Long-Term Barriers to the Diffusion of Innovations*

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Abstract

We document an empirical relationship between the cross-country adoption of technologies and the degree of long-term historical relatedness between human populations. Historical relatedness is measured using genetic distance, a measure of the time since two populations' last common ancestors. We find that the measure of human relatedness that is relevant to explain technology adoption is not the simple genetic distance between populations, but genetic distance relative to the world technological frontier. This evidence is consistent with long term historical relatedness acting as a barrier to technology adoption: societies that are more distant from the technological frontier tend to face higher imitation costs. The results can help explain current differences in total factor productivity and income per capita across countries.

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1 Introduction

Differences in technology adoption lie at the heart of differences in long-term economic performance and standards of living across societies. Total factor productivity (TFP), an indirect measure of technology based on the Solow residual, accounts for a vast share of differences in income per capita across countries (e.g. Caselli, 2005 and Hsieh and Klenow, 2010). Comin, Hobijn and Rovito (2008) have provided evidence of large lags in the usage of specific technologies, implying that technology usage disparities might account for a large part of cross-country TFP differentials. Technological innovation has also played a paramount role in the study of economic growth and development, both theoretically and empirically (e.g., see Aghion and Howitt, 2008). In this literature, the question of why the adoption of new productivity-enhancing technologies takes place so slowly and unequally across different societies remains a central puzzle.

In this paper, our goal is to shed light on the barriers and obstacles that prevent or delay the adoption of specific technologies across countries. We focus in particular on human barriers, holding fixed geographic barriers. We formulate and test the hypothesis that rates of technology adoption depend on measures of long-term historical relatedness between populations, i.e. on their degree of kinship. The main idea of this paper is twofold: (1) on average, populations that are more closely related tend to be more similar with respect to traits (habits, customs, beliefs, values, etc.) that are transmitted with variation from one generation to the next, and (2) similarity in intergenerationally transmitted traits tends to reduce the barriers to technology adoption - i.e., populations that share more similar intergenerationally-transmitted traits face lower costs when imitating each other's innovations.

We argue that long-term genealogical distance works as a *barrier* to the diffusion of innovations across populations. It is important to emphasize that we are not assuming that populations would necessarily inherit traits that make them directly more productive. In fact, in our theoretical framework, inherited traits have no direct effect on a population's productivity. What matters, in our model, is that random historical divergence introduces different customs, habits and norms across populations, and that these differences, on average, tend to decrease their ability to learn from each other. Even relatively trivial differences in attitudes, appearance or behavior between groups may lead to misunderstanding or discrimination, and may create significant barriers to communication and social interactions, reducing opportunities for learning and imitation.[1] In sum,

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[1] Indeed, the microeconomic literature on the diffusion of innovations (Rogers, 1995) is consistent with a central

our central hypothesis is that differences in technology adoption across societies can be explained by barrier effects inversely related to the degree of relatedness between human populations.

Building on our previous work on the diffusion of economic development (Spolaore and Wacziarg, 2009), we capture historical relatedness between populations using genetic distance. Genetic distance is calculated as a summary measure of the difference in *allele frequencies* across a set number of genes, or *loci*. As human populations split from each other over the course of history, they developed distinct genetic markers from random mutations. Most of these genetic mutations did not confer any environmental advantages and diffused as the simple result of randomness (they were not selected), so they are called *neutral genes* (Kimura, 1968). Genes used to compute common measures of genetic distance are chosen from among neutral genes. For such genes, random mutations arise and diffuse at a constant rate, so measures of genetic distance based on a large enough number of neutral genes reflect the time separating two populations from a common ancestor, as in a molecular clock. We argue that human traits that create barriers between populations on average diverge to an extent proportional to the separation time between two populations.

Thus, genetic distance is an ideal measure of the degree of historical relatedness between populations. An intuitive analogue is the concept of relatedness between individuals: two siblings are more closely related than two cousins because they share more recent common ancestors - their parents rather than their grandparents. Our key hypothesis is that technological innovations are more likely to be adopted across siblings than across more distant cousins: separation times between populations are associated with similarity in a wide range of traits, transmitted either genetically or culturally from parents to children, that matter for the ease of adoption of productive innovations.

Figure 1 (from Cavalli-Sforza, Menozzi and Piazza, 1994, p. 78) is a phylogenetic tree illustrating how different human populations have split apart over time. Such phylogenetic trees, constructed from genetic distance data, are the population analogs of family trees for individuals.

[INSERT FIGURE 1 HERE]

It must be emphasized that genetic distance is based on neutral change, and, therefore, is not meant to capture differences in specific traits that may directly matter for fitness and survival. Genetic distance is a general measure of long-term relatedness, and is associated with the whole

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role for subjective barriers between groups and populations.

set of traits that are transmitted "vertically" from parents to children, biologically and culturally. It is therefore a general metric for the average difference in traits passed on across generations over the very long run - that is, over the time horizon along which populations have split apart. In this paper we call "vertical traits" all characteristics that are passed on intergenerationally with variation within a population over the very long run.

This paper is the first to empirically document the effects of genealogical relatedness on the adoption of specific technologies across countries. To do so, we use historical and contemporary data on usage rates of a wide range of technologies, dating back to the year 1500. We use two recently developed databases of technology adoption: The Cross-Country Historical Adoption of Technology (CHAT) dataset, which covers a wide range of detailed technologies going back to the year 1800 (Comin and Hobijn, 2009), and the database of historical technology adoption used in Comin, Easterly and Gong (2010) to study technological persistence since antiquity (this database goes back to 1000 BC, but we only make use of data since 1500 AD). We compare the empirical effects of the simple genetic distance between populations to that of genetic distance relative to the technological frontier, finding that the latter trumps the former as a determinant of bilateral differences in technological adoption rates. This empirical test is consistent with a barrier effect of long-term historical distance, whereby societies that are more distant from the technological frontier tend to face higher imitation costs. We find large and statistically significant effects of genetic distance relative to the frontier on technology use differences. These large effects at the level of individual technologies can help explain current differences in total factor productivity and income per capita across countries.

This paper is organized as follows. Section 2 presents a stylized model of the diffusion of technologies as function of differences in vertically transmitted traits across human populations, and ultimately as a function of the degree of genealogical relatedness between them. Section 3 presents our data and empirical methodology. Section 4 describes the empirical results, and Section 5 concludes.

2 A Theory of Relatedness and Technology Adoption

In this section we present a simple framework linking long-term relatedness (measured by genetic distance), intergenerationally transmitted traits, and the adoption of technologies across populations. The main ideas are that (1) genetic distance measures the degree of long-term genealogical relatedness of different populations over time, (2) on average, populations that are more closely related tend to be more similar with respect to traits that are transmitted with variation from one generation to the next, (3) similarity in intergenerationally transmitted traits tends to reduce the barriers to technology adoption: populations that share more similar intergenerationally-transmitted traits face lower costs when imitating each other's innovations. These hypotheses have testable empirical predictions: intensive and extensive margins of technology adoption should be a function of different populations' relative genetic distance from the technological frontier, rather than the simple distance between them. The empirical section then tests this prediction.

2.1 Genetic Distance and Vertically Transmitted Traits

As discussed earlier, genetic distance measures the difference in allele distributions between two populations, where the chromosomal loci under consideration are neutral - that is, they change randomly and independently of selection pressure. When two populations split apart, random genetic mutations result in genetic differentiation over time. The longer the separation time, the greater the genetic distance computed from a set of neutral genes. Therefore, genetic distance captures the time since two populations have shared common ancestors - i.e., the time since they have been the same population. Overall, genetic distance is a general metric for average differences in traits passed on across generations over the very long run - that is, over the time horizon along which populations have split apart. We call "vertical traits" all those traits that are passed from one generation to the next within a population, with variation, over the very long run.

These concepts can be illustrated with a simple analytical example. For simplicity, let all vertical traits of a population be summarized as a point on the real line. At time 0 ("the present") population i has vertical traits $v_i(0)$, where $v_i(0)$ is a real number. In general, populations inherit their vertical traits from their ancestor populations with variation. Specifically, population i living at time 0, and descending from ancestral population a_i living at time $-T$, will have traits given by:

$$v_i(0) = v_{a(i)}(-T) + \varepsilon_i(-T, 0) \tag{1}$$

where $v_{a(i)}(-T)$ are ancestral population $a(i)$'s vertical traits at time $-T$, and $\varepsilon_i(-T, 0)$ measures random variation between time $-T$ and time 0.

Consider the simplest possible mechanism for variation: vertical change as a random walk, whereas $\varepsilon_i(-T, 0) = \varepsilon > 0$ with probability 1/2 and $\varepsilon_i(-T, 0) = -\varepsilon < 0$ with probability 1/2. In addition, consistently with a "neutral" view of intergenerational change, we assume that such shocks are independent across different populations - i.e., shock $\varepsilon_i(-T, 0)$ is independent of shock $\varepsilon_j(-T, 0)$ for $j \neq i$. By the same token, at time $-T$ population $a(i)$'s vertical traits are inherited from its ancestor population $a(a(i))$, living at time $-T\prime < -T$, according to the following equation:

$$v_{a(i)}(-T) = v_{a(a(i))}(-T') + \varepsilon_{a(i)}(-T', -T) \tag{2}$$

where $\varepsilon_{a(i)}(-T', -T) = \varepsilon' > 0$ with probability 1/2 and $\varepsilon_{a(i)}(-T', -T) = -\varepsilon' < 0$ with probability 1/2. Again, shocks are independent across populations.

Now, consider three populations ($i = 1, 2, 3$). Population 1 and population 2 descend from the same last common ancestor population $a(1) = a(2) \equiv a(1\&2)$ living at time $-T$. In contrast, population 3 only shares common ancestors with populations 1 and 2 going back to time $-T\prime$: $a(3) \neq a(1\&2)$, and $a(a(3)) = a(a(1\&2)) \equiv a(1\&2\&3)$. The phylogenetic tree of the three populations is illustrated in Figure 2.

[INSERT FIGURE 2 HERE]

By construction, genetic distance $g(1, 2)$ between population 1 and population 2 is smaller than genetic distance between population 1 and population 3 (and smaller than genetic distance between population 2 and population 3). Formally:

$$g(1, 2) = F < g(1, 3) = g(2, 3) = F\prime \tag{3}$$

Vertical traits in each population are given by the following equations:

$$v_1(0) = v_{a(1\&2)}(-T) + \varepsilon_1(-T, 0) \tag{4}$$

$$v_2(0) = v_{a(1\&2)}(-T) + \varepsilon_2(-T, 0) \tag{5}$$

$$v_3(0) = v_{a(3)}(-T) + \varepsilon_3(-T, 0) \tag{6}$$

$$v_{a(1\&2)}(-T) = v_{a(1\&2\&3)}(-T') + \varepsilon_{a(1\&2)}(-T', -T) \tag{7}$$

$$v_{a(3)}(-T) = v_{a(1\&2\&3)}(-T') + \varepsilon_{a(3)}(-T', -T) \tag{8}$$

Let $d_v(i, j) \equiv |v_j - v_i|$ denote the distance in vertical traits between population i and population j. The expected vertical distance between population 1 and population 2, which share their last common ancestors at time $-T$, is:[2]

$$E[d_v(1,2)] = \varepsilon \tag{9}$$

Clearly, all variation between populations 1 and 2 is given by change that took place between time $-T$ and 0. In contrast, expected distance between population 1 and population 3 (and between population 2 and population 3) will reflect shocks that took place both between time $-T\prime$ and $-T$ and between time $-T$ and time 0. On average, such shocks bring about a larger expected distance:[3]

$$E[d_v(1,3)] = E[d_v(2,3)] = \max\{\frac{\varepsilon'}{2} + \varepsilon \ , \ \varepsilon' + \frac{\varepsilon}{2}\} > \varepsilon = E[d_v(1,2)] \tag{10}$$

Thus, larger genetic distance, on average, is associated with larger distance in vertical traits. Of course, this relation is not deterministic. Some pairs of populations that are genealogically more distant may end up with more similar vertical traits than two more closely related populations, but that outcome is less likely to be observed than the opposite outcome. On average, genetic distance and vertical distance go hand in hand.

2.2 Relative Vertical Distance from the Frontier and Technology Adoption

Over the millennia, populations have diverged in a series of traits transmitted vertically from parents to children. These vertical traits include physical and cultural characteristics. Most of these traits

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[2] The derivation is straightforward. With probability 1/4 both populations experience a positive shock ε, and with probability 1/4 both populations experience a negative shock -ε. Hence, with probability 1/2, their vertical distance is zero. With probability 1/2 one population experiences a positive shock ε and the other a negative shock $-\varepsilon$, implying a vertical distance equal to $|\varepsilon - (-\varepsilon)| = 2\varepsilon$. On average, the expected vertical distance is $E[d_v(1,2)] = \frac{1}{2}0 + \frac{1}{2}2\varepsilon = \varepsilon$.

[3] The derivation is as follows. With probability 1/4 population 1's ancestor populations and population 2's ancestor populations experienced identical shocks both between time -T' and time -T and between time -T and time 0. That is, with probability 1/4 we have $\varepsilon_{a(1\&2)}(-T,-T') = \varepsilon_{a(3)}(-T,-T')$ *and* $\varepsilon_1(0,-T) = \varepsilon_3(0,-T)$, implying $d_v(1,3) = 0$. By the same token, with probability 1/4 the two populations experienced identical shocks between time $-T'$ and $-T$ but different shocks between time $-T$ and time 0, implying $d_v(1,3) = 2\varepsilon$, and with probability 1/4 identical shocks between $-T$ and 0 but different between $-T'$ and $-T$, implying $d_v(1,3) = 2\varepsilon'$. With probability 1/8, one population linaeage has experienced two positive shocks $(\varepsilon' + \varepsilon)$ while the other has experienced two negative shocks $(-\varepsilon' - \varepsilon)$, therefore leading to a vertical distance equal to $2\varepsilon' + 2\varepsilon$. Finally, with probability 1/8 one population lineage has experienced a positive shock ε' and a negative shock $-\varepsilon$ while the other population lineage has experienced -ε' and ε. In this latest case, the vertical distance $d_v(1,3) = |2\varepsilon - 2\varepsilon'|$. In sum, expected vertical distance is given by

$$E[d(1,3)] = \frac{1}{4}2\varepsilon' + \frac{1}{4}2\varepsilon + \frac{1}{8}(2\varepsilon' + 2\varepsilon) + \frac{1}{8}|2\varepsilon - 2\varepsilon'|$$

which is equal to $\varepsilon + \frac{\varepsilon'}{2}$ if $\varepsilon \geq \varepsilon'$ and equal to $\varepsilon' + \frac{\varepsilon}{2}$ if $\varepsilon \leq \varepsilon'$, or, equivalently, $E[d_v(1,3)] = \max\{\frac{\varepsilon'}{2} + \varepsilon \ , \ \varepsilon' + \frac{\varepsilon}{2}\}$. The same expected vertical distance holds between populations 2 and 3.

have diverged randomly, and do not need to have a direct effect on survival and fitness. However, this divergence has led to differences across populations. Our key hypothesis is that such differences may act as barriers to the diffusion of technological innovations across populations in modern times. It is reasonable to expect that, on average, populations that share a more recent common history and are therefore closer in terms of intergenerationally transmitted traits, face lower costs and obstacles to adopting each other's innovations. The literature on the diffusion of innovations (Rogers, 1995) is consistent with a major role for subjective barriers between groups and populations. As Rogers points out, summarizing the lessons from decades of research, most people depend upon a subjective evaluation of an innovation that is conveyed to them from other individuals like themselves who have previously adopted the innovation. Overall, historical relatedness and similarity is likely to reduce imitation costs, while a higher vertical distance should be associated with higher imitation and adoption costs. In sum, our main hypothesis is that long-term divergence in vertically transmitted traits act as a barrier to more recent "horizontal" diffusion of innovations across societies.

2.2.1 Extensive margin

These ideas can be formalized very simply in a one-period model. At time 0, one of our three populations - say, population 1 - introduces a continuum of innovations of mass N.[4] An innovation $k \in [0, N]$ will be adopted by population $i = 2, 3$ if and only if the innovation's benefits b_k are higher than its costs c_{ki}.[5] Our key hypothesis is that *adoption costs for each population are a function of vertical distance from the frontier* (population 1):

$$c_{ki} = \chi_k + \phi d_v(i, f) \tag{11}$$

where $\chi_k > 0$ and $\phi > 0$. Different innovations come with different costs and benefits. To fix idea, assume that the ratio $(b_k - \chi_k)/\phi$ is distributed uniformly between 0 and $\omega > 0$, with innovation 0 having the highest ratio $(b_0 - \chi_0)/\phi = \omega$ and innovation N having the lowest ratio $(b_N - \chi_N)/\phi = 0$. In general, the ratio for innovation $k \in [0, N]$ is:

$$\frac{b_k - \chi_k}{\phi} = \omega[1 - \frac{k}{N}] \tag{12}$$

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[4] We assume here, for simplicity, that the probability of coming up with an innovation is independent of vertical traits. If vertical traits also explain the onset of innovations, the effects under consideration would be larger. These direct effects are not necessary for our results.

[5] We abstract from an effect of vertical traits on the benefits from adoption. Again, such effect would strengthen the relationship, but is not necessary for the results.

Population i will adopt N_i^* innovations, where, for each adopted innovations $k \in [0, N_i^*]$, $b_k \geq c_{ki}$. Hence, the marginal N_i^* is defined by:

$$b_{N_i^*} = \chi_{N_i^*} + \phi d_v(i, f) \tag{13}$$

which, by using equation (12) above, can be re-written as:

$$\frac{b_{N_i^*} - \chi_{N_i^*}}{\phi} = d_v(i, f) = \omega[1 - \frac{N_i^*}{N}] \tag{14}$$

which implies:[6]

$$N_i^* = N[1 - \frac{d_v(i, f)}{\omega}] \tag{15}$$

This equation shows that the number of innovations adopted by each population is decreasing in its vertical distance from the frontier. If vertical traits change according to the simple random-walk process illustrated in the previous subsection, the expected rate of adoption for population 2 (which is genetically closer to the frontier population 1: $g(1, 2) = F$) will be larger than the expected rate of adoption for population 3 (which is genetically more distant from the frontier $g(1, 3) = F' > F$):[7]

$$E\{N_2^*\} = N[1 - \frac{E[d_v(1, 2)]}{\omega}] = N[1 - \frac{\varepsilon}{\omega}] > E\{N_3^*\} = N[1 - \frac{E[d_v(1, 3)]}{\omega}] = N[1 - \frac{\varepsilon}{\omega} - \frac{\varepsilon'}{2\omega}] \tag{16}$$

Let $d_N(i, j) \equiv |N_j^* - N_i^*|$ denote the difference in rates of technology adoption (extensive margins) between population i and population j. Our basic framework implies that such difference will depend on relative vertical distance from the frontier, and hence, on average, on relative genetic distance from the frontier population:

$$d_N(i, j) \equiv |N_j^* - N_i^*| = \frac{1}{\omega} |d_v(j, f) - d_v(i, f)| \tag{17}$$

Therefore, we predict a positive correlation between differences in rates of technology adoption $d_N(i, j)$ between two populations i and j, and their relative genetic distance (i.e., $|g(i, f) - g(j, f)|$) from the frontier.

This framework can also account for a positive correlation between differences in rates of technology adoption $d_N(i, j)$ and simple genetic distance $g(i, j)$, as long as $|g(i, f) - g(j, f)|$ and $g(i, j)$ are positively correlated (as they indeed are in the data). However, our theory also implies that relative genetic distance is a *better* predictor of technology adoption, because it is a more accurate measure

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[6] The equation holds for $d_v(i, f) \leq \omega$. For $d_v(i, f) > \omega$, $N_i^* = 0$ (no innovation has positive net benefits).

[7] In what follows we assume, without loss of generality, that $\varepsilon \geq \varepsilon'$.

of relative distance from the frontier in terms of vertical traits. For example, if one were to use simple genetic distance as a proxy for expected vertical differences, on average one should expect that differences in rates of technology adoption between population 2 and population 3 ought to be identical to differences in technology adoption between population 1 and population 3, because $g(1,3) = g(2,3)$. This would be possible if and only if $E|N_3^* - N_2^*| = E|N_3^* - N_1^*| = E|N_3^* - N| = N(\frac{\varepsilon}{\omega} + \frac{\varepsilon'}{2\omega})$, which would hold if and only if $E\{N_2^*\} = N$. But, as we have seen above, on average population 2 does *not* adopt all innovations, because it faces barriers associated with its own vertical distance from the frontier: $E|N_2^* - N| = N\frac{\varepsilon}{\omega} > 0$. Hence, using simple genetic distance $g(2,3)$ as a measure of barriers to technology adoption between population 2 and population 3 would lead us to overestimate the adoption gap between population 2 and population 3 (or, equivalently, to underestimate the adoption gap between population 1 and population 3). In general, our theory predicts that simple genetic distance is a biased proxy for the fundamental determinant of comparative adoption of innovations across societies. This fundamental determinant is the *relative distance in vertical traits*, which can be measured more accurately by *genetic distance relative to the frontier*.[8] We will test the prediction that genetic distance relative to the frontier should trump simple genetic distance as a determinant of technology adoption in the empirical section.

2.2.2 Intensive margin

An analogous illustration of the main idea can be provided with respect to intensive margins of adoption. This is important because much of our technology data focuses on the intensive margin. Let Z_{ki} denote the *level* at which a given innovation k is used by population i. Assume that benefits and costs of adoption are now given as follows:

$$B_k = \beta_k Z_k \tag{18}$$

$$C_k = \frac{\gamma_k}{2[\phi_0 - \phi_1 d_v(i,f)]} Z_k^2 \tag{19}$$

Hence, net benefits for population i are maximized at:

$$Z_{ki}^* = \frac{\beta_k[\phi_0 - \phi_1 d_v(i,f)]}{\gamma_k} \tag{20}$$

Again, the difference in adoption rates (this time at the intensive margin) will be a function of relative vertical distance from the frontier and hence, on average, relative genetic distance from the

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[8] For further discussion of the relation between relative genetic distance and simple genetic disatance, see Spolaore and Wacziarg (2009, p. 477).

frontier population:

$$d_{Z_k}(i,j) \equiv |Z^*_{kj} - Z^*_{ki}| = \frac{\beta_k \phi_1}{\gamma_k} |d_v(j,f) - d_v(i,f)| \tag{21}$$

The above results illustrate our hypothesis that technology adoption is a function of relative distance in intergenerationally transmitted traits. As we have already discussed, such relative distance between populations can be captured empirically by their relative genetic distance from the frontier.

2.3 A Dynamic Example

In the rest of this section we illustrate our general ideas in a dynamic framework, that will allow to establish a more explicit and microfounded link between the adoption of innovations, imitation costs, distance in vertical traits, and total factor productivity. Changes in vertical traits tend to take place much more slowly and at a longer horizon than the spread of technological innovations, especially if we focus on modern technological progress and growth in a post-Malthusian world. Therefore, in this simple dynamic example we assume for simplicity that populations do not change over time (their size is fixed and normalized to one), and that their inherited vertical traits do not change over the relevant time horizon (additional small random shocks to vertical traits would not affect the basic results, while they would greatly complicate the algebra). Hence, consider our three populations $i = 1, 2, 3$, with vertical traits v_1, v_2 and v_3, inherited from their ancestral populations as described above, and unchanged in modern times (i.e., for $t \geq 0$). Time is continuous. At each time $t \geq 0$ consumers in each economy i maximize:

$$U_i(t) = \int_s^\infty \ln C_i(s) e^{-\rho(t-s)} ds \tag{22}$$

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:

$$\frac{dC_i}{dt} \frac{1}{C_i(t)} = r_i(t) - \rho \tag{23}$$

where $r_i(t)$ is the real interest rate in society i (we assume that the three 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 produced according to:

$$Y_i(t) = \int_0^{A_i(t)} [X_{ki}(t)]^\alpha dk, \quad 0 < \alpha < 1 \tag{24}$$

where $X_{ki}(t)$ is the quantity of intermediate good of type k employed at time t in economy i. We assume that 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. In particular, as in Barro and Sala–i-Martin (1997 and 2003, 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 $P_k = 1/\alpha$, earning the profit flow $\pi = (1-\alpha)\alpha^{(1+\alpha)/(1-\alpha)}$ at each time t.[9] 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:

$$g \equiv \frac{\pi}{\lambda} - \rho > 0 \tag{25}$$

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

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 the intermediate goods to local conditions. Our key assumption is that such imitation costs are *increasing in the distance in vertical traits between the imitator and the frontier.* Specifically, we assume that economy i's imitation cost is:

$$\mu_i(t) = \lambda e^{\theta d_v(i,f)} \left(\frac{A_i(t)}{A_f(t)}\right)^{\psi} \tag{26}$$

The above specification is consistent with our main hypothesis: differences in vertical traits act as barriers to adoption and imitation. The parameter θ captures the extent to which dissimilarity in vertical characteristics increases imitation costs. 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. 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 traits. As we will see, in steady state societies

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[9] For a detailed derivation see Barro and Sala-i-Martin (1997 and 2003)

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). 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 (a lower $A_i(t)/A_f(t)$ in our framework).

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:

$$Y_i(t) = \alpha^{2\alpha/(1-\alpha)} A_i(t) \tag{27}$$

As shown in Barro and Sala-i-Martin (1997, 2003), with free entry into the "imitation" sector, economy i's real interest rate in equilibrium is:

$$r_i(t) = \frac{\pi}{\mu_i(t)} + \frac{d\mu_i}{dt}\frac{1}{\mu_i(t)} \tag{28}$$

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 $g = \dfrac{\pi}{\lambda} - \rho$. Hence, in steady state the real interest rates in all economies are identical and equal to $\dfrac{\pi}{\lambda}$. Consequently, we have:

$$\mu_i^* = \mu_j^* \tag{29}$$

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

$$|\ln A_i^*(t) - \ln A_j^*(t)| = |\ln Y_i^*(t) - \ln Y_j^*(t)| = \frac{\theta}{\psi}|d_v(i,f) - d_v(j,f)| \tag{30}$$

The intuition of the above equation is straightforward: long-term differences in total factor productivity and output between societies are an increasing function of their relative cost to imitate, which depends on their relative vertical distance from the frontier.[10] Therefore, this dynamic model confirms the key implications of the simplified static setup presented above.

In sum, our framework predicts a positive correlation between different adoption rates of innovations (at both the extensive and intensive margins, and as measured by total factor productivity) between society i and society j, and their relative vertical distance from the frontier $|d_v(i,f) - d_v(j,f)|$.

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[10] 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.

Since vertical distance is on average higher among societies that are genetically more distant, the framework predicts that, on average, differences in the rates of adoption of innovations and total factor productivity will be correlated with relative genetic distance from the frontier.

We have illustrated our main hypotheses in a highly simplified setting. The general idea could be formalized in more complex and realistic frameworks. In general, our approach is consistent with modeling barriers to technology adoption (in the sense of Parente and Prescott, 1994 and 2002) as a function of vertical distance from the frontier. For example, an interesting extension would be to include these effects in models of technology diffusion and growth, such as Comin and Hobijn (2010), where, in order to become the sole supplier of a particular capital vintage, the capital good producer must bear an up-front fixed cost (adoption cost). Our hypothesis is that such costs are affected by barriers that vary across societies as a function of their relative vertical distance from the technological frontier.[11] More generally, a large and important literature has studied the effects of barriers on the onset and pace of technology diffusion and economic growth. For example, Ngai (2004) argues that barriers to technology adoption affect both the beginning date and the subsequent pace of modern growth, and that current income differences, being transitional, can be accounted by relatively smaller barriers, relative to models that focus on the steady state (such as in our simple dynamic example). It would be interesting to link our approach more explicitly to this theoretical and empirical literature, but such explorations are left for further research. The bottom line of this section, more simply, is to illustrate the basic idea that relative genetic distance acts as a barrier to the adoption of technological innovations across societies - a hypothesis that we will test empirically in the rest of this paper.

3 Data and Methodology

3.1 Genetic Distance

To measure long-term relatedness between human population, we use genetic distance. In doing so, we follow a recent strand of research documenting strong correlations between genetic distance and a variety of political and economic outcomes, such as per capita income (Spolaore and Wacziarg, 2009) and bilateral conflict between nations (Spolaore and Wacziarg, 2009).

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[11] Specifically, our hypothesis is consistent with an extension of Comin and Hobjin (2010)'s model where the parameter b in their equation (17) varies across economies as a function of their relative vertical distance from the technological frontier.

The original data on genetic distance is from Cavalli-Sforza et al. (1994), who gathered a comprehensive dataset of allele frequencies for a large number of world populations. In this paper, we focus on their World matrix, providing allele frequency data for 120 gene loci covering 42 world populations. As a measure of heterozygosity, we focus on F_{ST} genetic distance, a functional form to map differences in allele frequencies into a single distance metric that has been shown to have desirable properties (in particular, if populations are of a sufficient size, F_{ST} genetic distance has been shown to be perfectly correlated with the time separating two populations' common ancestors). Figure 1 (from Cavalli-Sforza, Menozzi and Piazza, 1994, p. 78) is a phylogenetic tree illustrating how different human populations have split apart over time. As we already discussed, phylogenetic trees, which are built from genetic distance data, are the population analogs of family trees for individuals. In our data, the largest observed genetic distance is between Mbuti Pygmies and Papua New Guineans ($F_{ST} = 0.4573$), while the smallest distance is between the Danish and the English ($F_{ST} = 0.0021$).

Genetic groups were matched to current ethnic groups using data on the ethnic composition of countries from Alesina et al. (2003). Genetic groups were further matched to countries. We did so for two points in time: We first created a match for 1500, using the ethnic composition of countries as they were in the period preceding the discovery of the New World (in this match, for instance, the US is matched to the North Amerindian genetic group). In the 1500 match, each country is matched to a single genetic group. Next, we matched ethnic groups to the current populations of countries on the basis of the frequency data of ethnic groups by country also provided in Alesina et al. (2003). Ethnically diverse countries were matched to several of the 42 genetic groups, allowing the computation of different measures of genetic distance between countries (for instance, in this contemporary match, the US is matched to a combination of English, Asian, West African and North Amerindian). Further details on these matches of genetic groups to ethnic groups and on to countries can be found in Spolaore and Wacziarg (2009). For the contemporary period, we focus on a weighted measure, capturing the expected genetic distance between two randomly selected individuals, one from each country.[12] Formally, assume that country 1 is made up of populations $i = 1...I$ and country 2 is made up of populations $j = 1...J$. Denote by s_{1i} the share of population i in country 1 (similarly for country 2) and d_{ij} the F_{ST} genetic distance between populations i and

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[12] Using instead the genetic distance between genetic groups constituting a plurality of the populations of each country did not materially affect the results. The two measures only differ for pairs involving countries made up of more than one genetic group, so in practice the two measures are highly correlated.

j. The weighted F_{ST} genetic distance between countries 1 and 2 is defined as:

$$FST_{12}^{W} = \sum_{i=1}^{I} \sum_{j=1}^{J} (s_{1i} \times s_{2j} \times d_{ij}) \tag{31}$$

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. Using this method, the average weighted bilateral genetic distance between two countries in our sample, across $10,585$ country pairs, is 0.113,with a standard deviation of 0.082 (Table 1).

While FST_{12}^{W} is the *simple* genetic distance between countries 1 and 2, we can denote by FST_{12}^{R} the genetic distance between 1 and 2 *relative* to the technological frontier. Then, for instance if the frontier is the US (as is usually the case for recent technologies), $FST_{12}^{R} = |FST_{1,US}^{W} - FST_{2,US}^{W}|$. Here, simple and relative genetic distance are the direct empirical counterparts of the theoretical concepts developed in Section 2.

3.2 Technological Adoption

We employ two datasets to capture historical and current technological adoption levels. The first dataset, from Comin, Easterly and Gong (2010), (henceforth CEG) describes the level of technology adoption for a wide panel of countries at years 1000 BC, 1 AD, 1000 AD, 1500 AD and 2000 AD. In our empirical work, we only make use of data for the latter two dates, since we only observe genetic distance data for 1500 and the contemporary period. For 1500, the CEG data captures exclusively the extensive margin of technology adoption. They characterize whether each of 113 contemporary countries were using any of 24 technologies as of 1500. These technologies, listed in Appendix 1, are grouped into 5 categories: military technologies, agricultural technologies, transportation, communication, and industry. For each of the underlying technologies in each category, a country is given a score of 1 is the underlying technology was used in 1500, and zero otherwise.[13] The scores are then summed within each category, and divided by the maximum obtainable score, resulting in a value between 0 and 1. Additionally an overall index of technological sophistication is obtained by averaging the scores over all 5 categories (thus, each technological category is given equal weight in the overall technological sophistication score). In our empirical work we make use of both the categorical scores and the overall index.

For the contemporary period (1970-2000), the CEG dataset is constructed using a different

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[13] For agricultural technologies, the scoring is a bit different, with a score of zero assigned to hunter-gatherer countries, 1 for pastoralist countries, 2 for hand cultivation, and 3 for plough cultivation.

approach. Since the extensive margin diffuses very fast in the current period (for instance, it is very easy for a country, however technologically unsophisticated, to import and use a single computer), the measures include the intensive margin. Using the *per capita* usage intensity of 9 underlying technologies at various recent dates, CEG compute an overall index of technological adoption, based on Comin, Hobijn and Rovito (2008). The functional form for the current technological adoption index captures the usage lag from the technological frontier (i.e. the United States): it is based on where a country stands in terms of technology usage in terms of the number of years since the United States had the same usage intensity. The index is normalized to vary between 0 and 1. Again, the index is broken down into underlying sectoral components that mirror 4 of those for 1500 (all but the military technology category). Table 1 provides summary statistics for the contemporary technology use index, as well as its sectoral subcomponents.

The second dataset we use is the CHAT dataset, from Comin and Hobijn (2009). This allows a much more detailed investigation into the adoption of specific technologies without aggregating them into any sort of index. We focus on the 1990-1999 time period, and among the over 100 technologies we retain those for which at least 50 countries are available, to ensure sufficient sample size and variability. We average the the usage data over the 1990-1999 period, and divide each measure by the country's population, following Comin, Easterly and Gong (2010).[14] The resulting set of 33 technologies we explored from the CHAT dataset are listed in Appendix 1 - they cover a wide range of technological categories such as agricultural technologies, transportation technologies, communications technologies, medical technologies, and industrial technologies.

In addition to specific technologies, we also use data on per capita income from the Penn World Tables version 6.3, for the year 2005, to both replicate the baseline results in Spolaore and Wacziarg (2009) and to explore, as a first step, the determinants of differences in aggregate TFP (for which per capita income is a good proxy). Our model delivers predictions not only concerning the intensive and extensive margins of specific technologies, but also the resulting determinants of differences in aggregate TFP, and we briefly examine those at the beginning of our empirical investigation.

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[14] We prefer to use a consistent approach to determine the denominator of our technology usage intensity measures rather than varying the denominator from measure to measure. In only one case (the share of cropland area planted with modern variety) do we depart, since it would make little sense to divide this share by population.

3.3 Methodology

To test the predictions of our model, we adopt a bilateral approach which consists of calculating a measure of the *difference* in technology usage intensity across all available pairs of countries in our sample, and regressing it on characteristics of the pair, chiefly genetic distance. While in principle we could simply regress a country's technological use level on its genetic distance to the frontier country, the bilateral approach has the advantage of allowing for a horserace between simple and relative genetic distance.[15] Such a horserace is a central test of our barriers model, since under such a model, relative distance should come out stronger than absolute distance. Moreover, we can make more efficient use of a wealth of bilateral distance data as control variables - chiefly geographic distance data.

Denoting (i, j) the countries in a pair, our baseline specification is:

$$|T_i - T_j| = \beta_0 + \beta_1 FST_{ij}^R + \beta_2' X_{ij} + \varepsilon_{ij} \tag{32}$$

and (to conduct a horserace):

$$|T_i - T_j| = \gamma_0 + \gamma_1 FST_{ij}^R + \gamma_2 FST_{ij}^W + \gamma_3' X_{ij} + \nu_{ij} \tag{33}$$

where T_i is a measure of technology use by country i, X_{ij} is a set of measures of geographic distance, and ε_{ij} and ν_{ij} are disturbance terms. In all the regressions we present below, we control for a wide range of metrics of geographic barriers captured by X_{ij}. It is essential to do so, as geographic barriers compete with genealogical barriers as a candidate explanation for technological diffusion. Moreover, geographic distance is correlated with genetic distance, since human populations that live further apart are likely to have split up from each other earlier in human (pre)history. The geographic barriers we introduce as controls include geodesic distance, latitudinal and longitudinal distance, and a set of dummy variables for contiguity, whether one of the countries in a pair is an island, whether one of the countries in the pair is landlocked, and whether the pair shares a common sea or ocean.[16]

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[15] We have also completed a set of simple cross-sectional regressions, and these are available upon request. The results were very consistent with those obtained under our more involved bilateral approach.

[16] We also included a wider set of controls, including freight costs, with similar results. In our dataset, freight costs were so highly correlated with geodesic distance that it makes litle sense to include them both. See Spolaore and Wacziarg (2009) for further details on this point and on the broader issue of geographic controls.

The specifications in equations (32) and (33) are reduced forms. Differences in technology usage are presumably the result of differences in institutions, technologies, human capital, savings rates, etc., all of which are possibly endogenous with respect to technology differences, and themselves a function of geographic and human barriers. Our regressions are really an attempt to describe the human and geographic barriers to the diffusion of innovations, without (for now) asking how the effects of these human and geographic barriers might be mediated by specific mechanisms - through human capital, institutions, or otherwise.

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 (as we do), equations (32) and (33) 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, as an absolute difference of two countries' technology levels. To address the problem of spatial correlation, we rely on two-way clustering of the standard errors, following the approach in Cameron, Gelbach and Miller (2006). In our application, clustering arises at the level of country i and at the level of country j, and is non-nested: each individual observation on income differences, say $|T_i - T_j|$ belongs to the group that includes country i and the group that includes country j. The estimator in Cameron, Gelbach and Miller (2006) allows for an arbitrary correlation between errors that belong to "the same group (along either dimension)" (p. 7). Their method is therefore directly applicable to the specific econometric issue we face (on page 3 of their manuscript the authors specifically mention spatial correlation as a possible application of their estimator). See also Spolaore and Wacziarg (2009) for a previous application of this methodology and its advantages.

4 Empirical Results

4.1 Simple Correlations

Table 1 presents summary statistics for the main variables in our analysis, i.e. major technology usage lags from the CEG dataset, per capita income, and our two main measures of genetic distance - simple and relative to the USA. For the sake of space we do not present summary statistics for the historical CEG data and for the disaggregated series from the CHAT dataset, but these are available upon request and tell a similar substantive story.

Panel A presents means and measures of spread to aid in the interpretation of the magnitudes of our estimated effects. More substantively, Panel B presents simple correlations. Several observations are in order. Firstly, the various technology usage lag differences as well as bilateral differences in per capita income bear moderate correlations with each other, generally in the range of 0.4 to 0.6. This is instructive as it indicates that our technology usage measures do not all capture the same concept of differences in technological advancement, and actually measure different (albeit correlated) degrees of technological sophistication depending on the sector.[17] Secondly, these measures of pairwise differences in technology adoption (plus per capita income, our proxy for aggregate TFP) bear sizable positive correlations with genetic distance relative to the frontier - in the range of 0.1 to 0.3 - consistent with the main hypothesis derived from our model. Thirdly, the correlations between pairwise differences in technology adoption levels and simple genetic distance is much closer to zero, and even sometimes negative. Thus, the evidence from simple correlations is consistent with our barriers story: genetic distance relative to the frontier seems to matter more than simple genetic distance.

4.2 Aggregate TFP

Table 2 displays empirical results from regressions as specified in equations (32) and (33), where T_i is defined variously as PPP per capita income as of 2005, PPP per capita income in 1870 or population density as of 1500. The goal of these regressions is to capture the effect of long term barriers on aggregate TFP. The regressions build on those in Spolaore and Wacziarg (2009), but here we explicitly include a horserace between simple and relative genetic distance. The first three columns enter relative genetic distance, simple genetic distance and both variables together in a regression where the absolute difference in per capita income for 2005 is the dependent variable. We see exactly the pattern implied by the model of Section 2: Entered separately, the magnitude of the effect of relative distance, as measured by the standardized beta coefficient, is three times as large as the magnitude of the effect of simple genetic distance (both estimates being significantly positive). A standard deviation difference in relative genetic distance can account for 30% of a standard deviation in absolute income differences, a substantial portion of the variation, compared to only 10% for simple genetic distance. When both metrics of genetic distance are entered together,

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[17] The correlations of the sectoral indices with the overall index of technological differences of which they are part are greater - around $0.7-0.8$ - this is not surprising as the overall index is constructed as the average of the sectoral indices.

relative genetic distance is large and significant, while the coefficient on simple genetic distance is indistinguishable from zero.

Genetic distance, this time relative to the English population rather than the United States, is also a strong predictor of technology differences in 1870, right after the onset of the Industrial Revolution, and in 1500 as well (we follow the literature in using population density as a proxy for technology in the pre-industrial, Malthusian era). For 1500, we use historical genetic distance as of 1500 as a regressor, so the regression captures the effect of initial genetic distance on technological differences prior to the discovery of the New World and the (possibly) endogenous population movements that resulted from it. Northwestern Europe was then the technological leader, and technology differences in 1500 are an increasing function of genetic distance to the English.[18] For both 1500 and 1870, the standardized beta on genetic distance is around $15-17\%$, smaller than in 2005 but still a substantial portion of the variation, particularly considering the likely prevalence of error in the measurement of the dependent variable, which raises the standard error of the regression.

4.3 Contemporary Technological Differences

While aggregate TFP is interesting to fix ideas, this paper is mainly about the spread of *specific* technologies, so for the remainder of this paper we focus on data at the level of disaggregated technologies. We start with the CEG data. Tables 3 and 4 present estimates of equations (32) and (33), respectively, for all CEG sectoral measures of technology usage lags for the year 2000. Entered alone (Table 3), genetic distance relative to the United States is positively related with technological differences for all measures, and statistically significantly at the 5% level for 3 of the 4 sectoral measures, as well as the absolute difference in the overall technology usage lag index. The only sectoral category for which genetic distance is not significant is agricultural technology, which is perhaps more mature in 2000 and has diffused more broadly (since the 1960s many developing countries with strong comparative advantages in agriculture have widely adopted modern agricultural technologies). For communications, transportation and industrial technologies, the standardized effect of relative genetic distance ranges anywhere from 12.73% to 25.97%, and for the overall technology index it equals 19.81%, roughly in line with the results for aggregate TFP.

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[18] While we use distance from the English to define relative genetic distance from the frontier in these regressions, picking instead any of the Western European populations in our sample - Italian, German or Danish - would yield similar results.Genetic distances among these populations are very small relative to the World variation.

Turning to Table 4, which conducts a horserace between simple and relative genetic distance, we find that the latter trumps the former: when entered together in the regressions, relative genetic distance comes out significantly positive, while simple distance comes in either insignificant or even negative. The standardized magnitude of the effect of relative genetic distance across technological categories remains in line with those in Table 3, and the inclusion of simple genetic distance barely affects the regression R-squared. In sum, relative genetic distance carries virtually all of the explanatory power. This is perhaps the strongest evidence in favor of the main testable hypothesis in our model - namely the hypothesis that genealogical distance introduces significant barriers to the spread of innovations.

4.4 1500 Technological Differences

While the results for 2000 capture the intensive margin of technological adoption, the data for 1500 capture exclusively the extensive margin, and as such provide an alternative test of the hypothesis that genetic distance hinders the diffusion of innovations. Tables 5 and 6 show results using the CEG data for 1500 to construct the dependent variables - the difference in technology adoption indices at the sectoral and overall levels. The results here are even stronger than for the contemporary period in terms of the magnitude of the estimated barrier effects of genealogical relatedness. For every measure of bilateral technology difference, genetic distance relative to the UK enters with a positive sign, is statistically significant at the 10% level in all cases, and at the 1% level in 5 of the 6 cases. The weakest results, again, are for agriculture, and the strongest for transportation and military technologies. The magnitude of the effects, in terms of standardized betas, range from 10.41% (agricultural technologies) to 41.81% (transportation technologies), while the effect on the overall technological difference index is 31.63%. Thus, a standard deviation in genetic distance relative to the UK can account for about one third of a typical difference in technology adoption between countries.

Turning to the more direct test of our theory, namely the horserace with simple genetic distance, we find again in Table 6 that in all cases (save agricultural technologies) relative distance trumps simple genetic distance in terms of magnitude, sign and/or statistical significance. Moreover, the magnitude of the effect of relative genetic distance barely changes compared to Table 5, so that the inclusion of simple genetic distance in the regression has benign effect. To conclude, the strong evidence we uncovered in the contemporary period holds also for the pre-Industrial era. This was also the era prior to the vast migrations that followed the discovery of the New World, so one cannot argue that they reflect the endogeneity of genetic distance with respect to technological attractiveness.[19]

4.5 Results for Disaggregated Technologies

Our final test is to turn to even more disaggregated technologies, from the CHAT dataset. While the data from CEG provides useful sectoral characterizations of the technological achievements of nations throughout history, the sectoral indices are aggregated and do not allow us to determine which of the underlying technologies drive the results. The CHAT dataset allows us to address this shortcoming because it provides us with data on technology use for a wide range of specific technologies. As already mentioned, we use data on 33 technologies for which we observe data for more than 50 countries, and define our dependent variables, for each technology, as the absolute difference in the per capita use of the technology. For instance, for cell phone technology, our dependent variable is the absolute difference, between country i and country j, in the number of cell phones per capita. To maintain consistency, we assume that the technological leader for all these technologies was the US (this turns out to be the case in actuality in the vast share of the cases, and in the instances when it is not the case the leader is usually a country that is genetically very close to the US, such as a Northwestern European country).

The results are presented in Table 7. In *every single case*, the effect of relative genetic distance to the US is positive. Additionally, in 22 of the 33 cases, the effect is statistically significantly different from zero at least at the 10% level (in 19 of these the significance obtains at the 5% level). Here, the results are particularly strong for some agricultural technologies, for most communications technologies, and for all but one of the industrial technologies. The results are weakest for medical technologies and transportation. Turning to the magnitude of the effects, for the technologies where relative genetic distance is statistically significant, the standardized betas vary between about 8% and 24% - slightly smaller than for the CEG data but in the same rough order of magnitude.

For the sake of space we do not report the results of the horserace regressions which add simple genetic distance to the specification of Table 7 in order to test which of relative or simple genetic distance are better predictors of technology differences. The overall lesson from these horseraces is that relative genetic distance comes out more significant in 17 of the 22 cases where relative

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[19] We believe this argument is hard to make for the contemporary era as well as it is difficult to argue that the reason, say, that Europeans migrated to North America was because of superior technological potential there *ex ante*.

distance was significant, and in most of these cases simple genetic distance either is insignificant or even bears a negative sign. Thus, the preponderance of the evidence at the level of disaggregated technologies is consistent with our barriers model.

5 Conclusion

The history of human populations is characterized by successive splits which led populations to stray apart and develop specific cultural and biological traits over the course of time. The longer two populations have been separated, the more their vertically transmitted traits can be expected to differ. The central hypothesis in this paper is that differences in vertically transmitted traits between populations hinders the exchange of ideas, and hence the diffusion of innovations. Using genetic distance as a summary measure of differences in vertically transmitted human traits, we showed that, indeed, populations that are genetically far from the innovator display lower aggregate TFP, higher technology usage lags, lower uptake on the extensive margin of technology adoption, and overall lower rates of technology usage at the level of disaggregated technologies. These results are quantitatively strong and statistically significant in the vast majority of cases, and hold both in the contemporary period and historically, going as far back as 1500.

While this paper has provided clear evidence of a barrier effect of genetic distance, much work remains to be done to elucidate the precise mechanisms whereby differences in human traits hinder the diffusion of innovations. We have presented reduced form, descriptive patterns linking genetic distance and technology use, as well as a formal test of our barriers model based on comparing the effect of simple versus relative genetic distance. However, we have not answered the question of why genetically distant populations tend not to adopt each other's innovations. Is it for lack of trust or understanding across different populations? Is it because communication is difficult? Is it because adapting innovations developed for a different cultural context is hindered by differences in norms, habits or customs? We leave these important questions for future research.

References

Aghion, Philippe and Peter Howitt (2008), *The Economics of Growth*, Cambridge, MA: The MIT Press.

Alesina, A., A. Devleeschauwer, W. Easterly, S. Kurlat, and R. Wacziarg (2003), "Fractionalization," *Journal of Economic Growth*, 8: 55-194.

Barro, Robert J. and Xavier Sala-i-Martin (1997), "Technological Diffusion, Convergence and Growth", *Journal of Economic Growth*, vol. 2, no.1, pp. 1-26.

Barro, Robert J. and Xavier Sala-i-Martin (2003), Economic Growth, 2nd edition, Cambridge, MA: MIT Press

Cameron, A. Colin, Jonah B. Gelbach, and Douglas L. Miller, "Robust Inference with Multi-Way Clustering," NBER Technical Working Paper #T0327, 2006.

Caselli, Francesco (2005), "Accounting for Cross-Country Income Differences." in *Handbook of Economic Growth*, Vol. 1A, edited by Philippe Aghion and Steven N. Durlauf, 679–741. New York: North-Holland.

Cavalli-Sforza, Luigi L., Paolo Menozzi and Alberto Piazza (1994), *The History and Geography of Human Genes*, Princeton: Princeton University Press.

Comin, Diego and Bart Hobijn (2009), "The CHAT Dataset", Harvard Business School Working Paper # 10-035.

Comin, Diego, and Bart Hobijn (2010), "An Exploration of Technology Diffusion," *American Economic Review*, vol. 100, no. 5, December, 2031-59.

Comin, Diego, Bart Hobijn and Emilie Rovito (2008), "World Technology Usage Lags," *Journal of Economic Growth,* 13, 4.

Comin, Diego, William Easterly and Erick Gong (2010), "Was the Wealth of Nations Determined in 1000 B.C.?" *American Economic Journal: Macroeconomics* 2, no. 3: 65-97.

Fagerberg, J. (2004), "Innovation: A Guide to the Literature," Chapter 1 in Oxford Handbook of Innovation, edited by J. Fagerberg, D. C. Mowery, and R.R.Nelson, Oxford: Oxford University Press.

Hsieh, Chang-Tai and Peter J. Klenow (2010), "Development Accounting," *American Economic Journal: Macroeconomics*, 2:1, 207–223.

Kimura, Motoo (1968), "Evolutionary Rate at the Molecular Level", *Nature*, vol. 217, pp. 624-626.

Ngai, L. Rachel (2004), "Barriers and the Transition to Modern Growth," *Journal of Monetary Economics,* 51, pp. 1353–1383.

Parente, Stephen L. and Edward C. Prescott (2002), *Barriers to Riches*, Cambridge: MIT Press

Rogers, E. M. (1995). Diffusion of innovations (4th ed.). New York: Free Press.

Romer, Paul M. (1990), "Endogenous Technological Change", *Journal of Political Economy*, vol. 98, no. 5, pp. S71-S102.

Spolaore Enrico and Romain Wacziarg (2009), "The Diffusion of Development," *Quarterly Journal of Economics*, 124(2): 469-529.

Spolaore Enrico and Romain Wacziarg (2009), "War and Relatedness", *NBER Working Paper* #15095, June.

Appendix 1 - Technologies used in the various datasets

A. 24 Technologies in the CEG 1500 AD Dataset.

1. *Military*: Standing army, cavalry, firearms, muskets, field artillery, warfare capable ships, heavy naval guns, ships (+180 guns).

2. *Agriculture*: Hunting and gathering, pastoralism, hand cultivation, plough cultivation.

3. *Transportation* : Ships capable of crossing the Atlantic Ocean, ships capable of crossing the Pacific Ocean, ships capable of reaching the Indian Ocean, wheel, magnetic compass, horse powered vehicles.

4. *Communications*: Movable block printing, woodblock or block printing, books, paper.

5. *Industry*: Steel, iron.

B. 10 Technologies in the CEG 2000 AD Dataset.

Electricity (in 1990), Internet (in 1996), PCs (in 2002), cell phones (in 2002), telephones (in 1970), cargo and passenger aviation (in 1990), trucks (in 1990), cars (in 1990), tractors (in 1970).

C. 33 Technologies in the CHAT dataset for 1990-1999.

1. *Agriculture*: Harvest machines, tractors used in agriculture, metric tons of fertilizer consumed, area of irrigated crops, share of cropland area planted with modern varieties (% cropland), metric tons of pesticides.

2. *Transportation*: civil aviation passenger km, lengths of rail line, tons of freight carried on railways, passenger cars in use and commercial vehicles in use.

3. *Medical*: Hospital beds, DPT immunization before age 1, measles immunization before age 1.

4. *Communications*: Cable TV, cell phones, personal computers, access to the Internet, items mailed/received, newspaper circulation, radios, telegrams sent, mainline telephone lines, television sets in use.

5. *Industry and other*: Output of electricity, KwHr, automatic looms, total looms, crude steel production in electric arc furnaces, weight of artificial (cellulosic) fibers used in spindles, weight of synthetic (non cellulosic) fibers used in spindles, weight of all types of fibers used in spindles, visitor beds available in hotels and elsewhere, visitor rooms available in hotels and elsewhere.

Table 1 - Summary Statistics for genetic distance and the CEG data, contemporary period

Panel A - Means and variation

Variable	# of Obs.	Mean	Std. Dev.	Min	Max
Avg. tech adoption in agriculture in 2000 AD	6,105	0.200	0.233	0	0.855
Avg. tech adoption in communications in 2000 AD	7,381	0.260	0.189	0	0.791
Avg. tech adoption in transportation in 2000 AD	6,441	0.199	0.160	0	0.844
Avg. tech adoption in industry in 2000 AD	5,565	0.301	0.215	0	1.028
Avg. of the sectoral tech adoption indexes in 2000 AD	7,503	0.213	0.181	0	0.838
Absolute difference in log income, 2005	10,440	1.384	0.989	0	4.878
Fst gen. dist. relative to the USA, weighted	10,585	0.062	0.047	0	0.213
Fst Genetic Distance (absolute)	10,585	0.113	0.082	0	0.336

Panel B - Correlations

	Avg. tech adoption in agriculture in 2000 AD	Avg. tech adoption in communi-cations in 2000 AD	Avg. tech adoption in transpor-tation in 2000 AD	Avg. tech adoption in industry in 2000 AD	Avg. of the sectoral tech. adoption indexes in 2000 AD	Absolute difference in log income, 2005	Fst gen. dist. relative to the USA, weighted
Avg. tech adoption in communications in 2000 AD	0.566	1.000					
Avg. tech adoption in transportation in 2000 AD	0.529	0.632	1.000				
Avg. tech adoption in industry in 2000 AD	0.537	0.682	0.536	1.000			
Avg. of the sectoral tech adoption indexes in 2000 AD	0.756	0.830	0.808	0.785	1.000		
Absolute difference in log income, 2005	0.401	0.650	0.551	0.753	0.700	1.000	
Fst gen. dist. relative to the USA, weighted	0.108	0.202	0.173	0.279	0.225	0.316	1.000
Fst Genetic Distance (absolute)	-0.063	0.072	-0.015	0.138	0.026	0.163	0.597

Table 2 – Regressions for overall TFP differences, contemporaneous and historical
(TFP proxied with log per capita income in 1870 and 2005 period, and with population density for 1500)

	(1)	(2)	(3)	(4)	(5)
	2005 income	**2005 income**	**2005 income**	**1870 income**	**1500 density**
Fst gen. dist. relative to the USA, Weighted	**6.290** **(1.175)*****		**6.029** **(1.239)*****		
Fst Genetic Distance		**2.164** **(0.596)*****	**0.275** **(0.541)**		
Relative Fst genetic distance to the UK, weighted				**1.691** **(0.836)****	
Relative Fst genetic distance to the UK, 1500 match					**29.751** **(7.168)*****
Absolute difference in latitudes	0.232 (0.245)	0.559 (0.279)**	0.255 (0.248)	1.184 (0.273)***	3.297 (2.684)
Absolute difference in longitudes	-0.025 (0.220)	-0.196 (0.240)	-0.007 (0.213)	0.710 (0.264)***	5.365 (2.033)***
Geodesic Distance	-0.012 (0.026)	-0.008 (0.027)	-0.016 (0.025)	-0.092 (0.034)***	-0.781 (0.248)***
=1 for contiguity	-0.418 (0.060)***	-0.495 (0.060)***	-0.414 (0.061)***	-0.259 (0.048)***	-3.562 (0.719)***
=1 if either country is an island	0.174 (0.083)**	0.143 (0.083)*	0.174 (0.083)**	0.064 (0.099)	4.820 (2.673)*
=1 if either country is landlocked	0.008 (0.085)	0.024 (0.090)	0.005 (0.087)	0.170 (0.078)**	0.346 (0.956)
=1 if pair shares at least one sea or ocean	-0.001 (0.067)	0.028 (0.077)	-0.0001 (0.067)	0.071 (0.050)	-1.632 (0.727)**
Constant	1.022 (0.089)***	1.143 (0.086)***	1.017 (0.090)***	0.365 (0.076)***	6.693 (0.981)***
Observations (countries)	10,440 (144)	10,440 (144)	10,440 (144)	1,485 (54)	10,153 (142)
Standardized Beta (%)	30.18	10.39	28.93	15.02	17.77
R-Squared	0.11	0.07	0.11	0.16	0.07

Standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%

Table 3 – Bilateral regressions of technological distance on genetic and geographic distance metrics (CEG dataset for 2000, dependent variable as in first row)

	(1)	(2)	(3)	(4)	(5)
	Agricultural Technology	**Communications Technology**	**Transportation Technology**	**Industrial Technology**	**Overall Technology**
Fst gen. dist. relative to the USA, weighted	**0.402** **(0.268)**	**0.500** **(0.212)****	**0.608** **(0.185)*****	**1.149** **(0.288)*****	**0.745** **(0.216)*****
Absolute difference in latitudes	0.687 (0.121)***	0.274 (0.066)***	0.306 (0.057)***	0.329 (0.081)***	0.361 (0.082)***
Absolute difference in longitudes	0.405 (0.129)***	0.089 (0.055)	0.305 (0.072)***	0.174 (0.069)**	0.243 (0.088)***
Geodesic Distance	-0.050 (0.014)***	-0.016 (0.006)**	-0.036 (0.008)***	-0.024 (0.007)***	-0.032 (0.010)***
=1 for contiguity	-0.050 (0.014)***	-0.077 (0.012)***	-0.053 (0.013)***	-0.090 (0.018)***	-0.071 (0.012)***
=1 if either country is an island	0.118 (0.077)	0.057 (0.027)**	0.093 (0.047)**	0.062 (0.023)***	0.116 (0.048)**
=1 if either country is landlocked	-0.007 (0.028)	0.018 (0.017)	-0.008 (0.011)	0.013 (0.023)	-0.016 (0.014)
=1 if pair shares at least one sea or ocean	0.036 (0.027)	-0.010 (0.015)	0.014 (0.015)	0.000 (0.020)	0.009 (0.019)
Constant	0.089 (0.029)***	0.199 (0.018)***	0.148 (0.018)***	0.198 (0.023)***	0.147 (0.018)***
Observations (countries)	6,105 (111)	7,381 (122)	6,441 (114)	5,565 (106)	7,503 (122)
Standardized Beta (%)	8.38	12.73	18.68	25.97	19.81
R-Squared	0.25	0.10	0.14	0.16	0.17

Two-way clustered standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%

Table 4 – Bilateral regressions of technological distance on genetic and geographic distance metrics, horserace with absolute genetic distance (CEG dataset for 2000, dependent variable as in first row)

	(1)	**(2)**	**(3)**	**(4)**	**(5)**
	Agricultural Technology	**Communications Technology**	**Transportation Technology**	**Industrial Technology**	**Overall Technology**
Fst gen. dist. relative to the USA, weighted	**0.689** **(0.415)***	**0.504** **(0.276)***	**0.901** **(0.236)*****	**1.119** **(0.341)*****	**1.015** **(0.299)*****
Fst Genetic Distance	**-0.289** **(0.194)**	**-0.004** **(0.137)**	**-0.302** **(0.095)*****	**0.030** **(0.150)**	**-0.278** **(0.128)****
Absolute difference in latitudes	0.655 (0.129)***	0.274 (0.068)***	0.272 (0.058)***	0.332 (0.083)***	0.334 (0.083)***
Absolute difference in longitudes	0.387 (0.125)***	0.089 (0.052)*	0.279 (0.068)***	0.175 (0.067)***	0.224 (0.083)***
Geodesic distance	-0.046 (0.014)***	-0.015 (0.006)***	-0.032 (0.007)***	-0.025 (0.007)***	-0.028 (0.009)***
=1 for contiguity	-0.055 (0.014)***	-0.077 (0.012)***	-0.057 (0.013)***	-0.089 (0.018)***	-0.076 (0.012)***
=1 if either country is an island	0.118 (0.073)	0.057 (0.027)**	0.092 (0.042)**	0.062 (0.024)***	0.114 (0.045)**
=1 if either country is landlocked	-0.003 (0.029)	0.018 (0.017)	-0.006 (0.012)	0.013 (0.023)	-0.014 (0.014)
=1 if pair shares at least one sea or ocean	0.036 (0.027)	-0.010 (0.015)	0.012 (0.015)	0.001 (0.020)	0.008 (0.019)
Constant	0.093 (0.028)***	0.199 (0.018)***	0.153 (0.017)***	0.198 (0.023)***	0.152 (0.017)***
Observations (countries)	6,105 (111)	7,381 (122)	6,441 (114)	5,565 (106)	7,503 (122)
Standardized Beta (%)	14.37	12.83	27.68	25.31	26.97
R-Squared	0.26	0.10	0.15	0.16	0.18

Two-way clustered standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%

Table 5 – Bilateral regressions of technological distance on genetic and geographic distance metrics (CEG dataset for 1500, dependent variable as in first row)

	(1)	(2)	(3)	(4)	(5)	(6)
	Agricultural Technology	**Military Technology**	**Communications Technology**	**Transportation Technology**	**Industrial Technology**	**Overall Technology**
Relative Fst genetic distance to the UK, 1500 match	**0.551** **(0.281)***	**1.752** **(0.326)*****	**1.279** **(0.288)*****	**1.926** **(0.299)*****	**1.673** **(0.271)*****	**1.524** **(0.229)*****
Absolute difference in latitudes	0.189 (0.096)**	0.383 (0.094)***	0.758 (0.092)***	0.172 (0.064)***	0.138 (0.061)**	0.377 (0.065)***
Absolute difference in longitudes	-0.329 (0.082)***	-0.018 (0.066)	-0.017 (0.068)	-0.039 (0.048)	0.061 (0.091)	-0.066 (0.061)
Geodesic Distance	0.049 (0.010)***	0.009 (0.010)	0.009 (0.008)	0.014 (0.007)**	0.048 (0.010)***	0.025 (0.007)***
=1 for contiguity	0.037 (0.026)	-0.025 (0.019)	-0.042 (0.024)*	-0.006 (0.021)	0.023 (0.025)	0.014 (0.014)
=1 if either country is an island	-0.049 (0.058)	-0.087 (0.029)***	-0.095 (0.053)*	-0.073 (0.020)***	-0.180 (0.031)***	-0.092 (0.024)***
=1 if either country is landlocked	0.017 (0.026)	-0.051 (0.018)***	-0.020 (0.016)	-0.048 (0.011)***	0.006 (0.023)	-0.022 (0.011)**
=1 if pair shares at least one sea or ocean	-0.006 (0.020)	-0.105 (0.034)***	-0.018 (0.033)	-0.046 (0.029)	0.050 (0.029)*	-0.019 (0.025)
Constant	0.082 (0.034)**	0.166 (0.036)***	0.086 (0.026)***	0.069 (0.024)***	-0.126 (0.039)***	0.016 (0.020)
Observations (countries)	5,253 (102)	5,886 (108)	5,886 (108)	5,253 (102)	5,253 (102)	5,886 (108)
Standardized Beta (%)	10.41	29.26	19.95	41.81	25.27	31.63
R-Squared	0.23	0.27	0.36	0.32	0.46	0.44

Two-way clustered standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%

Table 6 – Bilateral regressions of technological distance on genetic and geographic distance metrics, horserace with absolute genetic distance (CEG dataset for 1500, dependent variable as in first row)

	(1)	(2)	(3)	(4)	(5)	(6)
	Agricultural Technology	**Military Technology**	**Communications Technology**	**Transportation Technology**	**Industrial Technology**	**Overall Technology**
Relative Fst genetic distance to the UK, 1500 match	**0.337** **(0.261)**	**1.883** **(0.344)*****	**1.346** **(0.311)*****	**2.073** **(0.312)*****	**1.558** **(0.271)*****	**1.615** **(0.244)*****
Fst Genetic Distance, 1500 match	**0.576** **(0.185)*****	**-0.369** **(0.120)*****	**-0.188** **(0.125)**	**-0.397** **(0.098)*****	**0.309** **(0.104)*****	**-0.257** **(0.095)*****
Absolute difference in latitudes	0.236 (0.090)***	0.353 (0.093)***	0.742 (0.095)***	0.140 (0.063)**	0.163 (0.062)***	0.356 (0.064)***
Absolute difference in longitudes	-0.279 (0.073)***	-0.053 (0.063)	-0.035 (0.065)	-0.074 (0.046)	0.088 (0.091)	-0.091 (0.059)
Geodesic Distance	0.038 (0.009)***	0.017 (0.009)*	0.013 (0.008)*	0.022 (0.006)***	0.042 (0.011)***	0.030 (0.007)***
=1 for contiguity	0.061 (0.024)***	-0.039 (0.020)**	-0.050 (0.026)*	-0.023 (0.021)	0.036 (0.025)	0.004 (0.015)
=1 if either country is an island	-0.046 (0.058)	-0.090 (0.030)***	-0.097 (0.053)*	-0.075 (0.022)***	-0.178 (0.030)***	-0.094 (0.025)***
=1 if either country is landlocked	0.007 (0.026)	-0.046 (0.018)***	-0.018 (0.016)	-0.041 (0.012)***	0.001 (0.023)	-0.018 (0.011)*
=1 if pair shares at least one sea or ocean	-0.013 (0.020)	-0.101 (0.034)***	-0.016 (0.032)	-0.042 (0.029)	0.047 (0.030)	-0.016 (0.024)
Constant	0.063 (0.036)*	0.179 (0.036)***	0.093 (0.028)***	0.082 (0.024)***	-0.136 (0.038)***	0.026 (0.020)
Observations (countries)	5,253 (102)	5,886 (108)	5,886 (108)	5,253 (102)	5,253 (102)	5,886 (108)
Standardized Beta (%)	6.37	31.45	20.99	45.01	23.54	33.52
R-Squared	0.24	0.27	0.36	0.34	0.46	0.44

Two-way clustered standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%

Table 7 - Bilateral regressions of technological distance on relative genetic distance (CHAT dataset averaged over 1990-1999)

		Fst gen. dist. relative to the USA, weighted	Observations (countries)	Standardized Beta (%)	R-Squared
Agricultural technologies					
(1)	**Harvest machines**	2.044 (1.134)*	3,486 (84)	5.91	0.17
(2)	**Tractors used in agriculture,**	19.615 (8.245)**	5,778 (108)	9.05	0.25
(3)	**Metric tons of fertilizer consumed**	73.393 (23.062)***	5,778 (108)	11.68	0.23
(4)	**Area of irrigated crops**	0.453 (0.276)*	5,565 (106)	7.21	0.03
(5)	**Share of cropland area planted with modern varieties (% cropland)**	0.182 (0.080)**	3,321 (82)	7.20	0.02
(6)	**Metric tons of pesticides**	0.738 (0.893)	4,465 (95)	2.62	0.12
Transportation technologies					
(7)	**Civil aviation passenger km**	0.484 (0.254)*	3,828 (88)	11.29	0.21
(8)	**Lengths of rail line**	0.397 (0.275)	4,656 (97)	5.26	0.28
(9)	**Tons of freight carried on railways**	2.330 (1.421)	4,005 (90)	10.63	0.16
(10)	**Passenger cars in use**	0.245 (0.082)***	5,886 (109)	15.88	0.26
(11)	**Commercial vehicles in use**	0.066 (0.025)***	5,050 (101)	23.50	0.29

		Fst gen. dist. relative to the USA, weighted	Observations (countries)	Standardized Beta (%)	R-Squared
Medical technologies					
(12)	**Hospital beds**	1.481 (4.319)	5,565 (106)	1.31	0.17
(13)	**DPT immunization before age 1**	0.137 (0.156)	5,778 (108)	3.54	0.01
(14)	**Measles immunization before age 1**	0.141 (0.162)	5,778 (108)	3.71	0.01
Communications technologies					
(15)	**Cable TV**	74.485 (56.305)	4,753 (98)	4.23	0.16
(16)	**Cell phones**	0.109 (0.044)**	5,778 (108)	8.21	0.12
(17)	**Personal computers**	0.247 (0.099)**	4,950 (100)	12.53	0.21
(18)	**Access to the Internet**	0.192 (0.072)****	5,778 (108)	14.25	0.28
(19)	**Items mailed/received**	0.097 (0.074)	2,346 (69)	11.00	0.21
(20)	**Newspaper circulation**	0.245 (0.101)**	5,886 (109)	10.43	0.25
(21)	**Radios**	0.064 (0.139)	5,886 (109)	1.87	0.12
(22)	**Telegrams sent**	0.312 (0.260)	2,211 (67)	5.74	0.07
(23)	**Mainline telephone lines**	0.185 (0.067)***	5,886 (109)	11.54	0.28
(24)	**Television sets in use**	0.492 (0.141)***	5,886 (109)	18.78	0.31

		Fst gen. dist. relative to the USA, weighted	Observations (countries)	Standardized Beta (%)	R-Squared
Industrial technologies and other					
(25)	**Output of electricity, KwHr**	34.477 (13.849)**	5,565 (106)	8.16	0.23
(26)	**Automatic looms**	0.828 (0.304)***	3,570 (85)	11.19	0.06
(27)	**Total looms**	1.200 (0.361)***	3,570 (85)	8.95	0.08
(28)	**Crude steel production in electric arc furnaces**	0.091 (0.031)***	2,278 (68)	8.10	0.08
(29)	**Weight of artificial (cellulosic) fibers used in spindles**	0.425 (0.354)	2,145 (66)	3.89	0.10
(30)	**Weight of synthetic (non cellulosic) fibers used in spindles**	2.045 (0.819)**	2,145 (66)	9.89	0.20
(31)	**Weight of all types of fibers used in spindles**	7.832 (2.759)***	2,850 (76)	12.10	0.07
(32)	**Visitor beds available in hotels and elsewhere**	24.245 (7.518)***	5,565 (106)	9.31	0.10
(33)	**Visitor rooms available in hotels and elsewhere**	13.518 (3.884)***	5,778 (108)	10.50	0.10

Two-way clustered standard errors in parentheses; * significant at 10%; ** significant at 5%; *** significant at 1%
Unless specified in parentheses, the dependent variable is the absolute difference in *per capita* prevalence of the technology between country *i* and country *j*.
All regressions include controls for absolute difference in latitudes, absolute difference in longitudes, geodesic distance, dummy=1 for contiguity, dummy=1 if either country is an island, dummy=1 if either country is landlocked, dummy =1 if pair shares at least one sea or ocean.

Figure 1 - Genetic distance among 42 populations.
Source: Cavalli-Sforza et al., 1994.

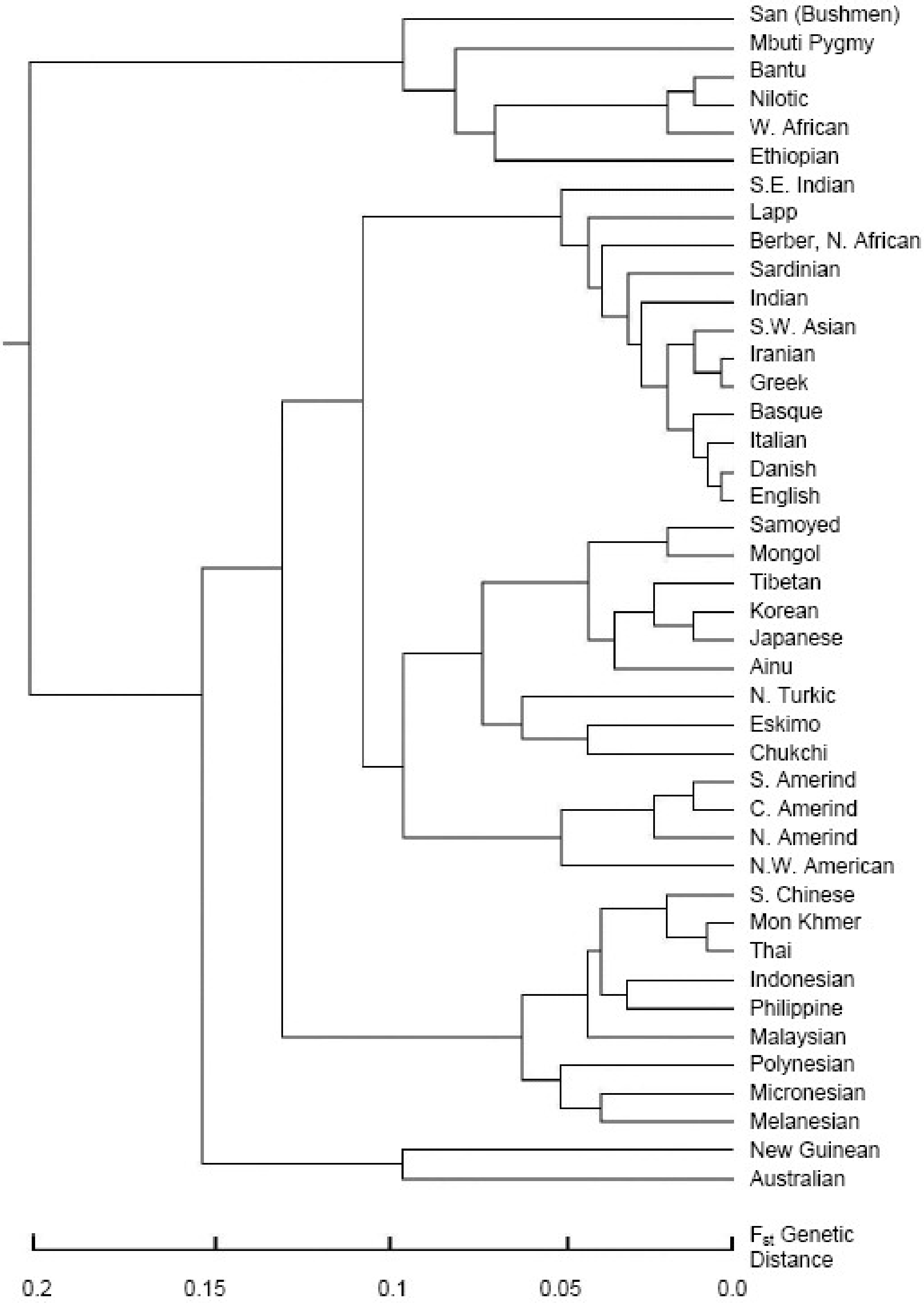

Figure 2 - Population Tree