = \int_s^\infty \ln C_i(s) e^{-\rho(t-s)} ds \tag{12}$$

under a standard budget constraint, where $C_i(t)$ is consumption, and $\rho > 0$ is the subjective discount rate. The Euler equation for the optimal growth rate of consumption holds:

$$\frac{dC_i}{dt}\frac{1}{C_i(t)} = r_i(t) - \rho \tag{13}$$

where $r_i(t)$ is the real interest rate in society i (we assume that the M societies are not financially integrated). At time t, in each society i, there is a continuum of intermediate goods, measured on the interval $[0, A_i(t)]$. Each intermediate good is produced by a local monopolist. In each society i final output $Y_i(t)$ is produces according to:

$$Y_i(t) = \int_0^{A_i(t)} [X_{ki}(t)]^\alpha dk, \quad 0 < \alpha < 1 \tag{14}$$

where X_{ki} is the quantity of intermediate good of type k employed at time t in economy i. We assume that at time t_0 society f is at the technological frontier, which means that $A_f(t_0) > A_i(t_0)$ for all $i \neq f$. Innovation at the frontier economy takes place endogenously, as in Romer (1990) and related literature.[16] In particular, as in Barro and Sala–i-Martin (1997 and 2004, chapters 6 and 8), we assume that the inventor of intermediate good k retains perpetual monopoly power over the production of that input in society f, and henceforth sells it at price $P_k = \dfrac{1}{\alpha}$, earning the profit flow $\pi = (1-\alpha)\alpha^{(1+\alpha)/(1-\alpha)}$ at each time t.[17] The cost of inventing a new intermediate good at the frontier is λ units of final output. Free entry into the innovation sector implies that the real interest rate $r_f(t)$ must be equal to π/λ. We assume $\pi/\lambda > \rho$, which implies that consumption grows at the constant rate:

$$g \equiv \frac{\pi}{\lambda} - \rho > 0 \tag{15}$$

Consequently, output $Y_{if}(t)$ and the frontier level of intermediate goods $A_f(t)$ will also grow at the rate g.

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[16] Textbook surveys of this literature are provided by Aghion and Howitt (1998) and Barro and Sala-i-Martin (2004).

[17] For a detailed derivation see Barro and Sala-i-Martin (1997 and 2004)

The other societies cannot use the intermediate goods invented in economy f directly, but, as in Barro and Sala-i-Martin (1997), must pay an imitation cost μ_i in order to adapt (or translate) the intermediate goods to local conditions. Our key assumption is that such imitation costs are *increasing in the distance in vertically characteristics between the imitator and the frontier.* Specifically, we assume that economy i's imitation cost is:

$$\mu_i(t) = \lambda e^{\theta d_v(i,f)} \left(\frac{A_i(t)}{A_f(t)} \right)^{\psi} \tag{16}$$

The above specification is consistent with Hypothesis 2: differences in vertical characteristics increase the costs of horizontal imitation. The parameter θ captures the extent to which dissimilarity in vertical characteristics increases imitation costs.[18] For a given distance in vertical characteristics, an imitator in society i faces lower imitation costs when there is a larger set of intermediate goods available for imitation (that is, when $A_i(t)/A_f(t)$ is low). The rationale for this assumption is that the intermediate goods that are easier to imitate are copied first. The parameter $\psi > 0$ captures this advantage from technological backwardness.[19]

Again, we assume that an imitator who pays cost $\mu_i(t)$ to imitate good k has perpetual monopoly power over the production of that input in economy i, and hence can charge $P_k = 1/\alpha$, earning the profit flow $\pi = (1-\alpha)\alpha^{(1+\alpha)/(1-\alpha)}$, while output is proportional to available intermediate goods $A_i(t)$ in equilibrium:

$$Y_i(t) = \alpha^{2\alpha/(1-\alpha)} A_i(t) \tag{17}$$

As shown in Barro and Sala-i-Martin (1997, 2004), with free entry into the "imitation" sector, economy i's real interest rate in equilibrium is:

$$r_i(t) = \frac{\pi}{\mu_i(t)} + \frac{d\mu_i}{dt} \frac{1}{\mu_i(t)} \tag{18}$$

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[18] The parameter θ plays a function analogous to β in the framework of Subsection 2.1.

[19] Whether imitators whose technology is farther from the technological frontier face lower or higher imitation costs is debated in the empirical literature (for a recent survey, see Fagerberg, 2004). Our perspective suggests that, when assessing the relationship between imitation costs and technological backwardness empirically, one should control for distance in long-term vertical characteristics. As we will see, in steady-state societies that are farther technologically (and hence should face *lower* imitation costs for this reason) are also farther in terms of vertical distance from the frontier (and hence should face *higher* imitation costs through this channel). Hence, failure to account for this vertical distance from the frontier may lead to overestimate the imitation costs directly associated with a given technology gap - that is, to underestimate the advantages directly associated with technological backwardness (i.e., with a lower $\frac{A_i(t)}{A_f(t)}$ in our framework).

2.2.1 Economic distance in steady-state

In steady-state, the level of imitation costs μ_i^* is constant, while the number of intermediate goods in economy i, as well as output and consumption, all grow at the same rate as in economy f - that is, at rate $g = \frac{\pi}{\lambda} - \rho$. Hence, in steady-state the real interest rates in all economies are identical and equal to $\frac{\pi}{\lambda}$. Consequently, we have:

$$\mu_i^* = \mu_j^* \tag{19}$$

for all i and j, which implies the following relationship in steady state:

$$\ln Y_i^*(t) - \ln Y_j^*(t) = \ln A_i^*(t) - \ln A_j^*(t) = \frac{\theta}{\psi}[d_v(i,f) - d_v(j,f)] \tag{20}$$

The intuition of the above equation is straightforward: long-term differences in output between societies is an increasing function of their relative cost to imitate, which depends on their relative distance from the frontier in terms of vertical characteristics.[20] Therefore, this microfounded dynamic model of horizontal diffusion confirms the key implications of the simplified reduced-form setup presented in Subsection 2.1.

2.2.2 Regime Change in R&D Technology

The above analysis has been developed for a given innovation and imitation technology (for a given parameter λ, in our setting). However, one can argue that the past two centuries have witnessed a major regime change in the very mechanisms through which societies improve their technologies over time. Alfred North Whitehead (1931, p.38) famously said that "the greatest invention of the 19th century was the invention of the method of invention".[21] In our framework, we can formalize this major regime change as a one-shot change in R&D technology at the frontier (say, a dramatic reduction in λ at the frontier at the onset of the Industrial Revolution). Since followers' R&D activities are focused on imitation, better R&D methods, if successfully adapted, may allow a reduction in *imitation* costs. But there is no reason why that adjustment should happen instantaneously. In fact, one should expect that a major change in R&D technology at the frontier may spread only slowly to the imitation technology at the periphery. This motivates the

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[20] Interestingly, the effect of relative genetic distance from the frontier is decreasing in parameter ψ, which measures the benefits (lower imitation costs) associated with technological backwardness.

[21] Building on this historical insight, Howitt and Mayer-Foulkes (2004) provide a Shumpeterian model in which economies converge to the high-growth steady-state path only if they can successfully adopt "modern R&D" introduced at the beginning of the industrial revolution.

important question: "How does the change in R&D technology itself spread to imitating societies?" Consistent with our general approach - and, in particular, with Hypothesis 2 - we should expect that followers that are closer to the frontier society in terms of long-term vertical characteristics would also be in a better position to adopt those improvements in R&D technology, and hence would be able to reduce their imitation costs at an earlier date. In what follows, we will model these ideas within our simplified framework - namely, we will study the transitional dynamics associated with a shock to R&D technology at the frontier, and the gradual diffusion of the improvement to imitation technologies at the periphery.[22]

Let $\lambda_f(t)$ denote the cost of inventing a new intermediate good at the frontier at time t, while the imitation cost for society i is:

$$\mu_i(t) = \lambda_i(t) e^{\theta d_v(i,f)} \left(\frac{A_i(t)}{A_f(t)} \right)^{\psi} \tag{21}$$

Assume that, for $t < T$, the parameters are given as in the above analysis: $\lambda_f(t) = \lambda_i(t) = \lambda$ for all $i \neq f$, and the system is in steady-state.

Now, assume that at time T the frontier society reduces its innovation cost to $\lambda' < \lambda$. We assume that this change in R&D technology does not trickle down immediately to the other societies, but spreads as a function of their distance from the frontier in terms of vertical characteristics. In particular, we assume that each society i will reduce its imitation parameter from $\lambda_i(t) = \lambda$ for $t < T_i$ to $\lambda_i(t) = \lambda' < \lambda$ for $t \geq T_i$, where T_i is increasing in $d_v(i,f)$. To fix ideas, assume:

$$T_i = T + \zeta d_v(i,f) \qquad \zeta > 0 \tag{22}$$

As shown in Appendix 1, the transitional dynamics of the economic distance between the frontier society and a society at a distance $d_v(i,f) > 0$ follows the path in Figure 2, with the economic distance between society i and the frontier peaking at time $T' < T + \zeta d_v(i,f)$.

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[22] Analogous effects could be obtained if one were to model the shock as a major improvement in total factor productivity. For simplicity, we abstract from this straightforward extension.

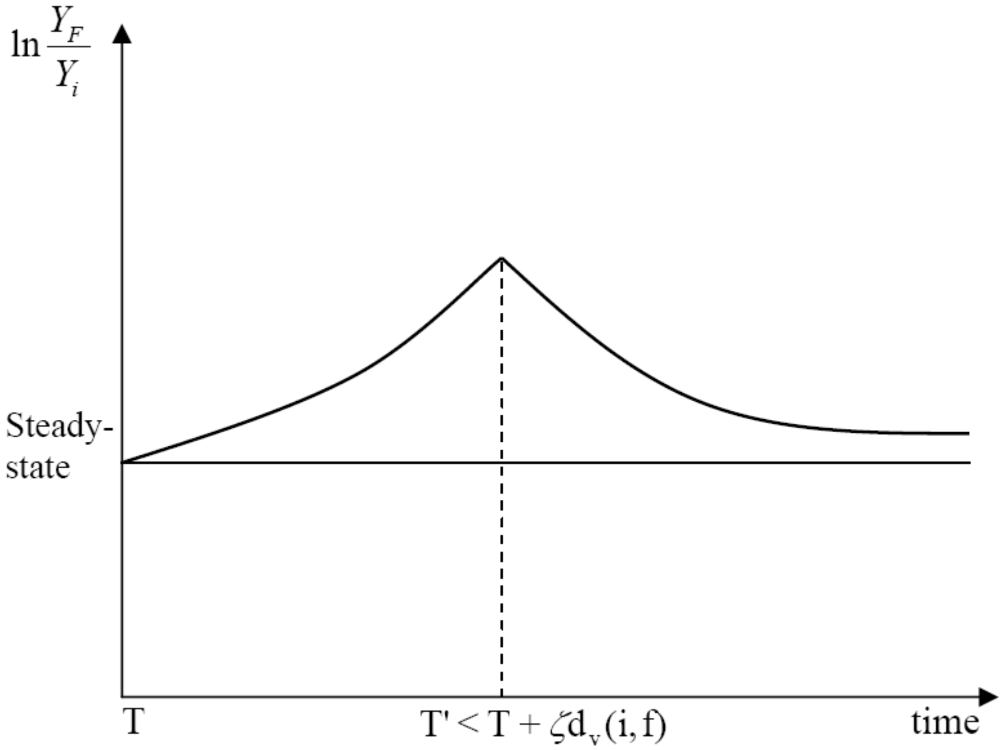

Figure 2 - Path of relative income following a regime change.

Henceforth, in general, the diffusion of modern R&D implies an increase of the effect of genetic distance on economic distance in the immediate period after the regime change, when most societies are still too far from the frontier to have adopted the new R&D methods, followed by a decline of the effect as more societies adopt the better R&D methods and become more effective imitators. The system will gradually converge to the new steady-state, in which, once again, income differences will be only a function of the barriers to the diffusion of innovations related to the production of final output (i.e., they will be equal to $\frac{\theta}{\psi}[d_v(i,f) - d_v(j,f)]$, as before the regime change). This result can be summarized as follows:

Implication 3. *Following a regime change in R&D, the effect of relative genetic distance on economic distance will be temporarily higher than in steady-state, until all societies have improved their imitation technology.*

In other words, after a regime change in R&D that gradually diffuses to imitating societies according to their relative distance from the world technological frontier, the effect of genetic distance should look like an inverted U: it would first increase, when only the societies that are very close to the frontier adopt the R&D improvement, and then decrease back to its long-term (positive) level as more societies adopt the improvement in R&D. As we will see in the Section 4, the actual variation of the effect of genetic distance on economic distance around the Industrial Revolution follows a pattern that is consistent with Implication 3.

2.3 A General Taxonomy

In the analytic framework presented above, we have illustrated economic mechanisms of diffusion implying a positive correlation between relative genetic distance from the frontier and income differences. A key feature underlying the model is the link between genetic distance and the vertical transmission of characteristics across generations. In our model, we showed how differences in neutral characteristics (that is, characteristics that do not have a direct effect on productivity and innovations) can explain income differences by acting as barriers to the diffusion of innovation across populations. In order to clarify the nature of the links between genetic distance and economic distance in our framework, it is useful to introduce a broader classification of different channels and mechanisms through which the vertical transmission of characteristics across generations may in principle affect economic outcomes.

First of all, we should stress again that these characteristics can be transmitted not only biologically (through reproduction) but also culturally. In fact, as we have already mentioned, a direct link from DNA-transmitted characteristics to economic outcomes is not necessary for our results, as long as vertical transmission of cultural characteristics takes place among genetically-related individuals. Our focus is on income differences across different populations of Homo Sapiens Sapiens, taking place over a relatively short period in terms of genetic evolution. Therefore we expect that, over that time frame, divergence in cultural characteristics have played a paramount role.

In general, characteristics can be transmitted across generations through DNA (genetic transmission, or GT - e.g. eye color) or through pure cultural interactions (cultural transmission, or CT - e.g., a specific language). Moreover, vertical characteristics, whether passed on through GT or CT, may affect income differences because of a direct (D) effects on productivity or because they constitute barriers (B) to the transmission of innovations across populations. Hence, in principle there are four possible combinations of mechanisms through which vertical characteristics may affect income differences: a GT direct effect, a GT barrier effect, a CT direct effect, and a CT barrier effect.[23] The following chart summarizes the four possibilities.

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[23] It is important to notice that these conceptual types should not be viewed as completely separable, but rather as points on a logical continuum, which may involve a mix of them. For a recent general discussion of the interactions

	Direct Effect (D)	Barrier Effect (B)
Genetic Transmission (GT)	Quadrant I	Quadrant II
Cultural Transmission (CT)	Quadrant III	Quadrant IV

Taxonomy of the effects of vertical characteristics

For instance, genetic traits affecting the trade-off between quality and quantity of children in the theoretical framework proposed by Galor and Moav (2002) to explain the Industrial Revolution would be examples of GT direct effects (Quadrant I). GT barrier effects (Quadrant II) could stem from visible genetically-transmitted characteristics (say, physical appearance) that do not affect productivity directly, but introduce barriers to the diffusion of innovations and technology by reducing exchanges and learning across populations that perceive each other as different.[24] Direct effects of cultural characteristics have been emphasized in a vast sociological literature that goes back at least to Max Weber.[25] A recent empirical study of the relationship between cultural values and economic outcomes that is consistent with the mechanisms of Quadrant III is provided by Tabellini (2004). The link between differences in vertically-transmitted characteristics - including cultural characteristics, as in Quadrant IV - is at the core of our own model..As we will see in Section 4, our empirical analysis provides support for our hypothesis that genetic distance - and in particular, relative genetic distance from the technological frontier - captures *barriers* to the horizontal diffusion of development.

Finally, it is worth pointing out that the distinction between GT and CT may be useful to fix ideas, but is not a clear-cut dichotomy. In fact, this distinction, essentially that between nature and nurture, may be misleading from an economic perspective, as well as from a biological perspective. Generally, the economic effects of human characteristics are likely to result from interactions of cultural and genetic factors, with the effects of genetic characteristics on economic outcomes changing over space and time depending on cultural characteristics, and vice versa. To illustrate this point, consider differences across individuals within a given population (say, the U.S.). Consider a clearly genetic characteristic of an individual, for instance having two X chromosomes. This

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between biological and cultural transmission, see Richerson and Boyd (2004). Recent results in genetics that are consistent with complex gene-culture interactions are provided by Wang et al. (2006).

[24] This effect is related to recent work by Guiso, Sapienza and Zingales (2004), who argue that differences in physical characteristics may affect the extent of trust across populations. Visible differences across ethnic groups also play an important role in the analysis of ethnic conflict by Caselli and Coleman (2002).

[25] More recent references can be found in the edited volume by Harrison and Huntington (2000).

purely genetic characteristic is likely to have had very different effects on a person's income and other economic outcomes in the year 1900 and in the year 2000, because of changes in culturally transmitted characteristics over the century. This is a case where the impact of genes on outcomes varies with a change in cultural characteristics.[26]

By the same token, one can think of the differential impact of a given cultural characteristic (say, the habit of drinking alcohol) on individuals with different genetic characteristics (say, genetic variation in alcohol dehydrogenase, the alcohol-metabolizing enzyme). An example of a complex interactions in which culture affects genes is the spread of the gene for lactose tolerance in populations that domesticated cows and goats. In the interpretation of our empirical analysis we will not dwell much on the distinction between genetic and cultural transmission of characteristics, but interpret genetic distance as an overall measure of differences in the whole set of vertically transmitted characteristics. That is, rather than addressing the "nature versus nurture" debate, which is beyond the scope of our analysis, we interpret our findings as evidence for the economic importance of long-term divergence in vertically-transmitted characteristics of different populations (i.e., the diffusion of development is impeded by barriers arising from differences in vertical characteristics). That said, it is also true that we find clues pointing to cultural transmission rather than purely genetic transmission as a likely mechanism behind our results. For instance, we find large effects of genetic distance on income differences within Europe: genetic distance explains income differences between populations that are geographically close, have shared very similar environments, and have had a very short time to diverge genetically (in many cases, less than a few thousand years). Since cultural change is much faster than genetic change, and most genetic change, especially in the short-run, is neutral (i.e. unrelated to natural selection), our findings are consistent with cultural transmission as a key mechanism explaining persistent income differences.[27]

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[26] This is a variation on an example by Alison Gopnik in her comment to the now-famous Pinker vs Spelke debate at http://www.edge.org/discourse/science-gender.html#ag. Pinker's response is also available at http://www.edge.org/discourse/science-gender.html.

[27] The view that cultural transmission trumps genetic transmission in explaining differences within human populations is standard among geneticists and anthropologists. For nontechnical discussions of these issues, see Diamond (1992, 1997), Cavalli-Sforza and Cavalli-Sforza (1995), Olson (2002) and Richerson and Boyd (2004).

3 The Genetic Distance Data

3.1 Measuring Genetic Distance

Since the data on genetic distance that we use as a measure of distance in vertical characteristics is not commonly used in the economics literature, and constitutes a central contribution of our paper, it is worth spending some time describing it.[28] Genetic distance measures genetic differences between two populations. The basic unit of analysis is the *allele*, or the variant taken by a gene. By sampling populations for specific genes, geneticists have compiled data on allele frequencies, i.e. the proportion of the population with a gene of a specific variant.[29] Differences in allele frequencies are the basis for computing summary measures of distance based on aggregated differences in allele frequencies across various genes (or *loci* on a chromosome). Following Cavalli-Sforza et al. (1994), we will use measures of F_{ST} distance, also known as coancestor coefficients (Reynolds et al., 1983). F_{ST} distances, like most measures of genetic differences, are based on indices of heterozygosity, the probability that two alleles at a given locus selected at random from two populations will be different. The construction of F_{ST} distances can be illustrated for the simple case of two populations (a and b) of equal size, one locus, and two alleles (1 and 2). Let p_a and q_a be the gene frequency of allele 1 and allele 2, respectively, in population a.[30] The probability that two randomly selected genes at a given locus are *identical* within the population (homozygosity) is $p_a^2 + q_a^2$, and the probability that they are different (heterozygosity) is:

$$h_a = 1 - \left(p_a^2 + q_a^2\right) = 2p_a q_a \tag{23}$$

By the same token, heterozygosity in population b is:

$$h_b = 1 - \left(p_b^2 + q_b^2\right) = 2p_b q_b \tag{24}$$

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[28] As far as we know, this is the first study of the relationship between genetic distance and differences in income per capita across countries. Guiso, Sapienza and Zingales (2004), in a parallel study, use genetic distance between European populations as an instrument for a measure of trust in order to explain bilateral trade flows. This is quite different from our application, as we are interested in explaining income differences, not trade flows. Their results are consistent with our interpretation of genetic distance as related to barriers. An economic application of measures of genetic distance across different species is provided by Weitzman (1992).

[29] Allele frequencies for various genes and for most populations in the world can be found at http://alfred.med.yale.edu/

[30] Therefore we have $p_a + q_a = 1$ and $(p_a + q_a)^2 = p_a^2 + q_a^2 + 2p_a q_a = 1$.

where p_b and q_b be the gene frequency of allele 1 and allele 2, respectively, in population b. The average gene frequencies of allele 1 and 2 in the two populations are, respectively:

$$\overline{p} = \frac{p_a + p_b}{2} \tag{25}$$

and:

$$\overline{q} = \frac{q_a + q_b}{2} \tag{26}$$

Heterozygosity in the *sum* of the two populations is:

$$h = 1 - \left(\overline{p}^2 + \overline{q}^2\right) = 2\overline{pq} \tag{27}$$

By contrast, *average* heterozygosity is measured by:

$$h_m = \frac{h_a + h_b}{2} \tag{28}$$

F_{ST} measures the variation in the gene frequencies of populations by comparing h and h_m:

$$F_{ST} = 1 - \frac{h_m}{h} = 1 - \frac{p_a q_a + p_b q_b}{2\overline{pq}} \tag{29}$$

If the two populations have identical allele frequencies ($p_a = p_b$), F_{ST} is zero. On the other hand, if the two populations are completely different at the given locus ($p_a = 1$ and $p_b = 0$, or $p_a = 0$ and $p_b = 1$) , F_{ST} takes value 1. In general, the highest the variation in the allele frequencies across the two populations, the higher is their F_{ST} distance. The formula can be extended to account for L alleles, S populations, different population sizes, and to adjust for sampling bias. The details of these generalizations are provided in Cavalli-Sforza et al. (1994, pp. 26-27).[31]

These measures of genetic distance have been devised mainly to reconstruct phylogenies (or family trees) of human populations. F_{ST} (which is also known as the coancestor coefficient) can be interpreted as the distance to the most recent common ancestors of two populations, or, equivalently, as the degree of genealogical *relatedness* between populations. F_{ST} genetic distance is strongly related to how long two populations have been isolated from each other.[32] If two populations split apart as the result of outmigration, their genes start to change as a result of random genetic drift and natural selection. When calculating genetic distances in order to study population history

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[31] For a general discussion of measures of genetic distances, see also Nei (1987).

[32] Isolation here refers to the bulk of the genetic heritage of a given population. As stressed by Cavalli-Sforza et al. (1994), small amounts of intermixing between members of different populations do not change the big picture.

and phylogenesis, geneticists concentrate on neutral characteristics that are not affected by strong directional selection (Cavalli-Sforza et al., 1994, p. 36): the term "neutral markers" refers to genes affected only by random drift.[33] It is important to stress that our measures of genetic distance are based on such neutral markers only, and not on selected traits.

When populations become separated, the process of random drift will take them in different directions, raising their genetic distance. The longer the period of separation, the greater genetic distance becomes. If drift rates are constant, genetic distance can be used as a molecular clock - that is, as the time elapsed since two populations separated can be measured by the genetic distance between them. When genetic distance is based on neutral markers, and populations are sufficiently large, geneticists have shown that drift rates are indeed constant (very small populations are generally subject to faster random genetic drift).

To summarize, we use F_{ST} distance as a measure of genealogical relatedness between populations. We expect a larger F_{ST} distance to reflect a longer separation between populations, and hence, on average, a larger difference in vertical characteristics.

3.2 The World Sample

The genetic distance data is from Cavalli-Sforza et al. (1994), p. 75-76. Our main focus on the set of 42 world populations for which they report all bilateral distances, computed from 120 alleles.[34] These populations are aggregated from subpopulations characterized by a high level of genetic similarity. However, measures of bilateral distance among these subpopulations are available only regionally, not for the world as a whole. Among the set of 42 world populations, the greatest genetic distance observed is between Mbuti Pygmies and Papua New-Guineans, where the F_{ST} distance is 0.4573, and the smallest is between the Danish and the English, for which the genetic

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[33] The classic reference for the neutral theory of molecular evolution is Kimura (1968). For more details on the neutral theory, the *molecular clock* hypothesis, and the construction and interpretation of measures of genetic distance, a recent reference is Jobling et al. (2004).

[34] Cavalli-Sforza et al. (1994) also provide a different measure of genetic distance (Nei's distance). Nei's distance, like F_{ST}, measures differences in allele frequencies across a set of specific genes between two populations. F_{ST} and Nei's distance have slightly different theoretical properties, but the differences are unimportant in practice as their correlation is 92.9% (Table 1) We show below that the choice of measures does not affect our results.

distance is 0.0021.[35] The mean genetic distance among the 861 available pairs is 0.1338. Figure 2, from Cavalli-Sforza et al. (1994), is a phylogenetic tree illustrating the process by which different human populations have split apart over time. The figure was constructed in order to maximize the correlation between euclidian distances to common nodes measured along the branches in the figure, and the F_{ST} genetic distance computed directly from allele frequencies. Thus, genetic distance between two populations is approximately the horizontal distance separating them from the next common node in Figure 4. Such phylogenetic trees, constructed from genetic distance data, are the population analogs of genealogical trees for individuals.

Genetic distance data is available at the population level, not at the country level. It was thus necessary to match populations to countries. We did so using ethnic composition data by country from Alesina et al. (2003). In many cases, it was possible to match ethnic group labels with population labels from Cavalli-Sforza et al. (1994), using their Appendices 2 and 3 to identify the ethnic groups sampled to obtain genetic distances. This was supplemented with information from Encyclopedia Britannica when the mapping of populations to countries was not achievable from ethnic groups data. Obviously, many countries feature several ethnic groups. Whenever the shares of these groups were available from Alesina et al. (2003) and the match to a genetic group was possible, we matched each of a country's ethnic group to a genetic group. For instance, the Alesina et al. (2003) data on ethnic groups has India composed of 72% of "Indo-Aryans" and 25% "Dravidians". These groups were matched, respectively, to the Cavalli-Sforza groups labeled "Indians" and "Dravidhans" (i.e. S.E. Indian in Figure 4).[36]

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[35] Among the more disaggregated data for Europe which we also gathered, the smallest genetic distance (equal to 0.0009) is between the Dutch and the Danish, and the largest (equal to 0.0667) is between the Lapp and the Sardinians. The mean genetic distance across European populations is 0.013. As can be seen, genetic distances are roughly ten times smaller on average across populations of Europe than in the World dataset. However, we still find that they significantly predict intra-Europe income differences.

[36] The complete match of genetic groups to ethnic groups, and in turn to countries, is available upon request.

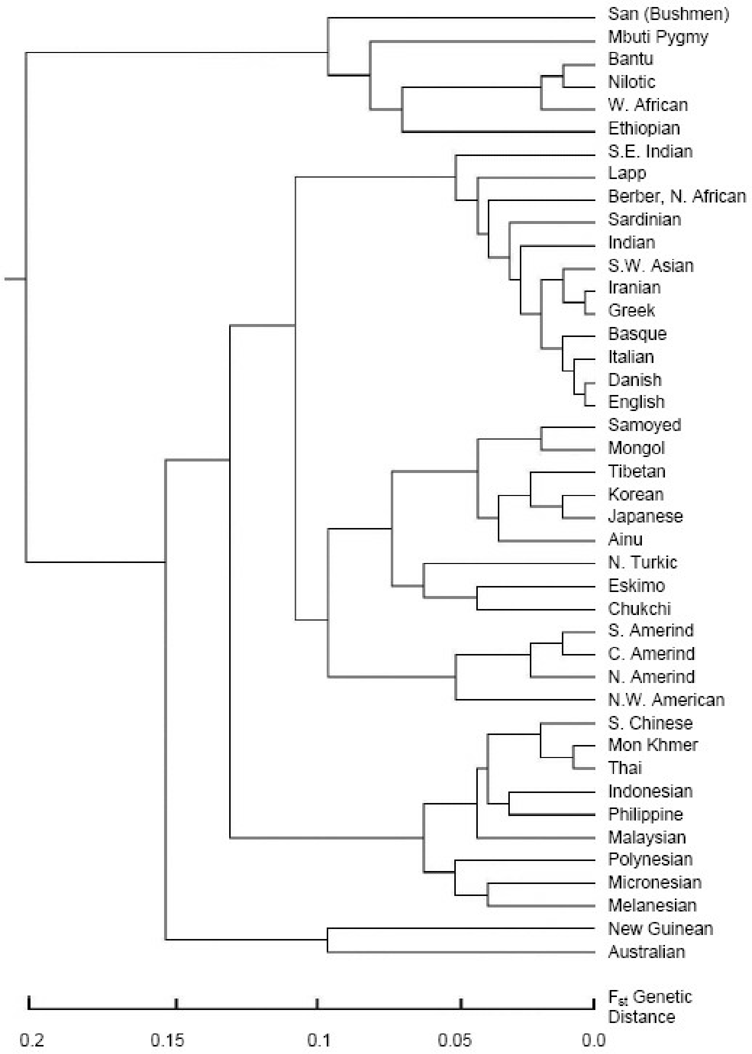

Figure 3 - Genetic distance among 42 populations. Source: Cavalli-Sforza et al., 1994.

This match served as the basis for constructing measures of genetic distance between countries, rather than groups. We constructed two such measures. The first was the distance between the plurality ethnic groups of each country in a pair, i.e. the groups with the largest shares of each country's population. This resulted in a dataset of $21,321$ pairs of countries (207 underlying countries and dependencies) with available genetic distance data. The second was a measure of weighted genetic distance. Some countries, such as the United States or Australia, are made up of sub-populations that are genetically distant, and for which both genetic distance data and data on the shares of each genetic group are available. Assume that country 1 contains populations $i = 1...I$ and country 2 contains populations $j = 1...J$, denote by s_{1i} the share of population i in country 1 (similarly for country 2) and d_{ij} the genetic distance between populations i and j. The weighted F_{ST} genetic distance between countries 1 and 2 is then:

$$F_{ST}^{W} = \sum_{i=1}^{I} \sum_{j=1}^{J} (s_{1i} \times s_{2j} \times d_{ij}) \tag{30}$$

where s_{ki} is the share of group i in country k, d_{ij} is the F_{ST} genetic distance between groups i and j.[37] The interpretation of this measure is straightforward: it represents the expected genetic distance between two randomly selected individuals, one from each country. As we show below, weighted genetic distance is very highly correlated with genetic distance based on dominant groups, so for practical purposes it does not make a big difference which one we use. We will use the F_{ST} distance based on plurality groups as the baseline measure throughout this study, as it allows us to maximize the number of available observations.

Error in the matching of populations to countries should lead us to understate the correlation between genetic distance and income differences. Several regions may be particularly prone to matching errors. One is Latin America, where it is sometimes difficult to identify whether populations are predominantly of European descent or of Amerindian descent. This is particularly problematic in countries with large proportions of "Mestizos", i.e. populations of mixed descent, such as Colombia (in this specific case the country's dominant group was matched to the "South Ameridian" category). Another is Europe, where countries can only be matched to one of three genetic groups (English, Danish and Italian). As a rule of thumb, we matched countries to groups that were the closest genetically to that country's population, using the regional genetic distance data in Cavalli-Sforza et al. (1994).

The ethnic composition in Alesina et al. (2003) refers to the 1990s. This is potentially endogenous with respect to current income differences if the latter are persistent and if areas with high income potential tended to attract European immigration since 1500. This would be the case for example under the view that the Europeans settled in the New World due to a favorable geographical environment.[38] In order to construct genetic distance between countries as of 1500, we also mapped populations to countries using their ethnic composition as of 1500, i.e. prior to the

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[37] Due to missing data on group shares, the weighted measure only covers $16,110$ pairs, or 180 countries.

[38] In fact, income differences are not very persistent at a long time horizon such as this - see Acemoglu et al. (2002). Our own data shows that pairwise log income differences in 1500 are uncorrelated with the 1995 series in the common sample (Table 1).

major colonizations of modern times. Thus, for instance, while the United States is classified as predominantly populated with English people for the current match, it is classified as being populated with North Amerindians for the 1500 match. This distinction affected mostly countries that were colonized by Europeans since 1500 to the point where the dominant ethnic group is now of European descent (New Zealand, Australia, North America and some countries in Latin America). Genetic distance in 1500 can be used as a convenient instrument for current genetic distance. The matching of countries to populations for 1500 is also more straightforward than for the current period, since Cavalli-Sforza et al. attempted to sample populations as they were in 1500, possibly reducing the extent of measurement error. The correlation between genetic distance for current populations and for 1500 is 0.658.

3.3 The European Sample

Cavalli-Sforza et al. (1994) also present matrices of genetic distance among populations within several regions. These sub-matrices cannot be merged with the world data, because they are based on sets of underlying genes distinct from the 120 genes used for the 42 populations in the world sample. They can, however, be used separately. We assembled a dataset of genetic distances between 26 European populations, a much finer classification than the world sample which only featured 3 distinct European populations. Matching populations to countries is much more straightforward for the European sample than for the world sample, because the choice of sampled European populations generally corresponds to nation-state boundaries. This should reduce the incidence of measurement error. The populations were matched to 26 countries, resulting in 325 country pairs.[39] The largest F_{ST} genetic distance among those pairs was 0.032, between Iceland and Slovenia. The smallest, among countries matched to distinct genetic groups, was between Denmark and the Netherlands ($F_{ST} = 0.0009$).

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[39] These 26 countries are Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Macedonia, Netherlands, Norway, Poland, Portugal, Russian Federation, Slovak Republic, Slovenia, Spain, Sweden, Switzerland the United Kingdom and Yugoslavia. The Basque, the Lapp and the Sardinian populations were not matched to any country, and some countries were matched to the same groups (Croatio, Slovenia, Macedonia and Yugoslavia were all matched to the "Yugoslavian" population, while the Czech Republic and Slovak Republics were both matched to the "Czech" population).

4 The Empirics of Income Differences

In this section we test the empirical implications of our model. We investigate the relationship between genetic distance and economic distance. Genetic distance is considered both relative to the technological frontier and in absolute terms. In line with our theory, we use the log income per capita as a metric of economic performance. The data on per capita income is purchasing power-parity adjusted data from the World Bank, for the year 1995.[40]

4.1 Genetic Distance to the Frontier

We start with a simple descriptive approach. Suppose that we can pinpoint the technological frontier. Does a country's genetic distance to the frontier correlate with its income level? To investigate this simple hypothesis, we ran income level regressions. For the World sample, we assumed the US was the technological frontier. In Europe, we use the UK. These choices seem reasonable a priori: in the World sample, only Luxemburg and Norway had incomes per capita higher than the US in 1995.[41] Few would dispute that the US is currently the world's major technological innovator. Although we measure distance to the US using our weighted measure, which is more appropriate since the US is a genetically diverse country, variation in this measure is dominated by the distance to the English population. In the Europe sample, genetic distance to the UK is effectively the distance to the English population, i.e. the distance to the birthplace of the Industrial Revolution, as well as the distance to the current World frontier (the US). Table 1 presents the results. The regressions include a number of controls, which will be described and motivated below. For now, it suffices to note that a country's genetic distance to the US is significantly associated with lower per capita income, even after controlling for a variety of metrics of geographic and other distances. In column 1, the t-statistic on genetic distance exceeds 10, and genetic distance entered alone accounts for 35% of the variation in log income levels. Moreover, this result holds within Europe as well, although the small number of observations (i.e. 25) reduces the significance of the coefficient on genetic distance to the English when geographic controls are added. Figures 4 and 5 display the univariate results graphically, so the reader can evaluate which

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[40] We also used data from the Penn World Tables version 6.1 (Summers, Heston and Aten, 2002), which made little difference in the results. We focus on the World Bank data for 1995 as this allows us to maximize the number of countries in our sample.

[41] It is likely both countries do not owe their economic superiority primarily to their technological inventiveness, but to natural resource wealth (Norway) and a specific specialization pattern (Luxemburg).

countries drive the result.

Figure 4 − Log Income in 1995 and Genetic Distance to the USA

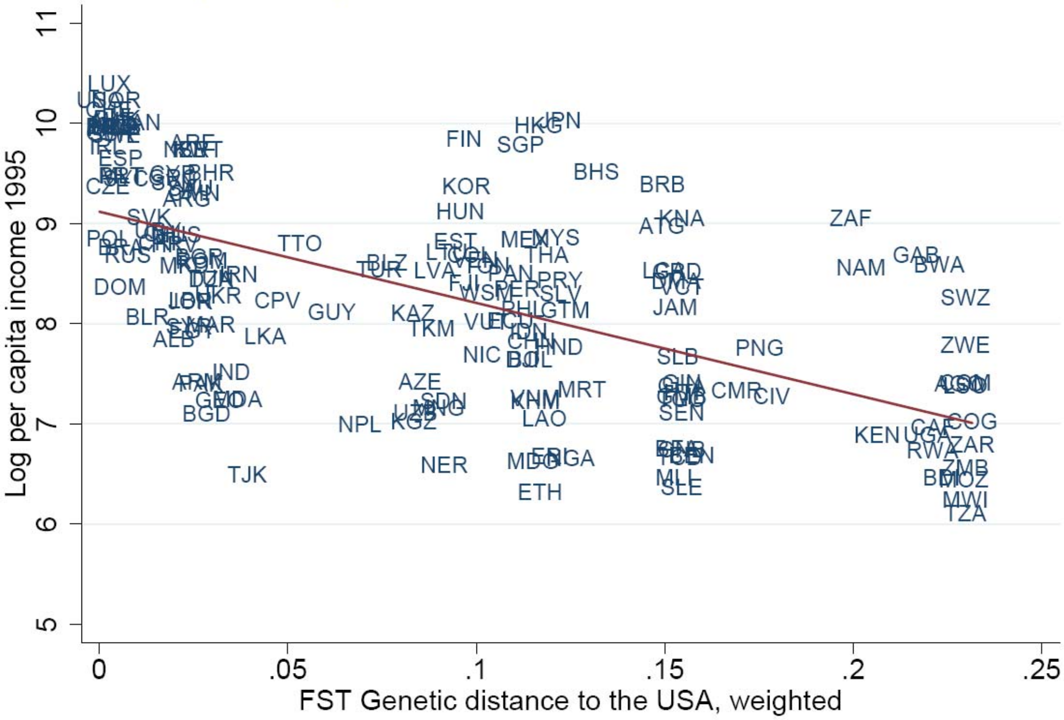
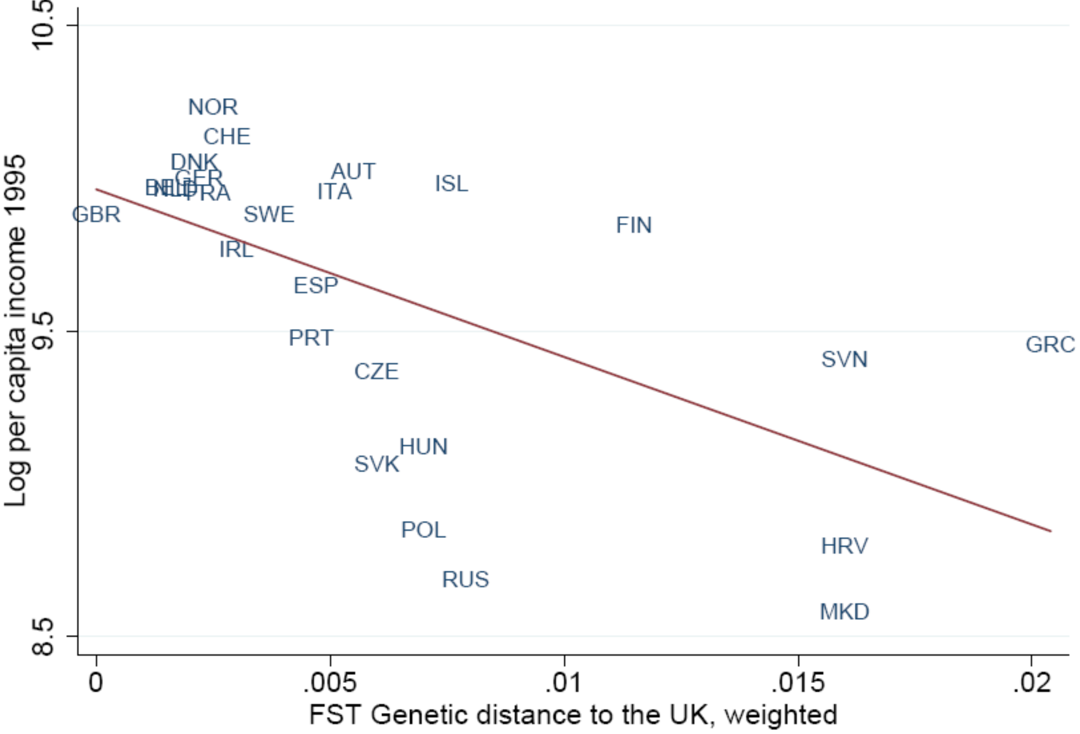


Figure 5 − Log Income in 1995 and Genetic Distance to the UK, Europe Sample



4.2 Bilateral Approach

To generalize the results of the previous subsection, we consider a specification in which the absolute difference in income between pairs of countries is regressed on measures of distance between the countries in this pair. This has two advantages. First, we no longer need to choose a technological leader to investigate the correlation between absolute genetic distance and income differences (our model led to predictions about the sign of this correlation, see equation 10). Second, we can make more efficient use of the wealth of bilateral distance data at our disposal. We will use this bilateral approach for the rest of this paper.

We computed income differences between all pairs of countries in our sample for which income data was available, i.e. $13,861$ pairs (based on 167 underlying countries). Define G_{ij}^{D} as the *absolute* genetic distance between countries i and j. Denote G_{ij}^{R} the genetic distance between i and j *relative* to the technological frontier. In most of what follows, we continue to assume the technological frontier is the United States (in the Europe sample we will continue to use the English). Then, by definition $G_{ij}^{R} = |G_{i,US}^{D} - G_{j,US}^{D}|$. Our baseline specifications are:

$$|\log y_i - \log y_j| = \beta_0 + \beta_1 G_{ij}^{D} + \beta_2' X_{ij} + \varepsilon_{ij} \tag{31}$$

and:

$$|\log y_i - \log y_j| = \gamma_0 + \gamma_1 G_{ij}^{R} + \gamma_2' X_{ij} + \nu_{ij} \tag{32}$$

where X_{ij} is a set of measures of geographic and cultural distance and ε_{ij} and ν_{ij} are disturbance terms.[42]

The reason our empirical specification must involve income differences rather than a single country's income level on the left hand side is that this makes the use of bilateral measures of distance possible. Conceptually, therefore, we depart from existing methodologies: our regression is not directional, i.e. our specification is not simply obtained by differencing levels regressions across pairs of countries.[43] We should also stress that our specifications are reduced forms. That

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[42] We also estimated an alternative specification where the distance measures were all entered in logs. This did not lead to appreciable differences in the economic magnitude or statistical significance of any of the estimates. Since several countries were matched to the same genetic group, so that the corresponding pairs had a genetic distance of zero, taking logs resulted in the loss of valuable observations.

[43] Our methodology is more akin to gravity regressions in the empirical trade literature than to levels or growth regressions in the literature on comparative development.

is, differences in income are presumably the result of differences in institutions, technologies, human capital, savings rates, etc., all of which are possibly endogenous with respect to income differences, and themselves a function of geographic and human barriers.

Before turning to the results, we must address a technical point regarding the disturbances ε_{ij} and ν_{ij}. In principle, if one is willing to assume that the measures of barriers are exogenous, equations (31) and (32) can be estimated using least squares. However, in this case usual methods of inference will be problematic due to spatial correlation resulting from the construction of the dependent variable. Appendix 2 demonstrates that introducing the difference in log income on the left hand side results in spatial correlation, and argues that introducing a set of common country dummy variables soaks up this spatial correlation. This is a set of N dummies, where D_j takes a value of 1 whenever country j appears in a pair. All of our regressions are least squares regressions with common country dummies and heteroskedasticity-consistent standard errors.

4.3 Unconditional Results

Table 1 presents some summary statistics for our variables. We consider various measures of genetic distance. Our baseline measure is the F_{ST} genetic distance between plurality groups in each country. We also used weighted F_{ST} genetic distance and Nei genetic distance based on plurality groups. These measures bear high correlations among themselves, so in practice it matters little which one we use. On the other hand, the theoretically more appropriate measure of relative distance to the frontier bears a correlation of only 0.55 with absolute F_{ST} genetic distance (for the measure based on plurality groups, this is simply the relative genetic distance to the English population). Finally, we considered F_{ST} genetic distance with countries matched to populations as they were in 1500. The correlation between this variable and the current measure is 0.68.

Our measure of absolute F_{ST} genetic distance G^D bears a positive correlations of 0.14 with the absolute value of log income differences in 1995. Genetic distance relative to the frontier G^R bears a higher correlation with income differences, equal to 0.23, in line with our model's prediction. These correlations are higher in the European sample, respectively 0.29 and 0.31.

Table 2 presents regressions of income differences on various measures of genetic distance. As a measure of the magnitude of the coefficients, we report the standardized beta coefficient on genetic distance for each regression.[44] Column 1 shows that, when entered alone in the regression,

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[44] The standardized beta is defined as the effect of a one standard deviation change in the regressor expressed as a

one standard deviation in F_{ST} genetic distance accounts for 21.77% of the variation in income differences. This effect rises in magnitude when we consider the effect of genetic distance relative to the frontier, as predicted by Implication 2 of our model (column 2). The effect is larger when Nei and weighted genetic distance are used instead of F_{ST} (columns 3 and 4). The effect is yet larger when we use the weighted F_{ST} genetic distance relative to the frontier, for which it reaches 30.49% (column 5).

We next make use of data from Cavalli-Sforza et al. (1994) on the standard deviation of the genetic distance estimates. Since these data are based on allele frequencies collected from samples of different sizes, they are estimated more or less precisely depending on population pairs. We have data on the standard errors of each estimate of genetic distance, obtained from bootstrap analysis. In column (6), we linearly downweigh observations with high standard errors on genetic distance. As expected, the magnitude of the resulting weighted least squares effect of F_{ST} genetic distance is larger than under simple OLS, consistent with the idea that measurement error is greater for pairs with high standard errors on genetic distance.

While providing suggestive evidence in favor of implications 1 and 2 of our theoretical model, these unconditional results may confound the effect of barriers linked to vertical characteristics with geographic barriers. In the next subsection, we control for a large number of measures of geographic distance. In what follows we will focus on the relative genetic distance to the frontier as the baseline measure of genetic distance, since it is the theoretically more appropriate measure. We also focus on the measure based on plurality match, since it allows for more observations - if anything using the weighted measure would raise the magnitude of the effect of genetic distance.

4.4 Controlling for Geographic Factors

Genetic distance and geographic isolation are likely to be highly correlated. The more isolated two groups become, the more they will drift apart genetically, since genetic admixture is made difficult by geographic barriers. It is therefore important to adequately control for geographic isolation: failing to do so would ascribe to genetic distance an effect that should be attributed to geographic distance. In this subsection, we control for a vast array of measures of geographic isolation.

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percentage of one standard deviation of the dependent variable

Distance Metrics. Our first set of measures of geographic isolation between countries includes various measures of distance. We consider a measure of the greater circle (geodesic) distance between the major cities of the countries in our sample, from a new dataset compiled by researchers at CEPII.[45] We also include latitudinal distance - i.e. simply the absolute value of the difference in latitude between the two countries i and j in each pair: $G_{ij}^{LA} = |\text{latitude}_i - \text{latitude}_j|$. Latitude could be associated with climatic factors that affect income levels directly, as in Gallup, Mellinger and Sachs (1998) and Sachs (2001). Latitude differences would also act as barriers to technological diffusion: Diamond (1997) suggests that barriers to the transmission of technology are greater along the latitude direction than along the longitude direction, because similar longitudes share the same climate, availability of domesticable animal species, soil conditions, etc. We should therefore expect countries at similar latitudes to also display similar levels of income. Third, we use for a measure of longitudinal distance, $G_{ij}^{LO} = \left|\text{longitude}_i - \text{longitude}_j\right|$, to capture possible geographic isolation along this alternative axis.[46]

Perhaps surprisingly, raw correlations between genetic distance and these simple measures of geographic distance are not as high as we might have expected. For instance, the correlation between geodesic distance and F_{ST} genetic distance is only 35.4% - though unsurprisingly it rises to 47.8% if genetic distance is measured based on populations as they were in 1500, because the colonization era acted to weaken the link between genetic distance and geographic distance by shuffling populations across the globe.

Table 4, column 1 includes these three measures jointly with F_{ST} genetic distance relative to the US. The effect of relative genetic distance falls slightly in magnitude, compared to column 2 of Table 3, as expected. We find evidence that geodesic distance acts as a barrier - the standardized beta on this variable is 13.77%. The economic significance of latitudinal and longitudinal distance is very close to zero.

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[45] The data is available at http://www.cepii.fr/anglaisgraph/bdd/distances.htm. This dataset features various measures of distance (between major cities, between capitals, weighted using several distances between several major cities, etc.), all of which bear pairwise correlations that exceed 99%. The dataset also includes other useful geographical and historical controls, such as whether pairs of countries whether the countries are contiguous, whether they had a common colonizer, were ever part of a single country, etc.

[46] In our regressions, we entered these distance measures in abolute terms. Using geographic distance *relative to the frontier* instead did not change our results - if anything doing so raised the magnitude of the genetic distance effect. Corresponding estimates are available upon request.

Microgeographic factors. In addition to these straightforward distance measures, we controlled for other measures of isolation between countries. In the context of gravity regressions, Giuliano, Spilimbergo and Tonon (2006) argued that genetic distance was likely correlated with features of the terrain that raise transport costs. These "microgeographic" features may not be well captured by simple metrics of distance. To account for this possibility, we included dummy variables taking a value of 1 if countries in a pair were contiguous, if they had access to a common sea or ocean, if any country in a pair was an island or was landlocked.[47] Column 2 of Table 4 shows these variables have the expected signs, but their inclusion does not affect the coefficient on genetic distance. In column 4, we attempt to control directly for transport costs, using the ratio of CIF to FOB exports.[48] The limited availability of the transport cost data leads to the loss of many observations, which largely accounts for the large increase in the effect of genetic distance that occurs when these variables are entered in the regression. To summarize, we find no evidence that geographic barriers induced by these microgeographic factors account for our findings.

Climatic Similarity. Next, we constructed measures of climatic similarity based on 12 Koeppen-Geiger climate zones.[49] One measure is the average absolute value difference, between two countries, in the percentage of land area in each of the 12 climate zones. Countries have identical climates, under this measure, if they have identical shares of their land areas in the same climates. As a simpler alternative, we use the absolute difference in the percentage of land areas in tropical

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[47] The common sea variable is the same as that used in Giuliano, Spilimbergo and Tonon (2006). Following their approach, we also included the difference in average elevation as a control. This led to a *larger* effect of genetic distance, although in large part due to the loss of 3,000 observations. We also included a measure of transport costs based on the difference between CIF and FOB trade flows, this time resulting in the loss of 10,000 observations due to the limited availability and quality of this proxy for transport costs. again, however, we found the effect of genetic distance *increased*. These results are available upon request.

[48] We follow the approach in Limao and Venables, 2001, Hummels, 2006 and Giuliano et al. (2006). The measure of indirect trade costs is $ITC_{ij} = \frac{CIF_{ij}}{FOB_{ij}} - 1$, and the data (for 1980-2005) come from the IMF Direction of Trade Statistics. We also control for elevation differences, as in Giuliano et al. (2006).

[49] The 12 Koeppen-Geiger climate zones are: tropical rainforest climate (Af), monsoon variety of Af (Am), tropical savannah climate (Aw), steppe climate (BS), desert climate(BW), mild humid climate with no dry season (Cf), mild humid climate with a dry summer (Cs), mild humid climate with a dry winter (Cw), snowy-forest climate with a dry winter (Dw), snowy-forest climate with a moist winter (Ds), tundra/polar ice climate (E) and highland climate (H). The data, compiled by Gallup, Mellinger and Sachs, is available at http://www.ciesin.columbia.edu/eidata/.

climates. As with latitude, climate may have direct effects on productivity, or barrier effects on technological diffusion: countries located in different climates may experience difficulties in adopting each other's mode of production, particularly in the agrarian era. Columns (4) and (5) of Table 4 report the results. As expected, climatic differences are associated with greater income differences, even controlling for latitude differences. However, the inclusion of these variables hardly affects the coefficient on genetic distance.

Continent Effects. The largest genetic distances observed in our worldwide dataset occur between populations that live on different continents. One concern is that genetic distance may simply be picking up the effect of cross-continental barriers to the diffusion of development, i.e. continent effects. If this were the case, it would still leave open the question of how to interpret economically these continent effects, but to test explicitly for this possibility, we added to our baseline specification two sets of continent dummies. We included one set of 7 dummies (one for each continent) taking on a value of one if the two countries in a pair are on the same continent. We also included a set of 7 dummies each equal to one if exactly one country belongs to a given continent, and the other not. The results are in column (6) of Table 4. The inclusion of continent dummies reduces by about one third the magnitude of the genetic distance effect, but the latter remains statistically significant. We will provide further evidence on the within-continent effects of genetic distance using our European dataset.

Possible Endogeneity of Current Genetic Distance. Next, we attempt to control for the possible endogeneity of genetic distance with respect to income differences. While differences in (neutral) allele frequencies between the populations of two countries do not result causally from income differences, migration could lead to a pattern of genetic distances today that is closely linked to current income differences. Consider for instance the pattern of colonization of the New World starting after 1500. Europeans tended to settle in larger numbers in the temperate climates of North America and Oceania. If geographic factors bear a direct effect on income levels, and were not properly accounted for in our regressions through included control variables, then genetic distance today could be positively related to income distance not because genetic distance precluded the diffusion of development, but because similar populations settled in regions prone to generating similar incomes.

To assess this possibility, column (1) of Table 5 excludes from the sample any pairs involving one or more countries from the New World (defined as countries in North America, Latin America, the Caribbean and Oceania), where the endogeneity problem is likely to be most acute. The effect of genetic distance falls slightly, but remains commensurate with the one we estimated before. The difference in latitudes becomes much larger, an observation to which we shall return below. Next, we use our data on F_{ST} genetic distance as of 1500 as an instrument for current genetic distance in column (2) of Table 5. This variable reflects genetic distance between populations as they were before the great migrations of the modern era, i.e. as determined since the Neolithic era, and yet is highly correlated (65.8%) with current genetic distance, so it fulfills the conditions of a valid instrument. Here, the magnitude of the genetic distance effect is raised by almost one third, with a standardized beta reaching 27.8%. As is usual in this type of application, the larger estimated effect may come from a lower incidence of measurement error under IV - as explained above the matching of populations to countries is much more straightforward for the 1500 match.

The Diamond Gap. Jared Diamond's (1997) influential book stressed that differences in latitude played an important role as barriers to the transfer of technological innovations in early human history, and later in the pre-industrial era, an effect that could have persisted to this day. Our estimates of the effect of latitudinal distance provided little evidence that this effect was still at play: in our regressions we found only weak evidence that differences in latitudes help explain income differences across countries, although this effect was much larger when excluding the New World from our sample. However, Diamond took his argument one step further, and argued that Eurasia enjoyed major advantages in the development of agriculture and animal domestication because a) it had the largest number of potentially domesticable plants and animals, and b) had a predominantly East-West axis that allowed an easier and faster diffusion of domesticated species. By contrast, differences in latitudes in the Americas and Africa created major environmental barriers to the diffusion of species and innovations. More generally, Eurasia might have enjoyed additional benefits in the production and transfer of technological and institutional innovations because of its large size.[50] It is important to properly control for Diamond's geography story as it is either a substitute or a complement to ours.

To test and control for a Eurasian effect, we constructed a dummy variable that takes on a value of 1 if one and only one of the countries in each pair is in Eurasia, and 0 otherwise (the "Diamond

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[50] This point is stressed in Kremer (1993). See also Masters and McMillan (2001).

gap").[51] In order to test Diamond's hypothesis, we added the Diamond gap to regressions explaining income differences in 1995 (column 3 of Table 5) and, using Maddison's historical income data, in 1500 (column 4). For the former regression, we restricted our sample to the Old World.[52] As expected, in the regression for 1995 income differences, the Diamond gap enters with a positive and significant coefficient, and its inclusion reduces (but does come close to eliminating) the effect of genetic distance. In column (4), using 1500 income differences as a dependent variable, the Diamond gap is also significant and large in magnitude, despite the paucity of observations. This provides suggestive quantitative evidence in favor of Diamond's observation that the diffusion of development was faster in Eurasia. We also conclude that genetic distance between populations plays an important role in explaining income differences even when controlling for the environmental advantages and disadvantages associated with Eurasia, so Diamond's hypothesis on the long-term diffusion of development is complementary to ours.

4.5 Controlling for Common History and Cultural Distance

In this subsection we control for additional possible determinants of income differences.[53] We first consider common history variables: countries that have shared a common history, for instance a common colonial past, may be closer both genetically, culturally and in income space. Second, we examine the issue of cultural distance, which is also potentially correlated with both genetic distance and income differences. As argued in Cavalli-Sforza et al. (1994) there is usually very little genetic admixture between populations that speak different languages, for instance, so irrespective of their physical distance these populations should be expected to drift apart genetically.[54] Moreover,

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[51] For further tests providing statistical support for Diamond's observations, see Olsson and Hibbs (2005).

[52] It is appropriate to exclude the New World from the sample when using 1995 incomes because Diamond's theory is about the geographic advantages that allowed Eurasians to settle and dominate the New World. If we were to include the New World in a regression explaining income differences today, we would include the higher income per capita of non-aboriginal populations who are there because of guns, germs and steel, i.e. thanks to their ancestors' Eurasian advantage.

[53] Throughout this subsection we will use the specification in column 2 of Table 4 as the baseline - i.e. we include a large array of geographic distance controls (estimates on these variables are not reported in Table 7).

[54] A well-known example is that of the hunter-gathering Mbuti Pygmies and the sedentary agragrian populations of Bantu descent in central regions of Africa. Despite living geographically close to each other for about 3000 years - sometimes only a few miles apart - these populations rarely intermixed, retained vastly different technologies, and correspondingly remained very distant genetically.

as we have argued in Section 2, genetic distance may be associated with differences in vertical characteristics transmitted culturally, rather than genetically. The types of barriers captured by genealogical relatedness (i.e. genetic distance) likely include slow-moving cultural barriers, such as linguistic barriers and difference in norms or values. Are there specific cultural traits that are correlated with genetic distance, and that are directly measurable? How much of the estimated effect of genetic distance is attributable to differences in specific measurable cultural characteristics? Measuring cultural distance is fraught with difficulties. In a well-known survey over fifty years ago Kroeber and Kluckhohn (1952) listed 164 definitions of culture proposed by historians and social scientists. We will adopt a more parsimonious approach, confining our attention to measures of linguistic and religious distance.

Common history controls. We first control for variables representing a pair's common historical experience. These are dummy variables for pairs that were ever part of the same country (for example Austria and Hungary), were ever in a colonial relationship, have shared a common colonizer since 1945 and are currently in a colonial relationship (such as France and French Polynesia). These variables all bear the expected signs (Table 7, column 1) - having had a common colonizer or having been part of the same country are associated with smaller income differences. Their inclusion in the regression does not affect the magnitude of the genetic distance effect.

Linguistic distance. The most salient example of a slowly changing culturally transmitted characteristic is language: it is transmitted across generations within a population, yet there is no gene for speaking specific languages. We attempt to measure linguistic distance in two ways.

Our first approach follows Fearon (2003). Fearon used data from Ethnologue to create linguistic trees, classifying languages into common families and displaying graphically the degree of relatedness of world languages. The linguistic tree in this dataset contains up to 15 nested classifications. If two languages share many common nodes in the tree, these languages are more likely to trace their roots to a more recent common ancestor language. The number of common nodes in the linguistic tree, then, is a measure of linguistic similarity. For instance, according to this measure, French and Italian share 4 common nodes - both belong to the Indo-European / Italic / Romance / Italo-Western linguistic groupings. Using data on the linguistic composition of countries (also from Fearon, 2003), and matching languages to countries, we can then construct indices of linguistic distance between countries. We did so, as for genetic distance, in two ways: first, we computed a measure of the number of common nodes shared by the dominant languages for each country pair. Second, we computed a weighted measure of linguistic similarity, representing the expected number of common linguistic nodes between two randomly chosen individuals, one from each country in a pair (the formula is the same as that of equation 30).[55] Following Fearon (2003), we transformed each of these series so that they are increasing in linguistic distance (LD) and bounded by 0 and 1:

$$LD = \sqrt{\frac{(15 - \#\text{ Common Nodes})}{15}} \tag{33}$$

Our second measure of linguistic distance is based on work in the field of lexicostatistics (a branch of linguistics). We use data from Dyen, Kruskal and Black (1992). They assembled data on 200 common "meanings" from all Indo-European languages. They then compiled for each language lists of words to express these meanings. When words from two languages to express a given meaning originated from a common source, these words were labelled as "cognate". For instance, the word "table" in French and "tabella" in Italian are cognate because both stem from the word "tabula" in Latin. Aggregating over the 200 meanings, a measure of linguistic similarity is the percentage of cognate words. Again, the greater the percentage of cognate words, the more recently the languages shared a common ancestor language. In contrast to the linguistic trees data, this measure has the advantage of being a continuous measure of similarity. Its main drawback is that it is only available for Indo-European languages, so the geographic coverage is reduced to 72 countries.

Pairwise correlations between measures of genetic and linguistic distances are displayed in Table 6. These correlations are positive, as expected, but contrary to our expectations they are not very large in magnitude. For instance, the correlation between F_{ST} genetic distance and linguistic distance based on dominant languages is 0.219, and almost zero for the lexicostatistical measure. Turning to regression analysis, in Table 7, columns 2 and 3, both linguistic distance and the % cognate measure enter with the expected signs and are statistically significant at the 5% level.[56] Thus, greater linguistic distance is associated with greater economic differences. The magnitude of the effect is very modest for the data based on linguistic trees, and larger for the lexicostatistical measure (with a standardized beta equal to 10%). However, these variables do not affect the

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[55] Using the measure based on the plurality language or the weigthed measure did not make any difference for the results. We focus on the former.

[56] As with geographic distance, we also used measures of cultural distance relative to the frontier (available upon request). This did not lead to any appreciable differences in our results.

coefficient on genetic distance.

Religious distance. Our second measure of cultural distance is based on religion. Religion also tends to be transmitted intergenerationally within populations. We followed an approach similar to that used for linguistic distance. We relied on a nomenclature of world religions obtained from Mecham, Fearon and Laitin (2006).[57] This nomenclature was broken down into religious families, first distinguishing between monotheistic religions of Middle-Eastern origin, Asian religions and "others", then subdividing each group into finer groups (such as Christians, Muslims and Jews) and so on. The number of common classifications (up to 5 in this dataset) is a measure of religious proximity. We matched religions to countries using Mecham, Fearon and Laitin (2006)'s data on the prevalence of religions by country and transformed the data in a manner similar to that in equation (33). Table 6 shows that while religious distance bears a correlation of 0.347 with linguistic distance, it is largely uncorrelated with genetic distance.

Columns (4) and (5) of Table 7 enters this measure of religious distance into our baseline specification, either alone or jointly with linguistic distance.[58] Religious distance is positively associated with income differences, and the standardized beta coefficient on this variable is about 10%. Again, however, its introduction only marginally affects the coefficient on genetic distance.

Interpretation and Observations. These results have several interpretations. The most straightforward interpretation is that differences in vertical characteristics captured by genetic distance are not primarily linguistic and religious in nature. This opens up the question of what they are, an important question for future research. Another interpretation is that the specific measures of linguistic and religious distance that we use are inadequate. Consider linguistic distance. It is well-known that linguistic and genetic trees look very similar, as demonstrated in Cavalli-Sforza et al. (1994, p. 98-105). The reason is straightforward: genes, like languages, are transmitted intergenerationally, and this insight is the basis for our interpretation of genetic distance as capturing the full set of vertical characteristics, both genetic and cultural. Yet the correlation between our measure of genetic distance and linguistic distance is quite low. This may be partly due to the fact that genetic distance is a *continuous* measure of distance, whereas the number of nodes is a

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[57] An alternative classification obtained from the World Christian Database, with only 3 nested classifications, did not lead to appreciably different results.

[58] Again, the results were unchanged when using religious distance relative to the US, or weighted religious distance.

discrete measure of linguistic distance: populations may share few common nodes but linguistic splits occurred recently, in which case one is overestimating distance, or they may share lots of common nodes but the last split occurred a long time ago, in which case one is underestimating distance. The lexicostatistical measure we used addresses this problem, but comes at a cost of losing almost half of the countries in our sample.

Whatever the interpretation, our results show that genetic distance, as an overall measure of differences in vertical characteristics, is robustly correlated with income differences, and we were not able to identify specific measures of cultural distance that could alter this conclusion.

4.6 Alternative Time Periods and Samples

4.6.1 Historical Income Data.

Our model led to testable predictions relating to the time path of the effect of genetic distance on income differences in the aftermath of a regime change in R&D technologies. In this section we examine the time variation in the effect of genetic distance in the 500 years that surrounded the Industrial Revolution. We find a pattern of coefficients that is supportive of our model of diffusion.

In Table 8, we use income per capita data since 1500 from Maddison (2003), and repeated our basic reduced form regression for 1500, 1700, 1820, 1870, 1913 and 1960.[59] As before, our measure of genetic distance is relative to the English. For the 1500 and 1700 regressions, we use the early match for genetic distance, i.e. genetic distance between populations as they were in 1492, prior to the discovery of the Americas and the great migrations of modern times.[60] For the subsequent periods we use the current match. Table 5 shows that across periods, the coefficient on relative genetic distance is statistically significant and positive. Moreover, the magnitudes are much larger than for the current period: considering regressions obtained from a common sample of 26 countries (275 pairs) for which data is continuously available, standardized beta coefficients range from 18.58% (1995) to 67.76% (1870). Thus, genetic distance is strongly positively correlated

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[59] The data on income for 1960 is from the Penn World Tables version 6.1. For comparison, column (7) reproduces the results for 1995.

[60] Regressions for these early periods feature at most 29 countries. These countries are Australia, Austria, Belgium, Brazil, Canada, China, Denmark, Egypt, Finland, France, Germany, Greece, India, Indonesia, Ireland, Italy, Japan, Korea, Mexico, Morocco, Netherlands, New Zealand, Norway, Portugal, Spain, Sweden, Switzerland, United Kingdom, United States. There were 275 pairs (26 countries) with available data for 1500 income, and 328 pairs (29 countries) for 1700.

with income differences throughout modern history. It is worth noting that genetic distance bears a large, positive and significant effect on income differences for the past five centuries, even though income differences in 1500 and in 1995 are basically uncorrelated (Table 2 shows this correlation to be -0.051 for the 325 country pairs for which data is available). This fact is consistent with our interpretation of genetic distance as a barrier to the diffusion of innovations across populations.

Strong evidence for our model of barriers to diffusion can be obtained from plotting the time path of coefficients, as is done in Figure 6. The result is striking. The slope coefficient of genetic distance decreases gradually from 1500 to 1820, then spikes up in 1870 during the Industrial Revolution and declines thereafter. The shape of the time path, described in Figure 6, is precisely that predicted by our theory (contrast this figure with Figure 2). This is fully consistent with our model where a major shift in the growth regime (the Industrial Revolution) initially results in large income discrepancies. These discrepancies persist in proportion to genealogical relatedness. As more and more countries adopt the major innovation, the impact of genetic distance progressively declines.

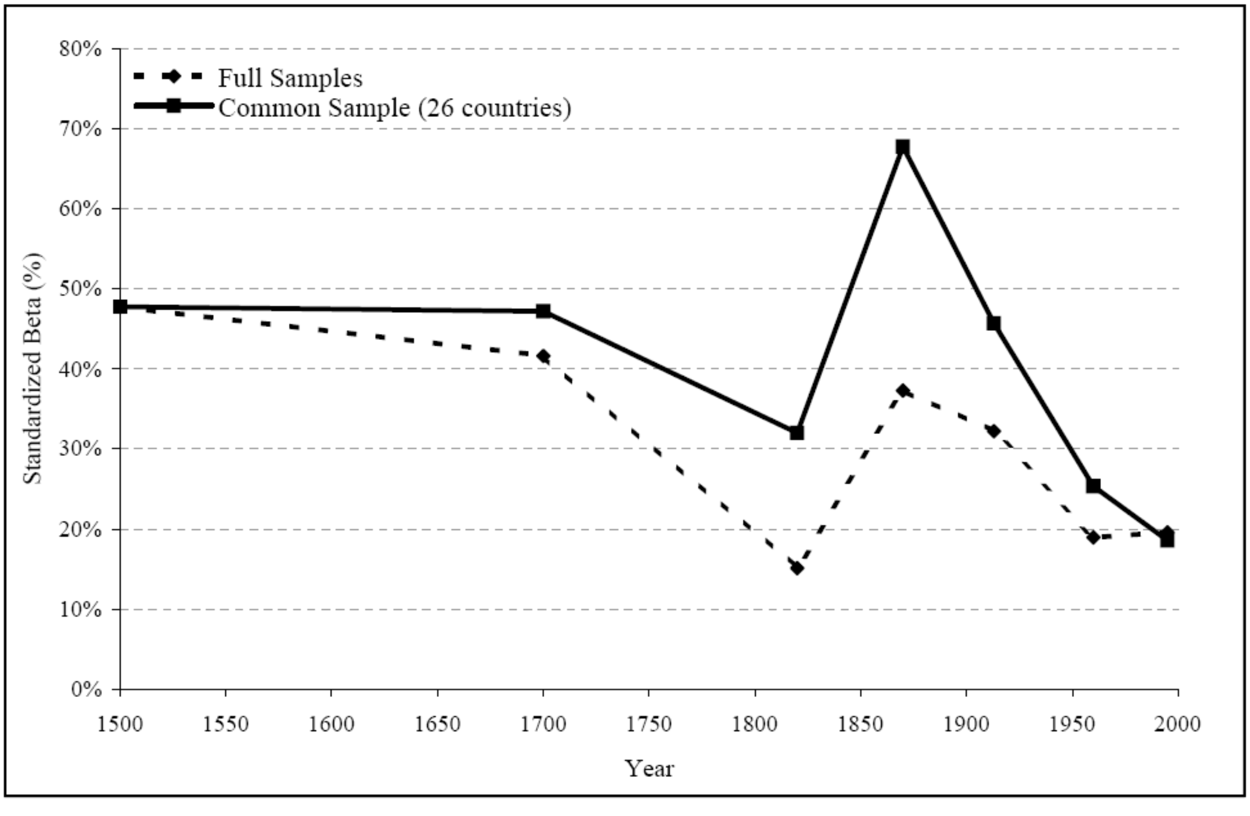

Figure 6 - Time path of the effect of relative genetic distance on income differences, 1500-1995.

4.6.2 Genetic Distance across European Countries.

Analyzing the European data can be informative for several reasons. First, it constitutes a robustness check on the worldwide results. Second, matching populations to countries is much more straightforward for Europe than for the rest of the world, because the choice of sampled European populations happens to match nation-state boundaries. This should reduce the incidence of measurement error. Third, genetic distances are orders of magnitude smaller across countries of Europe, and genetic specificities within Europe have developed over the last couple of thousand years (and not tens of thousands of years). It is very unlikely that any genetic traits have risen to prominence within Europe as the result of strong natural selection over such a short period of time, so a finding that genetic distance based on neutral markers within Europe is associated with income differences would be evidence that barriers to the diffusion of development are primarily induces by differences in culturally transmitted traits.

Table 9 presents the results. Genetic distance is again positively and significantly associated with income differences. Moreover, while genetic distance across European countries are smaller than in the World sample, so are the income differences to be explained. Thus, we find that the effect of F_{ST} distance is large in magnitude. In the baseline estimate in column (2) of Table 9, which includes geographic controls, the standardized beta coefficient on genetic distance relative to the English equals 44.44% - twice that obtained from the World sample. Physical distance measures bear small or insignificant coefficients, suggesting that geographic barriers are not a big hindrance to the diffusion of income across countries of Europe. The last column of Table 6 shows that genetic distance accounts for an even greater amount (79.59%) of the variation in income differences in 1870, during the Industrial Revolution. Again, we take these differences in estimated magnitudes as consistent with our barriers interpretation.

5 Conclusions

In this paper we make two contributions: (1) For the first time, we document a statistically and economically significant positive relationship between measures of genetic distance and cross-country income differences, even when controlling for various other measures of geographical, cultural and historical differences; and (2) we provide an economic interpretation of these findings, based on barriers to the diffusion of development.

Our economic model is based on two key hypotheses. The first hypothesis is that, on average, genetic distance captures divergence in characteristics that are transmitted vertically across generations within populations over the very long-run. Genetic distance, by acting like a molecular clock, measuring the time since two populations shared common ancestors, provides an ideal summary of divergence in slowly-changing genealogically-transmitted characteristics, including culturally-transmitted traits (habits, customs, etc.). Our second hypothesis is that such differences in long-term vertically-transmitted characteristics act as barriers to the horizontal diffusion of innovations from the world technological frontier. Societies that are genealogically farther from the innovators have faced higher costs to imitate and adapt new productivity-enhancing technologies and institutions.

As we have shown, the empirical evidence over time and space is consistent with the barriers interpretation. In particular, we have found, consistent with our theoretical framework, that the effect on economic distance associated with *relative* genetic distance from the technological frontier is larger than the effect of absolute genetic distance. We have also found that the effect has varied across time and space in ways that support our diffusion-from-the-frontier interpretation: the effect has increased in the first part of the 19th century, peaked in 1870, and has been decreasing afterwards, consistently with the view that relative genetic distance captures barriers to the diffusion of the Industrial Revolution. Some evidence, particularly the results for European countries, also suggests that these differences may stem in substantial part from cultural (rather than purely biological) transmission of characteristics across generations.

While our analysis provides a general macroeconomic framework to interpret our empirical findings, the study of the specific microeconomic mechanisms through which the effects operate is left for future research. For example, an analysis of microeconomic data may shed light on the relations among genetic distance, vertical characteristics, imitation costs, and the spread of specific innovations. So far, we were not able to show that linguistic or religious barriers, two culturally transmitted characteristics, are responsible for the effect of genetic distance. This does not preclude a role for other slow-changing culturally transmitted traits, such as norms or values. These are inherently harder to measure, particularly within the long term, macroeconomic perspective that we adopted, necessitating a more microeconomic approach. Another natural extension of our work would be to investigate whether and how genetic distance affects bilateral exchanges and interactions between different groups and societies, both peacefully (e.g., trade, foreign direct investment) and non-peacefully (conflict and wars).[61] Finally, it could be interesting to link our results to the vast literature on demography and economic growth, and explore the connections between genetic distance, vertically-transmitted characteristics, and demographic patterns.[62]

A final consideration is about policy implications. A common concern with research documenting the importance of variables like genetic distance or geography is pessimism about policy implications. What use is it to know that genetic distance explains income differences, if one cannot change genetic distance, at least in the short-run? These concerns miss a bigger point: available policy variables may have a major impact not on genetic distance itself, but on the coefficient that measure the effect of genetic distance on income differences. That coefficient has been changing over time, and can change further. If we are correct in interpreting our results as evidence for long-term barriers across different populations and cultures, significant reductions in income disparities could be obtained by encouraging policies that reduce those barriers, including efforts to translate and adapt technological and institutional innovations into different cultures and traditions, and to foster cross-cultural exchanges. More work is needed - at the micro as well as macro level - in order to understand the specific mechanisms, market forces, and policies that could facilitate the diffusion of development across countries with distinct long-term histories and cultures.

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[61] In preliminary work, using gravity equations, we indeed find a large and significant effect of genetic distance as a determinant of bilateral trade, controlling for a large number of geographical variables.

[62] See Galor (2005) for an in-depth discussion of this literature. See also Richerson and Boyd (2004) for an anthropological perpective.

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Appendix 1

Transitional Dynamics after a Regime Change in R&D

For simplicity and without much loss of generality, we will illustrate the effect of a regime-change in R&D for the case $\psi = 1$. Following Barro and Sala-i-Martin (1997; 2004 chapter 8), we describe the dynamic analysis for the variables $B \equiv A_i/A_f$ and $\chi \equiv C_i/A_i$. One can easily show that the growth rates of these two variables are given by:

$$\frac{dB}{dt}\frac{1}{B} = \frac{1}{\lambda_i e^{\theta d_v(i,f)} B}[\pi(\frac{1+\alpha}{\alpha}) - \chi] - \frac{\pi}{\lambda_f} + \rho \tag{34}$$

and:

$$\frac{d\chi}{dt}\frac{1}{\chi} = \frac{\pi}{\lambda_i e^{\theta d_v(i,f)} B} - \frac{\pi}{\lambda_f} \tag{35}$$

The dynamics of this system of differential equations can be described with a phase diagram in (B,χ) space, as in Figure A1.

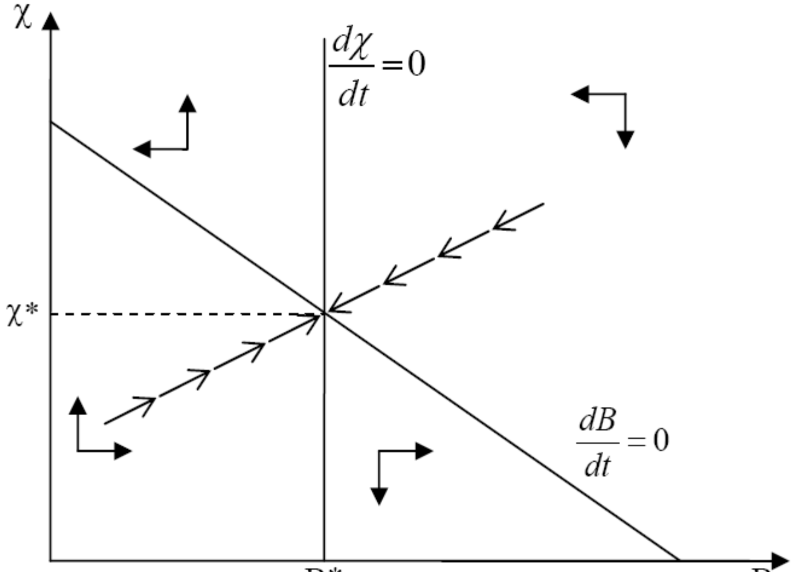

Figure A1 - Transitional Dynamics

The locus for $\frac{dB}{dt} = 0$ is given by the following linear relationhsip between χ and B:

$$\chi = \pi(\frac{1+\alpha}{\alpha}) - \lambda_i e^{\theta d_v(i,f)}[\frac{\pi}{\lambda_f} - \rho]B \tag{36}$$

while the locus for $\frac{d\chi}{dt} = 0$ is given by the following value of B:

$$B = \frac{\lambda_f}{\lambda_i} e^{-\theta d_v(i,f)} \tag{37}$$

Assume that the R&D parameters are $\lambda_f = \lambda_i = \lambda$ Then, in steady-state we have:

$$B^* = e^{-\theta d_v(i,f)} \tag{38}$$

and:

$$\chi^* = \frac{\pi}{\alpha} + \lambda\rho \tag{39}$$

If at time T both R&D parameters were to decrease to $\lambda' < \lambda$ instantaneously, the system would immediately jump to the new steady-state, as in Figure A2, with the same value for the state variable B^* and a lower steady-state value for the control variable $\chi^{*\prime} = \frac{\pi}{\alpha} + \lambda'\rho < \chi^*$.

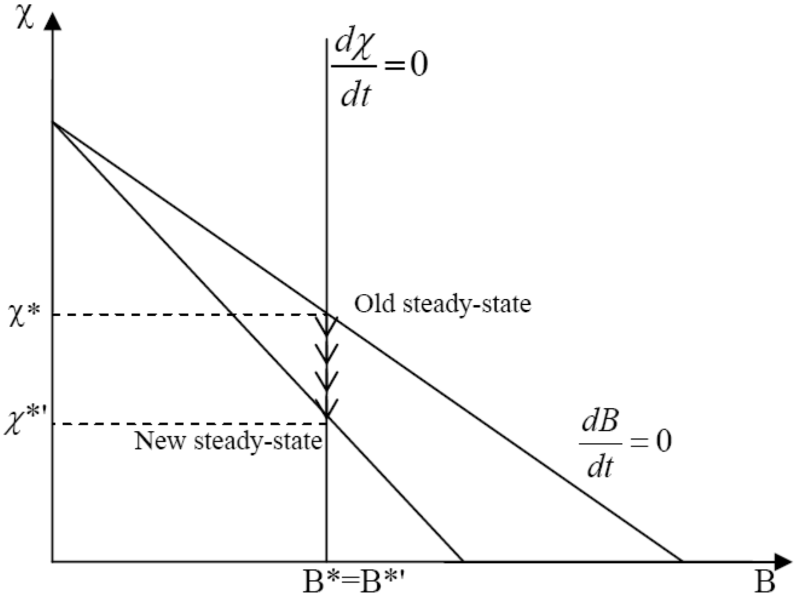

Figure A2 - Instantaneous diffusion of the new R&D technology

Therefore, an instantaneous adjustment of the R&D technology parameter in both societies (leader and follower) would imply a higher growth rate in both economies, and no change in their economic distance (i.e., $\ln Y_f - \ln Y_i = -\ln B^*$ would remain the same).

Now, in contrast, assume that at time T the frontier society introduces a lower unit cost for R&D ($\lambda_f(t) = \lambda' < \lambda$ for all $t \geq T$), while society i will be able to reduce its R&D parameter $\lambda_i(t)$ only with a delay $\zeta d_v(f,i)$, so that $\lambda_i(t) = \lambda$ for $t < T+ \zeta d_v(f,i)$ and $\lambda_i(t) = \lambda' < \lambda$ for $t \geq T+ \zeta d_v(f,i)$. Under the assumption that the time of the adjustment to the lower cost λ' is fully anticipated by the representative consumer at time T, the system will follow the dynamics of the following two "temporary" differential equations:

$$\frac{dB}{dt}\frac{1}{B} = \frac{1}{\lambda e^{\theta d_v(i,f)} B}[\pi(\frac{1+\alpha}{\alpha}) - \chi] - \frac{\pi}{\lambda'} + \rho \tag{40}$$

$$\frac{d\chi}{dt}\frac{1}{\chi} = \frac{\pi}{\lambda e^{\theta d_v(i,f)} B} - \frac{\pi}{\lambda'} \tag{41}$$

with a "temporary" locus for $d\chi/dt = 0$ at $B_1 = \left(\lambda'/\lambda\right) e^{-\theta d_v(i,f)}$ (the "temporary" loci for $d\chi/dt = 0$ and $dB/dt = 0$ are denoted with the dotted lines in Figure A3). After time T the system will follow the "temporary" dynamics consistent with the above differential equations. Since the future change in the R&D parameter is fully anticipated, the dynamic path of the system during the temporary phase - that is, for $T < T+ \zeta d(i,f)$, - must follow dynamics such that, at time $T+ \zeta d(f,i)$, the variables $\chi(t)$ and $B(t)$ are on the saddle path of the new "permanent" system. The new permanent system is constituted by the following two differential equations:

$$\frac{dB}{dt}\frac{1}{B} = \frac{1}{\lambda' e^{\theta d_v(i,f)} B}[\pi(\frac{1+\alpha}{\alpha}) - \chi] - \frac{\pi}{\lambda'} + \rho \tag{42}$$

$$\frac{d\chi}{dt}\frac{1}{\chi} = \frac{\pi}{\lambda' e^{\theta d_v(i,f)} B} - \frac{\pi}{\lambda'} \tag{43}$$

and has the same steady-state value for B as the old system before time T. Therefore, as shown in Figure A3, $B(t)$ will decrease for a while, and will reach a minimum B_2, when crossing the locus:[63]

$$\chi = \pi(\frac{1+\alpha}{\alpha}) - \lambda e^{\theta d_v(i,f)}[\frac{\pi}{\lambda'} - \rho]B \tag{44}$$

After that, $B(t)$ will start increasing again, and will converge back to its initial value $B^* = e^{-\theta d_v(i,f)}$. Therefore, the economic distance $\ln Y_f(t) - \ln Y_i(t) = -\ln B(t)$ will increase after T, peak before $T+ \zeta d(f,i)$, and then decrease back to the steady state level $-\ln B^*$, as shown in Figure 3 in Section 3. A similar patter will be followed by the economic distance between a society which is very close to the frontier and a society that is farther from the frontier. Eventually, after time $T+ \zeta \max d(f,i)$, all societies will have adopted imitation technologies with the lower parameter λ', and the effect of relative distance on economic distance will be back to the steady-state value before the regime change - that is, to $\ln Y_f - \ln Y_i = -\ln B^* = \theta[d_v(i,f) - d_v(j,f)]$ (Implication 3).

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[63] Clearly B_2 will be reached at a time T' smaller than $T+ \zeta d(f,i)$ since that point must be reached before the system converges to the new saddle path.

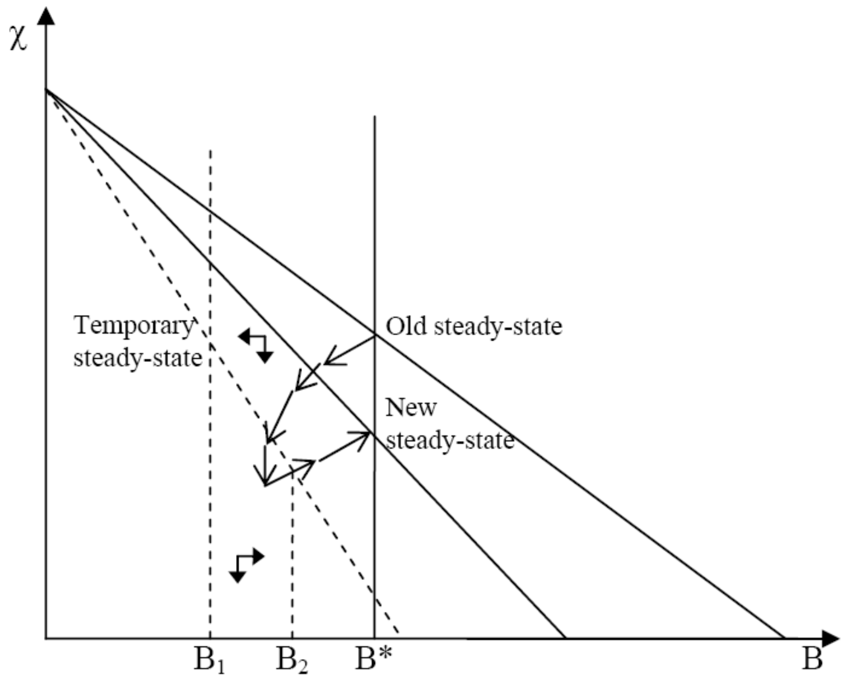

Figure A3 - Delayed diffusion of the new R&D technology

Appendix 2

Estimation method for the bilateral regressions

Consider three countries, 1, 2 and 3. Observations on the dependent variable $|\log y_1 - \log y_2|$ and $|\log y_1 - \log y_3|$ will be correlated by virtue of the presence of country 1 in both observations. Conditioning on the right-hand side variables (which are bilateral in nature) should reduce cross-sectional dependence in the errors ε_{12} and ε_{13}, but we are unwilling to assume that observations on the dependent variable are independent conditional on the regressors.[64] In other words, simple least squares standard errors will lead to misleading inferences due to spatial correlation.

Before proceeding, we note the following: with N countries, there are $N(N-1)/2$ distinct pairs. Denote the observation on absolute value income differences between country i and country j as

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[64] Another feature that reduces the dependence across pairs is the fact that the dependent variable involves the *absolute value* of log income differences. Simple simulations show that under i.i.d. Normal income draws with moments equal to those observed in our sample, the correlation between absolute value differences in income for any two pair containing the same country will be about 0.22. Without taking absolute values, it is straightforward to notice that the correlation would be exactly 0.5. Hence, taking absolute values reduces the cross-sectional dependence induced by the construction of the dependent variable..

dy_{ij}. Pairs are ordered so that country 1 appears in position i and is matched with all countries from 2...N appearing in position j. Then country 2 is in position i and is matched with 3...N appearing in position j, and so on. The last observation has country $N-1$ in position i and country N in position j. We denote the non-zero off-diagonal elements of the residual covariance matrix by σ_m where m is the country common to each pair.

A simple example when the number of countries is $N = 4$ is illustrative. In this case, under our maintained assumption that the error covariances among pairs containing a common country m are equal to a common value σ_m, the covariance matrix of the vector of residuals ε is of the form:

$$\Omega = cov \begin{pmatrix} \varepsilon_{12} \\ \varepsilon_{13} \\ \varepsilon_{14} \\ \varepsilon_{23} \\ \varepsilon_{24} \\ \varepsilon_{34} \end{pmatrix} = \begin{pmatrix} \sigma_\varepsilon^2 & & & & & \\ \sigma_1 & \sigma_\varepsilon^2 & & & & \\ \sigma_1 & \sigma_1 & \sigma_\varepsilon^2 & & & \\ \sigma_2 & \sigma_3 & 0 & \sigma_\varepsilon^2 & & \\ \sigma_2 & 0 & \sigma_4 & \sigma_2 & \sigma_\varepsilon^2 & \\ 0 & \sigma_3 & \sigma_4 & \sigma_3 & \sigma_4 & \sigma_\varepsilon^2 \end{pmatrix}$$

In this context, controlling for a common-country fixed effect should account for the correlated part of the error term. For this we rely on well-known results cited in Case (1991), showing that fixed effects soak up spatial correlation, though in a context quite different from ours: we do not have longitudinal data, and the panel nature of our dataset comes from the fact that each country is paired with all the other countries in the dataset.[65] Following this observation, we model:

$$\varepsilon_{ij} = \sum_{k=1}^{N} \gamma_k \delta_k + \nu_{ij} \tag{45}$$

where $\delta_k = 1$ if $k = i$ or $k = j$, $\delta_k = 0$ otherwise, and ν_{ij} is a well-behaved disturbance term. We treat δ_k as fixed effects, i.e. we introduce in the regression a set of N dummy variables δ_k each taking on a value of one $N-1$ times.[66] Given our estimator, the effect of the right-hand side

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[65] Note that simply treating ε_i and ε_j as fixed effects, by including corresponding dummy variables in the regression, will not fully address our concern. This is because, with the exception of country 1 and country N, all countries will appear either in position i or in position j in different observations, inducing spatial correlation between these pairs. In the example above, for instance, country 2 appears in position i in observation 1, and in position j in observation 4, inducing spatial dependence between ε_{12} and ε_{23}. Simple country fixed effects would not soak up this dependence.

[66] The inclusion of fixed effects did not greatly alter the signs or magnitudes of the estimates of the slope coefficients on our variables of interest, compared to simple OLS estimation. In contrast, in line with our expectations, our common-country fixed effects technique resulted in standard errors that were quite different from (and generally much larger than) the (wrong) ones obtained with simple OLS.

variables is identified off the variation within each country, across the countries with which it is matched.

It is in principle possible to test for the presence of spatial correlation both in the model with common country fixed effect and without. Such tests, known as Moran's I-tests, require specifying a neighborhood matrix along which non-zero correlations are allowed. In our case, the neighborhood matrix is easy to conceptualize: its entries are 1 whenever there is a common country in a pair, zero otherwise. Unfortunately, the dimensionality of the neighborhood matrix equals the square of the number of observations. In the case of our worldwide dataset, there would be $192,127,321$ entries, making the problem computationally intractable. We have run I-tests for our smaller dataset of European countries, where the matrix has $87,616$ entries.[67] Without dummies, Moran's I test suggested the presence of spatial correlation. With common country dummies added to the specification, it did not. We find this to be encouraging.

To summarize, for each country we create a dummy variable equal to 1 if the country appears in a given pair. We then include the full set of N dummy variables in the regression. The inclusion of these fixed effects soaks up the spatial correlation in the error term resulting from the presence of each country multiple times in various country pairs. In addition, our standard errors are heteroskedasticity-consistent (i.e. we correct standard errors to account for the fact that the diagonal elements of Ω might differ).[68]

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[67] The specification being tested is the baseline specification of Column 2 in Table 9. Details of these tests are available upon request.

[68] There are obviously several ways to address the issue of spatial correlation in our context. An alternative we considered would be to do feasible GLS by explicitly estimating the elements of Ω, and introducing the estimated Ω as a weighing matrix in the second stage of the GLS procedure. While apparently straightforward, this is computationally very demanding as the dimensionality of Ω is large - in our application we have over $13,000$ country pairs with available data on the variables of interest, and up to 167 covariance terms to estimate. We also pursued several bootstrapping strategies based on selecting subsamples such that the problem of spatial correlation would not occur, generating results very similar to those we present here. Details and results from these bootstraps are available upon request. In contrast to these alternatives, our approach is computationally easy to implement.