

POPULATION AND LONG-TERM ECONOMIC DEVELOPMENT: A RE-EXAMINATION AND SOME NEW EVIDENCE

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Abstract

The relationship between population and long-term economic development is of obvious importance. Past studies of this relationship have typically emphasized the favorable aspects of population. This paper re-examines the existing evidence and introduces new evidence derived from a multiplicity of demographic, archeological, and anthropological sources. The findings suggest important biases and confounding influences in current assessments, and point toward new mechanisms by which past population adversely influences economic development. A central aspect of the analysis is the role of population as a factor in generating ‘diversity’ (in a general sense). Potential influences are formalized in a model of technological leapfrogging.

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1 Introduction

The study of population is one of the oldest and farthest-reaching themes in social sciences. It is also one of the most controversial. Assessments of the long-term implications of population growth typically vary between Malthusian (or pessimistic) and Boserupian (or optimistic) extremes.¹ Fiscal concerns due to the emergence of below replacement fertility in many developed countries and concerns with environmental degradation due to the continuous expansion of the population of less developed countries have only exacerbated this controversy. The tension between optimistic and pessimistic views is apparently not likely to ease in the near future.

But while the understanding of the long-term consequences of population growth is widely held as a major economic problem, there is rarely any systematic empirical effort to bear on the *causal* effect of population on economic development. The challenge was taken up most prominently by Kremer [38] who used time series and cross-sectional evidence to argue that the long-run history of population growth and technological change is consistent with a view in which population spurs technological innovation.

Kremer [38] proposed a synthesis of Malthusian and Boserupian views and a very useful way of organizing economic-demographic interactions. In Kremer [38], spurs of innovation lead to faster population growth whereas faster population growth induces technological innovation.² This interaction generates two testable predictions: first, it suggests an increasingly increasing growth rate for population, and second, it suggests that out of two geographically isolated societies, the one with the larger initial population size should achieve greater population growth and greater technological sophistication

¹Malthus [44] considered the pressure of population against available resources as the fundamental cause of human misery. According to Malthus [44], changes in the technology for food production were essential for population growth since they temporarily relieved the pressure of population on the food supply. Rather than technological change determining population growth, Boserup [4] considered population pressure as the driving force behind technological change. Based on Southeast Asian observation and Western European cases, she showed that agricultural technologies improved in response to population pressure.

²Previous synthesis of Malthus and Boserup include Lee ([40], [41]). An additional synthesis is available in Wood [74]. Jones [33], Johnson [32], Galor and Weil [23], and Cohen [11] are some examples that build on the important contribution of Kremer [38]. Kuznets [39] is an earlier discussion that also favors a positive view of population. See also Dasgupta [13] and Simon [67] for important analyses of population.

over time. Kremer [38] examined both of these predictions using time series data on population that started as early as 1 million years ago (MYA henceforth) as well as a cross-sectional analysis based on the geographic isolation of the populations in the New World consequence of the melting of the ice caps.

In this paper I have a dual purpose. The first, is to further the empirical discussion Kremer [38] initiated on the role of population growth on long-term economic development. To that end, I re-examine Kremer's [38] analyses and introduce new data to bear on the empirical relationship between population growth and economic development. My empirical assessments use new information derived from detailed ethnographic data for current hunter-gatherers from Murdock and White [51], from Chandler's [10] archeological census of pre-modern cities, and from recent empirical findings about past human demography that stem from the anthropological analysis of genetic diversity in current populations, see, e.g., Cann et al. [7], Cavalli-Sforza et al. [9], and Relethford [58].

The findings differ substantially from those of Kremer [38]. For reasons that I will describe in detail later on, I find a weaker association between population and economic development and even contemplate the possibility of adverse effects of population. In light of this, my second goal in this paper is to suggest an alternative interpretation for the observed empirical association between population growth and economic conditions. In this alternative interpretation, as well as in the majority of the text, I treat technological sophistication as synonymous to economic development.³

With respect to the first goal, I find that the period over which increasingly increasing growth is observed is limited to the modern epoch and that current time series estimates of past populations are unreliable to test for increasingly increasing growth. By construction, these past estimates *assume* increasingly increasing growth. For example, Deevey [14], Kremer's [38] source, assumed that (i) the area populated by humans increased since 1MYA and that (ii) the density of the population in any given area has also increased since 1MYA. These assumptions would bias a time series analysis because they create an

³In general, these two concepts are not identical but on a long historical scale, as the one I consider here, economic development and technological change are closely interrelated. Technology plays a fundamental role in the transformation of any society in aspects such as wealth accumulation, economic growth, and improvements of the quality of life.

increasingly increasing population growth rate by construction. Now, the fact that these assumptions are used to estimate past population trends is not necessarily problematic if both assumptions are correct. However, I also present empirical evidence that suggests that there is no strong empirical support for Deevey's [14] assumption of an increasing trend in population densities since earlier times.

Further, I argue that Kremer's [38] cross-sectional tests, which are based on the geographic isolation of the New World, require a suitable *control* group. The basis of the cross-sectional comparison in Kremer [38] is the following. After the last glaciation, the populations in the New World became isolated from populations in the Old World. The isolation was quite complete prior to 1500 other than by the Norse voyages and the insignificant contact that may have existed in Alaskan communities. Thus, suppose populations were randomly allocated among the Old and the New World, and assume that population densities were the same in both regions some 12 thousand years ago (KYA henceforth) when hunter and gathering was the common mode of production in all populations. A view in which population favors economic development would predict that the Old World's size advantage, more precisely its population advantage (as all areas are assumed to have the same density), would generate an economic advantage for the Old World compared to the New World.

At first glance, the above conclusion seems reasonable. But there is one important qualification to be made about this conclusion. Strictly speaking, the above comparison depends on the similarities of other conditions, including geography, climate, and resource endowments, of the areas being compared. In the absence of a control for these differences, the previous comparison may lead to inadequate inferences. That is, factor endowments and geography were not equal in the different areas studied by Kremer [38] as the extensive discussion in Diamond [16] has shown. Thus, the importance assigned to the Old World's population size could be in part attributed to advantages in the number of domesticable species or Eurasia's East-West orientation which, according to Diamond [16], favored the origin of agriculture and the diffusion of post-agricultural technologies such as metallurgy and weaponry.

To rule out alternative explanations, I propose a “controlled” comparison of isolated geographical areas. This comparison minimizes confounding influences. For the many similarities discussed later on, I treat sub-Saharan Africa as a control region for South and Central America. In this comparison, the evidence associated with the geographic isolation of the New World suggests a much weaker influence of population on economic development. While sub-Saharan Africa had a larger population size and repeated contact with Eurasia through many trade routes, there were no large cities or large tributary empires south of the Sahara at the time of the European expansion (see, e.g., Connah [12]). In tropical America, Teotihuacán (currently Mexico city), was among the ten largest cities of the world in 400, Chandler ([10], 464).⁴

With respect to the second goal, I argue that technological change may be portrayed as a pattern of technological *leapfrogging* as studied initially by Brezis et al. [5]. The basic idea in the leapfrogging views of Brezis et al. [5] is that technological change is of two kinds. A “normal” technological change that evolves as predicted by models of endogenous growth and a “radical” technological change. I propose a simple model based on this alternative view. In the model, population creates an incentive for incremental investments in “normal” technical change but act as a barrier to the adoption of “radical” technological changes. I argue that such a model is useful for understanding current and past differences in economic conditions as it allows for sharp breaks as well as slow transitions between economic epochs and reversals in technological leadership. Further, a leapfrogging view offers a rationalization for the pervasive resistance to new technologies (Mokyr [49]).

The empirical evidence is insufficient for a detailed analysis of the pre-modern economic conditions in the different parts of the world. Nonetheless, I favor a leapfrogging view because the empirical evidence, at least in its present state, points toward higher populations and technological conditions early on in Africa. African societies, however, have

⁴I have developed the basic framework for the proposed comparison in greater detail elsewhere, see Birchenall [3]. Briefly, I will show later on that sub-Saharan Africa and South and Central America have similar geography in terms of their North-South orientation, landmass, and climate. Both lacked suitable animals for domestication and very few plants were available for agriculture (Diamond [16]). Furthermore, agriculture originated independently in both areas at about the same time (Smith [68]).

lagged in terms of agricultural and industrial achievements. Further, despite being less populous and technologically backward, industrialization first occurred in Europe rather than in Asia. This is a well established puzzle which I do not try to resolve here. However, a leapfrogging view suggests an interesting possibility: because the Near East and China experienced an early onset of settled agriculture (Smith [68]), their higher population densities and technological sophistication are not surprising. However, the relatively advanced technology and organization of these agricultural societies would make industrialization less profitable. Europe, in contrast, did not experience an independent origin of agriculture. Instead, Europe received migrants and innovations from the agricultural centers in Asia. In the same sense in which early advances in Africa may pose a barrier for “radical” changes, the absence of an independent origin of agriculture in Europe may give advantages for “radical” technological changes such as industrialization.⁵ This reasoning is reinforced by the fact that industrialization first diffused into regions where agriculture did *not* originate independently: North America and Australia.

To study past demography, I make extensive use of new evidence derived from the anthropological analysis of genetic diversity in current populations. By the use of these sources, this paper is related to Spolaore and Wacziarg [69], Galor and Ashraf [24], and a growing literature that use genetic information to examine current and past differences in economic development. The relationship of this paper and this literature is discussed in more detail at the end of this paper. I may just emphasize that these previous studies have not recognized the demographic implications of the observed patterns of human genetic diversity. The interpretation of the genetic patterns is also different from that in the literature. Previous studies in the economic literature value genetic information because they correctly assume that genetics coevolve with other variables, i.e., with culture in

⁵The reasons for why African economies have lagged behind comparable regions in the past is a broad theme and several ‘barriers’ related to the analysis I provide can be suggested. Because societies in Africa have high levels of genetic, anthropometric, and linguistic diversity, my analysis is consistent with interpretations that view ethnic and linguistic fractionalization as a barrier for the adoption of favorable technological and institutional changes conducive to modern economic growth, see, e.g., Easterly and Levine [17]. The main point of contrast with previous studies is that I emphasize an early population origin and a larger population size as a factor responsible for the high levels of diversity in Africa. In the current empirical literature, the sources of African diversity are not typically explained.

Spolaore and Wacziarg [69]. In this paper, I show that demographic factors rationalize the patterns observed and provided by previous studies.

The rest of the paper proceeds as follows. Section 2 re-examines current assessments of the relationship between population and technological change. Section 3 presents new data on past demography based on the patterns of genetic diversity within human populations and its implications for population and economic development. Section 4 offers remarks on technological leapfrogging. Section 5 concludes this paper. The Appendix discusses increasingly increasing growth and genetic diversity.

2 Background and current assessments of the relationship between population and technological change

In this section I provide a brief overview of the current assessments of the relationship between population and economic development and present alternative tests that complement current empirical analyses. My purpose in this section is limited because a definite assessment of the relationship between population and technological change is inherently difficult. I merely seek to raise concerns not previously addressed in the literature and to examine in greater detail existing qualifications that need to be resolved in order to provide a causal view of the observed association between population and long-term economic development.

My discussion is rooted in Kremer [38] where economic-demographic connections have been explicitly investigated. At the core of Kremer's [38] analysis is the following simple but illuminating endogenous growth model.⁶ Let $A(t)$ and $N(t)$ represent the level of technology and population size at date $t \geq t_0$. Assume technology changes according to:

$$\frac{dA(t)}{dt} = \theta A(t)^\phi N(t)^\gamma, \tag{1}$$

⁶Additional aspects beyond those considered by Kremer [38] may be found in Dasgupta [13], Kuznets [39], Simon [67], Kelley [36], and Johnson [32]. In these papers, as well as in Kremer [38], the effects of population on economic conditions are often channeled through a series of external effects.

with ϕ , γ , and θ as strictly positive and fixed parameters.

The previous parameters can be interpreted as follows. The role of the existing level of technology $A(t)$ is captured by ϕ . Thus, since $\phi > 0$, higher technological sophistication facilitates the creation of new technologies. The constant γ represents the influence of population on technological change. Because $\gamma > 0$, population size is a positive influence in technology creation. The influence of ‘exogenous’ variables, or variables other than $A(t)$ and $N(t)$, is captured by θ . On the Malthusian side, any change in technology translates into higher population,

$$\frac{dN(t)}{dt} \frac{1}{N(t)} = \frac{dA(t)}{dt} \frac{1}{A(t)}. \quad (2)$$

When $\phi = 1$, the dynamics of population are:

$$\frac{dN(t)}{dt} = \theta N(t)^\alpha, \text{ with } \alpha \equiv 1 + \gamma > 1. \quad (3)$$

Thus, (3) distinguishes between population growth due to exogenous and endogenous technological influences. Further, the dynamics in (3) are slightly more general than in Kremer [38] where $\theta = 1$.⁷

2.1 Re-examination of the time series evidence

The key testable prediction of (3) is that population should experience increasingly increasing growth rates.⁸ To examine this prediction, Kremer [38] used population estimates from Deevey [14]. These estimates and the econometric analysis of Kremer [38] strongly support increasingly increasing growth. In fact, $\gamma = 1$ provides a reasonable approximation to the evolution of population from 1MYA to 1990.

⁷Kremer [38] considered a much richer set of possibilities for technological change that includes $\phi < 1$. Variations in population densities have been considered by Klasen and Nestmann [37]. In the generalizations, population growth is still a function of population as in equation (3). Kremer [38] also discussed the reversal of the income-population growth relationship at the later stages of the demographic transition. An inverted U-shaped relationship has been studied in unified models of growth initially considered by Galor and Weil [23].

⁸Increasingly increasing growth turned out to be very accurate in predicting modern population growth although the ideas have been objected theoretically at least since the 1960s (see, e.g., Foerster et al. [20], Serrin [65], and Umpleby [71]). Additional remarks on increasingly increasing growth are available in the Appendix to this paper.

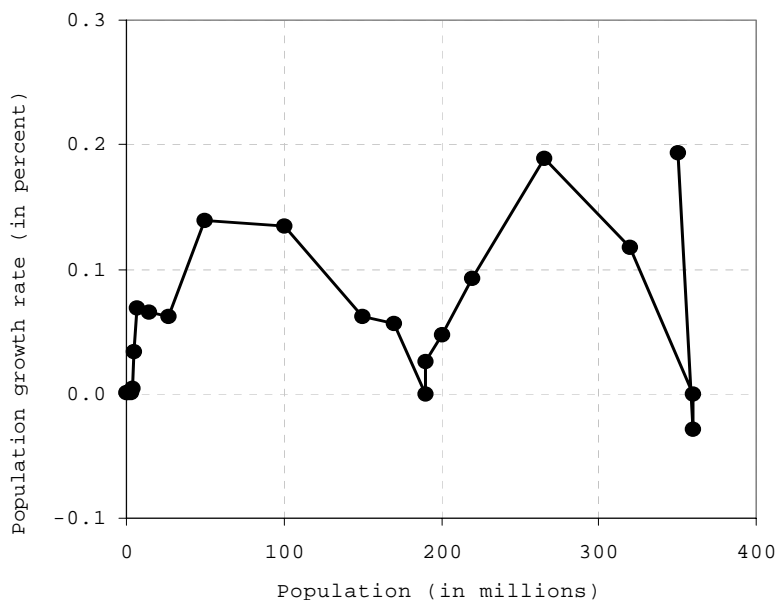


Figure 1: Scatter plot of population levels and population growth in pre-modern samples, 1MYA to 1400. Data from Kremer ([38], Table 1).

For the modern period, the available empirical evidence also confirms this prediction on a simple basis: it took almost all of human’s history up to 1800 to reach 1 billion people. The second billion took 125 years, the third 35 years, the fourth 15 years, the fifth 10 years and the sixth less than 10 years, Kremer ([38], Table 1). This pattern of population change is not consistent with exponential growth which predicts constant and not decreasing doubling times.

However, time series evidence depends heavily on recent historical trends. In Figure 1, I relate the level of population to its growth rate. This relationship can be seen as a prediction taken from (3). The figure basically excludes the last 500 years from Kremer ([38], Figure 1). As Figure 1 shows, there is no systematic association between population levels and growth rates before 1500.⁹ Thus, the period over which an increasingly increasing growth rate has prevailed is too brief compared with preceding epochs with

⁹In a linear regression between the growth rate of population, and its level, as described in (3), the coefficient on the population size is 0.051 (s.e. 0.0005) when all the sample points in Kremer [38] are used. If the sample is restricted to points before 1500, the estimated coefficient is 0.012 (s.e. 0.013), not statistically different from zero. The standard errors in the previous estimates have been corrected for heteroscedasticity due to the nature of the data.

quite different demographic patterns.

A larger span of data may help the econometric evaluation of (3). While desirable, these tests are also less informative because population data typically assume increasingly increasing growth. That is, past estimates of the human population assume that the area inhabited by humans has increased over time and that the population densities within each of these areas has also increased since 1MYA (see, e.g., Deevey [14] and Hassan [28]).

The empirical evidence needed to examine past demographic patterns is imperfect and examining past populations involves high degrees of speculation. The calculations are also inherently uncertain. Yet, the assumption of an increasing trend in population densities is problematic because the demography of current hunter-gatherers contradicts this assumption.¹⁰

It is known that modern human populations originated in tropical Africa some 150KYA and then migrated into non-African regions as hunter-gatherers (Jobling et al. [31]). Thus, to examine the possibility of an increasing trend in population density consider two simple tests. First, given that human populations entered into the New World only after some 25KYA, the hunter-gatherers in sub-Saharan Africa and in the New World are separated by a considerable number of years. If there is an observable trend in population densities as hunter-gatherers colonize new territories, as assumed by Deevey [14], the hunter-gatherers in the New World should have, on average, higher population densities than the hunter-gatherers of Africa. Second, past migrations took place mainly from tropical areas into temperate zones. Thus, population densities should also be higher for societies located further away from the Equator.

Although few hunter-gatherers exist today, they are well documented in the ethnographic record. Thus, I rely on the demography of current hunter-gatherers to provide a glimpse of the historical variation in population density across different geographic areas

¹⁰These assumptions seems quite counterintuitive for a variety of reasons. In fact, Deevey himself remarked: “my own treatment of this, published some years ago in *Scientific American*, was not very professional,” Deevey ([15], 248). For example, extinction and re-colonization in hunter-gatherer societies makes difficult to interpret range expansions as permanent increases in occupied area. Further, the idea of a continuous increase in population densities is also problematic since there is more food available per km² in the tropics, i.e., Hassan ([28], Table 12.5). For evidence in favor of higher densities and a range expansion during the middle Paleolithic in Africa, see Hawks et al. ([29], 12).

and latitudes. The analysis that follows uses Murdock and White’s [51] Standard Cross Cultural Sample (SCCS). The SCCS consists of detailed societal data from 186 ethnographically well-described societies including 55 hunter-gatherers throughout the world. These societies are described from historical and ethnographical accounts just after contact with western cultures.¹¹

My analyses of differential population densities are based on the following OLS regression:

$$Y_i = \alpha + \lambda \times |\text{Latitude}_i| + \rho \times \text{Region}_i + \varepsilon_i, \quad (4)$$

in which Y_i represents population density defined as the number of people per square mile. These demographic variables are coded in an ordinal scale in the SCCS. However, the ordinal scale from 1 to 7 is essentially the logarithm of size and population density respectively. The coefficient λ measures the role of latitude (defined as distance to the Equator), and ρ is the region of the society. Thus, a positive ‘trend’ in population densities according to the tests just outlined suggest $\rho > 0$ for societies in the New World and $\lambda > 0$ overall.

Table 1 presents the results of the estimation of (4). I provide several specifications and two measures of population density. Since hunter-gatherers are quite mobile, a precise estimate of population density is not easy to obtain. The SCCS considers several of these estimates including non-inferential estimates. I use these measures in specifications (5)-(8). Specifications (1) and (5) consider differences between the New and the Old World whereas (2) and (6) consider differences between tropical America (South and Central America) and sub-Saharan Africa. As I will discuss in the next sub-section, these areas are quite comparable in terms of resource endowments, climate, and geography.

It is difficult to draw definite conclusions due to the nature of the data, but all the specifications in Table 1 reject the idea that population densities are higher for hunter-gatherers in the New World or for hunter-gatherers in temperate areas. Distance to

¹¹The SCCS is representative of pre-industrial societies and it was constructed to maximize independence in terms of cultural and historical origin. Hunter-gatherers are defined based on the amount of food obtained from agriculture, i.e., if less than 10 percent of the food is from such source. The geographic distribution of the hunter-gatherers is as follows: In Africa there are 6 societies, in South America 9, in Eurasia 11, in the Insular Pacific 4, in North America 21, in the Circum-Mediterranean 4.

the Equator is also negative and statistically significant in specifications that include regional controls. The evidence in Table 1 thus suggests that population movements into temperate areas and into the New World were probably not associated with an increase in population density as typically assumed in ecological estimates, see, e.g., Deevey [14] and Hassan ([28], Chapter 12).

Table 1. Population size and densities of hunter-gatherers in the SCCS.

Dependent variable	Population density				Non-inferential population density			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Intercept	2.16** (0.24)	2.05** (0.34)	2.31** (0.33)	1.83** (0.34)	2.64** (0.40)	2.18** (0.37)	2.64** (0.40)	2.18** (0.37)
New World	-0.39 (0.32)				-0.35 (0.37)			
Tropical America		-0.60 (0.26)				-0.41 (0.30)		
Sub-Saharan Africa		-0.05 (0.40)				-0.28 (0.41)		
Latitude			-0.010 (0.007)	-0.017** (0.08)			-0.017** (0.08)	-0.023** (0.009)
Region dummies	NO	NO	NO	YES	NO	NO	NO	YES
R ²	0.02	0.03	0.03	0.08	0.02	0.02	0.08	0.12
N. Obs.	55	55	55	55	46	46	46	46

Source: In parentheses are robust standard errors. ** and * denote statistical significance at the 5 and 10 percent level. Hunter-gatherers are societies in which with less than 10 percent of their food is obtained from agriculture, $v3 \leq 3$ in the SCCS. Non-inferential measures are based on $v1131$ in the SCCS. The New World coefficient is a dummy variable for hunter-gatherers in the New World. Tropical America and sub-Saharan Africa are defined correspondingly. The regional dummies in (4) and (8) are indicators for the areas in the world described in the text.

In more recent periods, after agriculture, population data also relies on the assumption of increasing population densities. This is the key assumption behind the population estimates in McEvedy and Jones [46]. Population size and densities have indeed increased due to settled agriculture, Livi-Bacci ([42], 45). Thus, these assumptions are less prob-

lematic in recent periods. This point has been extensively discussed by Kremer ([38], 699-700).

Another aspect that will also bias statistical results in (3) deserves a brief mention. Current estimates of world population rarely present episodes of population decline. In part this is so because available methods in archeology are better suited to find population increases rather than population crashes (see, e.g., Schacht [64] and Petersen [53]). Yet, in areas where archaeological material covers a long span of time, the available evidence shows several episodes of population declines, see, e.g., Whitmore et al. [72]. With the exception of the Black Death, there are no episodes of negative growth in the estimates of world population employed by Kremer ([38], Table 1).¹²

2.2 Re-examination of the cross-sectional evidence

In this sub-section, I consider cross-sectional analyses that examine the relationship between population change and economic development. As in the previous sub-section, I first review current assessments and then provide a re-examination of the available evidence.

As noted by Kremer [38], (3) is a Bernoulli differential equation whose solution, written in terms of population, is:

$$\ln [N(t)] = \frac{\ln[\theta(1 - \alpha)t + N(t_0)^{1-\alpha}]}{1 - \alpha}, \quad (5)$$

for $N(t_0) > 0$ given.

A useful way to interpret (5) is the following. Because population varies in proportion to technology, population and technological sophistication at date t are increasing functions of the initial population size, $N(t_0)$, time since origin, $t - t_0$, and exogenous influences in technology creation, θ . Equation (5) thus makes it possible to evaluate the impact of population size on technology using the melting of the ice caps that divided the

¹²Population change in the Egyptian Nile valley, the Tigris-Euphrates lowlands, the Basin of Mexico, and the central Mayan lowlands of Mexico and Guatemala has been studied by Whitmore et al. [72] since 6KYA. Genetic anthropologists have also studied the time series patterns of population since 150KYA. Examples include Rogers and Harpending [61], Excoffier and Schneider [18], and Sherry et al. [66]. See also Hawks et al. [29] and Eswaran et al. [19].

continents as a “natural experiment.” Because the land bridges that connected the New World with Asia and New Guinea with Australia (also Tasmania and Flinders Island) disappeared some 12KYA, some populations became geographically isolated. Isolation, in a sense, induced exogenous differences in the initial population size $N(t_0)$.¹³

As in Kremer [38], I will consider the isolation of the New World as a dichotomous “treatment” in the modern statistical sense. To evaluate the effect of isolation as a “natural experiment,” in addition to a treatment group, I need a suitable control group with similar pre-treatment characteristics. The selection of this control group is essential because it should be able to eliminate exogenous influences formally captured by θ in (5).

One possible control area is the Old World. This comparison would suggest important advantages associated with the Old World’s large population size prior to 1500, see, e.g., Kremer [38]. However, there are important differences unaccounted for in a comparison between the Old and the New World. As I noted in the introduction, these regions differed in aspects beyond their demography such as in their orientation, their size, and their endowments. In fact, these differences were used by Diamond [16] to argue in favor of the role of geographical differences in long term development (i.e., regional differences in θ).

In order to eliminate confounding factors, I use sub-Saharan Africa as a “control” for the isolation of tropical America. Sub-Saharan Africa and South and Central America have similar geography: in both, axes run mostly from North to South, Diamond ([16], 177), and the total area of these continents is relatively equal, see Table 2. Climate is also similar since both cross the Equator. Further, both lacked suitable animals for domestication and very few plants were available for agriculture (in contrast to Eurasia whose favorable endowments were a consequence of its relatively large size, as Diamond

¹³The tests are a direct application of (5), see for example equation (16) in Kremer [38]. A general version of Kremer’s [38] model is available in Klasen and Nestmann [37] where densities are different between populations. Differences in densities would be part of θ in equation (5). Since $\ln[N(t)]$ is roughly a linear function of log-time in equation (5), increasingly increasing growth can be detected through a double logarithmic plot between population and time. Under increasingly increasing growth, log-population and log-time should lie on a straight line with slope $(1 - \alpha)^{-1}$. When α tends to one, population growth becomes exponential so a direct test of the model is to test whether or not $\alpha = 1$ in estimates of equation (5). Those tests (available upon request) also reject increasingly increasing growth in pre-modern samples.

[16] argues). Agriculture originated independently in both areas at about the same time, see, e.g., Smith ([68], 13).¹⁴ More importantly, sub-Saharan Africa was not isolated from Eurasia. Repeated contact with Eurasia existed through the Nile River because of ancient Egypt, through the Sahara by the Arab trade that started during the seventh century A.D., and by the East African trade through the Indian ocean in medieval times.

Table 2. Estimated pre-modern population in Africa and the Americas.

Region	Area	Biraben [2]				McEvedy and Jones [46]		
		400 B.C.	A.D.	1000	1500	A.D.	1000	1500
Africa								
North	2	10	14	9	9	8	11	8
Sub-Saharan	25	7	12	30	78	8	22	38
The Americas								
North	20	1	2	2	3	0.4	0.7	1.3
South and Central	20	7	10	16	39	4	8	13
Indian subcontinent	5	30	46	40	95	34	77	100
World population		153	252	253	461	170	265	425

Notes: Population in millions. Area (mill. km²) from McEvedy and Jones [46]. North Africa includes the Maghreb, Libya and Egypt. The area in North Africa does not include the Sahara. North America includes the US, Canada, and the Caribbean.

To examine the role of population in economic development I rely on modern estimates of past regional populations that begin in 400 B.C., see Table 2. Table 2 presents estimates from Biraben [2] and McEvedy and Jones [46]. According to Caldwell and Schidlmayr [6], these estimates used independent sources. In fact, the estimates differ in many aspects including the magnitude and timing of population change. In both, however, sub-Saharan

¹⁴The number of large-seeded grass species needed for agriculture in sub-Saharan Africa (4) is closer to South and Central America (with 2 and 5 respectively) than to Eurasia (with more than 30), see Diamond ([16], Table 8.1). Also, in neither of them there were many domesticable animals. In the Americas there was the llama while there were no mammalian candidates for domestication in sub-Saharan Africa, Diamond ([16], Table 9.2). The time and region of origin of agriculture (taken from Smith [68]) are the following: Near East (Fertile crescent) 10KYA, Yangtze river (South China) 8.5KYA, Yellow river (North China) 7.75KYA, Central Mexico 4.75KYA, South Central Andes 4.5KYA, Eastern United States 4.5KYA, Sub-Saharan Africa 4.0KYA. In North America, however, there was no domesticated cereal. Corn diffused from Central Mexico but only after the first millenia.

Africa had a large population size and the fastest population growth in the world in the years between 400 B.C. (or A.D.) and 1500 (or 1000).

To provide a “test,” consider a series of difference-in-difference estimates. First, a cross-sectional difference in population levels between sub-Saharan Africa and South and Central America in 1500 is $\Delta_D = N^{S.Africa} - N^{S.C.America}$. As Table 2 shows, population in sub-Saharan Africa was about twice as large as the population in South and Central America; that is, $\Delta_D > 0$.¹⁵ Second, consider a double difference or a difference in growth rates, $\Delta_{DD} = n^{S.Africa} - n^{S.C.America}$, with n as the population growth rate. These differences are presented in Table 3. As this table shows, population in sub-Saharan Africa increased between four- and ten-fold, much faster than the populations in tropical America. In other words, $\Delta_{DD} > 0$ as well.

Finally, the previous comparisons assume that sub-Saharan Africa had no contact with Eurasia so they represent a lower bound for the influence of population. One way to determine Eurasia’s influence is through a double difference estimator $\Delta_{DDD} = (n^{S.Africa} - n^{Eurasia}) - n^{S.C.America}$, with $n^{Eurasia}$ representing a control for the contact of sub-Saharan Africa and Eurasia. The difference in growth rates would then discount from Africa’s growth rate the contribution attributed to Eurasian influences. If the Eurasian influence is large, the estimate Δ_{DDD} should be small. Table 3 presents these estimates. Table 3 includes estimates of African population growth that discount the population increase in the Indian subcontinent (which also has a North-South axis) and in Eurasia. An alternative would be to use North Africa directly, but North Africa’s population growth was negative in most of the years considered in Table 3. As the table shows, even after the

¹⁵Evidence on the size of the population in America before Columbus varies substantially. For tax purposes, Spanish authorities in 1574 reported a total of about 8 to 10 million inhabitants in Hispanic America although there are much higher estimates, Livi-Bacci ([43], Table 1). Numbers in Africa also vary widely but early estimates suggested an African ‘consensus’ around 100 million inhabitants in 1650, see, e.g., Caldwell and Schidlmayr [6]. Although some earlier estimates are based on an “extraordinary amount of material,” they are either informed guesses based on travelers’ observations or impressions based on relative densities, Caldwell and Schidlmayr ([6], 188). Caldwell and Schidlmayr ([6], Table 2) present additional estimates of regional populations circa 1650. In all estimates but in Riccioli’s 1661 figure, Africa is more populous than the Americas. As Livi-Bacci [43] notes, a large population in the Americas is used mostly to give credit to “germs” as an important factor in the population decline after the Conquest. Livi-Bacci [43] also argues that the new pathologies were important in the depopulation of the Americas but additional factors related to violence, civil conflicts, famine and hunger, confiscation of labor, and economic and social disruptions were also powerful factors in the decline.

growth rate of a control region is subtracted, population growth in Africa was faster than in South and Central America. That is, $\Delta_{DDD} > 0$. The only instance in which there is a negative difference is for the first millennia in the population data from McEvedy and Jones [46].¹⁶

Table 3. Population growth in Africa and the Americas.

	Biraben [2]				McEvedy and Jones [46]	
	400 B.C. to 1000		A.D. to 1500		A.D. to 1500	
	Baseline population increase					
A. Sub-Saharan Africa	3.3	10.1	1.5	5.5	3.5	1.6
B. The Americas						
B ₁ . North	1.0	2.0	0.0	0.5	2.3	0.8
B ₂ . South and Central	1.3	4.6	0.6	2.9	2.0	1.0
	First difference, Δ_{DD}					
C ₁ (=A-B ₁). North America	2.3	8.1	1.5	5.0	1.2	0.8
C ₂ (=A-B ₂). South and Central	2.0	5.5	0.9	2.6	1.5	0.6
	Controls for Eurasian influence over Africa					
Population increase in						
D ₁ . Indian subcontinent	0.7	2.2	0.0	1.1	1.9	0.6
D ₂ . Eurasia	0.0	1.4	0.0	0.4	1.3	0.0
	Double difference, Δ_{DDD}					
With respect to Indian subcontinent						
E ₁ (=C ₁ -D ₁). North America	1.6	6.0	1.5	3.9	-0.7	0.3
E ₂ (=C ₂ -D ₁). South and Central	1.3	3.4	0.9	1.5	-0.4	0.1
With respect to Eurasia						
F ₁ (=C ₁ -D ₂). North America	2.3	6.7	1.5	4.6	0.0	0.9
F ₂ (=C ₂ -D ₂). South and Central	2.0	4.2	0.9	2.2	0.2	0.6

Notes: Data from Table 2. Population increase is not taken on uniform time units but simple normalizations will make rates comparable between periods.

In summary, during the post-agricultural period, sub-Saharan Africa had contact with

¹⁶Hopkins ([22], 121) suggests an estimate of 25 million in West Africa alone during 1700. Caldwell and Schindlmayr [6] suggest an estimate of the population in Africa around 50 million inhabitants in 1500. Note also that about 10 million slaves were transported mostly from West Africa during the Atlantic slave trade, Fogel and Engerman ([21], Figure 2).

Eurasia and a larger population size compared to South and Central America. A comparison between these regions, however, suggests a weaker role for population because the technological and economic conditions in tropical America prior to 1500 were not behind the conditions in sub-Saharan Africa, see, e.g., Chandler [10].

3 New evidence and new mechanisms

The results presented thus far, while not definite, suggest that the historical variation of long-term economic outcomes may not be caused primarily by population changes and technological feedbacks. In part, the previous findings also highlight implicitly exogenous differences in endowments and geography as a ‘third’ factor behind economic and demographic changes. In this section, I bring new data to bear on the dynamics of human populations in the past and entertain the possibility that population has, on the whole, been unfavorable to long-term development in sub-Saharan Africa. I also examine new mechanisms by which past population size may influence economic outcomes that extend beyond the technological considerations presented in the previous section. These mechanisms seem especially relevant for sub-Saharan Africa as they recognize Africa’s unique heritage with hunter-gathering and the evolutionary history of the continent. The usual disclaimer applies: because little is known with absolute certainty about past economic and demographic conditions, the discussion that follows is conjectural.

I first review recent evidence on past human demography that relies on the pattern of genetic diversity within human populations and then examine the implications derived from these findings for the analysis of population and economic themes. Anthropological analyses of human genetics have shed light on important historical questions such as the divergence of humans from other hominoids, the patterns of migration into Europe associated with the Neolithic agricultural revolution, the origin of Polynesian populations and the settlement of the New World (see Jobling et al. [31] and Relethford [59] for technical analyses. Cavalli-Sforza and Bodmer [8] and Cavalli-Sforza et al. [9] are classical references on human genetics).

3.1 A model of population and diversity

In this sub-section I review a basic model of population and diversity. The model serves to examine past demographic differences using current observations and it is useful to describe the association between population and general aspects of ‘diversity.’ That is, the model that follows describes one way in which diversity is produced in stationary populations.

The underlying principle that connects current genetic diversity with past demography is straightforward. Species develop over long periods of time and as they develop, they accumulate genetic variations. Therefore, a large population in the past implies a larger diversity in the present whereas a small population in the past, i.e., one brought about by a population decline, implies smaller diversity (Relethford [57] and Jobling et al. [31]).

The previous intuitive ideas can be formalized mathematically. The model that I outline in the following discussion is based on Cavalli-Sforza and Bodmer ([8], 504-505). To describe how genetic diversity is produced, consider a population of constant effective size N^e and assume individuals mate randomly within such population.¹⁷ These assumptions imply that the genetics of the next generation can be viewed as a sampling process with replacement.

Let F_t represent the fraction of the population that possess two identical forms of a given gene with each form (or allele) inherited from one parent. F_t defines homozygosity or identity by descent. $H_t \equiv 1 - F_t$ represent heterozygosity or genetic diversity. Two randomly drawn genes from the offspring generation $t + 1$ will share the same form if they are copies of the same gene in generation t or if they are copies of different but already identical genes in t . One way to understand this logic is to relate genetic changes to the transmission of last names in most societies. Two individuals share the same last name if they have the same father or if they have different fathers, but those fathers already have the same last name.¹⁸

¹⁷Effective population size is a genetic concept that measures the number of breeding individuals who have the same amount of genetic dispersion than the population under consideration. That is, it is the number of genetically representative individuals. The Appendix contains a detailed discussion of these aspects.

¹⁸For example, the Y-chromosome is transmitted only by fathers while mtDNA is only transmitted

Because there are N^e parents (and $2N^e$ genes), the probability of carrying identical genes (i.e., of having the same father) is $1/2N^e$. The second event takes place with a probability $(1 - 1/2N^e) F_t$ (i.e., having different fathers but with the same last name). This generates the following recurrence:

$$F_{t+1} = \frac{1}{2N^e} + \left(1 - \frac{1}{2N^e}\right) F_t.$$

In the absence of mutations, all genetic diversity is lost in the steady-state (i.e., $F^* = 1$ or $H^* = 0$). Assuming that all types of neutral mutations μ are equivalent and produce genes that never existed before (the infinite-sites model), two genes will have the same form if there is no mutation in the path that connects them. Thus,

$$F_{t+1} = (1 - \mu)^2 \left[\frac{1}{2N^e} + \left(1 - \frac{1}{2N^e}\right) F_t \right], \quad (6)$$

with $(1 - \mu)^2$ representing the probability that neither of the two genes has mutated in the past generation. Ignoring small terms, the steady-state probability that two individuals share the same gene can be approximated by: $F^* \simeq 1/(1 + 4\mu N^e)$, and the amount of genetic diversity is:

$$H^* = \frac{4\mu N^e}{1 + 4\mu N^e} \simeq 4\mu N^e, \quad (7)$$

which is an increasing function of effective population size N^e and the mutation rate μ .

Two implications from the previous expression are the following: first, larger populations are expected to have higher genetic diversity. If populations are very large (as microbial organisms) or if mutation rates are high, heterozygosity will approach one. Second, a transitory reduction in the effective population size reduces the amount of genetic diversity in the population. Diversity will reach H^* again because F_t is a stable difference equation.

by mothers. Nuclear DNA is inherited from both parents. Generalizations that allow for differences in sex ratios are discussed in Cavalli-Sforza and Bodmer ([8], chapter 8). Further, I have assumed that population is constant to simplify the discussion of the model. This aspect can be relaxed without major changes in the conclusions.

3.2 Overview of empirical findings about human diversity

Empirical measures of diversity show that humans are less diverse than other hominoids and that genetic diversity in human populations is allocated mostly within rather than between populations. Empirical analyses have also found that populations in Africa are the most genetically diverse group, see, e.g., Jorde et al. [35], Jorde et al. [34], Relethford [59], Relethford ([58], Figure 5.2), and Tishkoff and Verrelli [70]. For a survey of the geographical distribution of genetic diversity see Jobling et al. ([31], section 8.5.2). The Appendix presents a brief overview and discussion of genetic diversity.

These patterns of genetic diversity have been primarily used in anthropology to examine the origins of modern humans.¹⁹ Two interpretations have been offered for the high levels of genetic diversity within Africa: first, current genetic diversity may be interpreted as reflecting an exclusive African origin of the human population, see, e.g., Cann et al. [7].²⁰ Alternatively, diversity may be due to differences in past population size as predicted by equation (7), see, e.g., Relethford [57], Relethford and Jorde [56], and Relethford and Harpending [55]. The distinction between both views is important for the debate on human origins but a precise distinction in favor of size or ‘molecular age’ is not important for the purpose of this paper. Anthropological analyses of human populations suggest that sub-Saharan Africa had the largest and/or the oldest human populations.

Many other characteristics share the patterns observed in genetic diversity. Craniometry also suggest more diversity in sub-Saharan Africa, see Relethford and Harpending [55]. High African diversity is also featured in body size variation. Central Africa hosts one of the tallest and the shortest populations of the world: the Tutsi and “Pygmy”

¹⁹Crudely described, the debate on human evolution is centered on whether evolution takes place as adaptations within a specie or by speciation. The most extreme version of the “African replacement” hypothesis assumes that speciation generated modern humans as a separate specie in East Africa, as early as 150KYA, from where they expanded and fully replaced the other human forms that existed at the time. The “multiregional evolution” view assumes similar evolution within each region of the world. Jobling et al. [31] and Relethford [59] provide summaries and references on the different views.

²⁰Additional support for the importance of Africa in human evolution comes from the observation that in nearly all human genetic systems there is a primary division between African and non-African populations. That is, interpopulation genetic distances cluster in two major groups of African and non-African populations, see Jobling et al. [31] and Cavalli-Sforza et al. [9]. If correct, an exclusive African origin of the human population suggests that populations living outside of Africa before 150KYA were *not* ancestral to living humans.

tribes. Other measures of quantitative traits such as skin color also lend support to higher African diversity, Relethford ([58], Figure 5.4). Language and genetic maps show considerable concordance in human populations (see Cavalli-Sforza et al. [9]). Linguistically, Africa is also the most diverse continent. Sub-Saharan Africa, a relatively restricted geographical area, contains four distinct and very diverse language families whereas in North Africa, Europe, and Asia there is a single Eurasic family. In the Americas, there is also a single linguistic family, the Amerind, see Ruhlen ([62], Map 8). Diversity within Africa has also been highlighted in economic analyses of ethnolinguistic fractionalization. For example, 14 of the world’s 15 most diverse countries are in Africa (the non-African country being India), see, e.g., Easterly and Levine [17].

3.3 Implications for economic development and population theory

The previous sub-section highlighted the genetic distinctiveness of sub-Saharan Africa. This sub-section explores the implications of this special pattern for economic development and population theory. This sub-section also contrasts the analysis with previous studies, especially with Galor and Ashraf [24] and Spolaore and Wacziarg [69].

Some implications for population theory. Genetic diversity *per se* is not interesting from an economic or demographic point of view. However, the model sketched above and the previous discussion serves a broader purpose because several attributes coevolve with genes.²¹ For instance, language maps show high concordance with genetic maps as genes and languages in human populations have a common mode of transmission and mutation, see, e.g., Cavalli-Sforza et al. [9]. Further, other forms of ‘diversity’ may be randomly manufactured as in equation (7).

²¹It is important to avoid misunderstandings in the study of genetic homogeneity. Genetic homogeneity is neither good nor bad and it provides no indication of genetic inferiority. Homogeneity, has advantages as well as disadvantages. On one hand, genetic homogeneity means that the population lacks deleterious genes. On the other hand, homogeneity increases susceptibility to disease. For example, while Africans (whose genetic diversity is large) have some resistance to malaria by the sickle cell trait, the Americas before Columbus (one of the more homogeneous regions genetically speaking) were apparently free of a number of genetically transmitted diseases, see Mann ([45], 103-105).

Diversity, whether genetic, linguistic, or of any other form influence economic outcomes in a multiplicity of ways. For example, the link between population size and genetic diversity in equation (7) is quite close to Kuznets [39] view in which technological innovations take place *randomly* within a population. According to Kuznets [39], if talent is randomly distributed in the population, an increase in population size will increase the absolute number of “geniuses” or talented individuals who will in turn increase the production of knowledge. Thus, the creation of “new knowledge” may also be described in ways analogous to (7). That is, as in the case of the creation of “new genes” by mutation, a larger population may create new varieties of useful knowledge by mutation. Further, in evolutionary analyses of technological change, new technologies are essentially a manifestation of diversity, see, e.g., Nelson and Winter [52].

Despite the possibility of positive effects, empirical assessments of the role of diversity on actual economic outcomes are typically negative.²² As I have stressed, diversity may be a consequence of past demographic differences, see (7). Thus, past population may have an indirect influence on current economic conditions beyond Malthusian considerations based on diminishing returns and competition for resources. That is, past population may have an independent role as a contributor to diversity. This new role is especially relevant for sub-Saharan Africa. The fact that human populations had an early origin in Africa implies that these populations have acquired more ‘diversity.’ As I will discuss later on, an early origin also implies that societies in Africa have accumulated more experience as hunter-gatherers than comparable regions in other parts of the world.

Although only indirectly related to diversity, there is another potential demographic mechanism that has also been unfavorable to sub-Saharan Africa. It is known that disease environments in Africa differ markedly from those in temperate areas. These differences are perhaps not surprising since most diseases in Eurasia are consequence of agricultural

²²Current studies have examined measures of genetic, religious, and ethnolinguistic diversity and their effects on outcomes such as civil conflict and modern economic performance. Whereas in principle diversity may be a positive or negative influence on economic outcomes, the majority of empirical assessments has found negative effects, especially in sub-Saharan Africa, see, e.g., Alesina et al. [1], Easterly and Levine [17], Miguel and Gugerty [48], Montalvo and Reynal-Querol [50], and Spolaore and Wacziarg [69]. The mechanisms behind differences in diversity and the reasons for why diversity may lead to unfavorable outcomes have been much less studied in the literature.

developments and the proximity of domesticated animals, see, e.g., Diamond [16].

Disparities within tropical areas are also remarkable as most of the significant infectious tropical diseases originated in sub-Saharan Africa but not in tropical America, see, e.g., Wolfe et al. [73]. As I have just noted, sub-Saharan Africa has greater diversity in many aspects. This greater diversity extends to primates, monkeys, and other small animals which have served as source and reservoir for human tropical diseases. That is, sub-Saharan Africa produced more ancestral pathogens than South and Central America and these pathogens have survived for longer periods than in any other region. The survival of these diseases is in part a consequence of Africa's past 'demography.' Humans have had more and longer-lasting interactions with Old World primates than with the genetically distant New World primates, Wolfe et al. [73]. Some of these interactions have also led to 'genetic adaptations' that protect individuals from infectious diseases such as the sickle cell gene which is especially prevalent in areas of Africa with endemic malaria. This role of past human populations (including the Old World primates) as a potential factor that has worsened disease environments in Africa differs from the direct role of population in production or technology creation.

Previous use of genetic information in analyses of economic development.

Despite the fact that genetic diversity conveys no economic advantage directly, genetic information has been used to draw empirical conclusions about economic growth. Galor and Ashraf [24] considered a detailed empirical analysis of the relationship between genetic diversity within a given society and economic development in pre-modern economies. Their main dependent variable is the population density around 1500. They measure genetic diversity in a way consistent with equation (7) and find a hump-shaped relationship between genetic diversity and population density. This relationship, robust to the inclusion of controls for agricultural origins and land quality, implies that diversity had positive and negative influences on the development of pre-modern societies.

But Galor and Ashraf [24] did not recognize the relationship between diversity and past demography. As the previous discussion has pointed out, diversity arises in response to interactions within and between populations. In this sense, the shape uncovered by Galor

and Ashraf [24] can be rationalized on pure demographic grounds. In 1500, the major centers of agricultural production were Asia, South and Central America, and sub-Saharan Africa. Because the settlement of the New World began much later than for any other continent, societies in the New World were genetically homogeneous. As I just noted, Africa, on the other hand, had much higher levels of genetic diversity. Because South and Central America and sub-Saharan Africa were similar in terms of their demography in 1500 (see Table 2), but were at opposite sides of genetic diversity, it is natural to expect a hump-shaped relationship between genetic diversity and population density for these regions. (The controls in the OLS regressions in Galor and Ashraf [24] essentially serve to compare genetic diversity within tropical areas.) Consistent with my previous discussion, continent dummies drastically weaken the hump-shaped relationship and the role of genetic diversity in Galor and Ashraf [24], see their Table 3.²³

A separate study has been undertaken by Spolaore and Wacziarg [69]. They considered an alternative comparison of “genetic distance” between populations (not within populations as I have considered thus far). Spolaore and Wacziarg [69] also considered genetic diversity as a measure of elapsed time between populations and argued that genetic homogeneity facilitates technological diffusion because it reduces cultural barriers to adoption. Cavalli-Sforza et al. [9], the main source in Spolaore and Wacziarg [69], also suggest high levels of genetic diversity between African societies so this paper and Spolaore and Wacziarg [69] are complements in many dimensions. That is, in both papers, the high levels of genetic diversity within and between African societies are a distinctive aspect of the analysis.²⁴

²³Separately, the R^2 of the OLS regression in Galor and Ashraf [24] explains 42 percent of the variation in population densities in 1500. By equation (7), these result should be little surprising. There is a strong theoretical and empirical link between population size and genetic diversity so a regression between these variables provides a good fit because a higher population is a factor that produces diversity. This association is the reverse of the causality assumed in Galor and Ashraf [24]. That is, higher population size leads to high genetic diversity. In fact, the results presented by Galor and Ashraf [24] make the case of this paper stronger and provide additional empirical support to my claim that diversity proxies past demography.

²⁴Spolaore and Wacziarg [69] considered a wide variety of geographic and cultural factors that could account for the effect of genetic distance on economic variables. Despite the controls, genetic distance remains important in explaining income differences today. They also studied the diffusion of industrialization within Europe and showed that genetic homogeneity also mattered within Europe. Genetic differences also had predictive power for understanding income differences in 1500.

Spolaore and Wacziarg [69], however, focused on cultural barriers to the diffusion of innovations. This provides a partial view of the causes and many potential effects of diversity. For example, the findings in Spolaore and Wacziarg [69] help explain why European industrialization first diffused into homogeneous regions such as North America and Australia. But both of these regions were homogeneous in 1500 because they had a small population size since farming was not adopted in any of these regions. In other words, differences in demography and past technological conditions may be behind the diversity measures used by Spolaore and Wacziarg [69]. Further, diversity may not always be unfavorable for economic development and the mechanisms by which diversity influences economic outcomes are largely unexplored. For instance, the analysis of Spolaore and Wacziarg [69] may also provide insights for the origin of European industrialization. In a broad scale, Europe itself was perhaps less diverse than Asia since Europe had a lower population size and European populations were in part descendants from populations in the Near East.²⁵ Thus, the fact that industrialization first originated in Europe may be a consequence of their low levels of ‘diversity.’

4 An alternative view of long-term technological change

The preceding discussion leads to a related point that perhaps has not been stressed enough in current debates on long-term development. It is known that agriculture had several independent origins. Agriculture originated in Asia, South and Central America, and sub-Saharan Africa, see, e.g., Smith [68] and Harlan [26].

Agriculture did *not* originate independently in Europe, Australia, and North America. Because agriculture did not originate in what are now the wealthiest regions in the world, the *absence* of agricultural origins is perhaps as important as the *origin* of agriculture for understanding current patterns of the distribution of income in the world. Similarly,

²⁵The contribution of Neolithic farmers to the gene pool of modern Europeans is still debated. The contribution varies from around a quarter or less to more than half in regions closer to the Near East (see Relthford [59] and Cavalli-Sforza et al. [9]). The interpretation of the genetic evidence suggests that diffusion of ideas was as important as mass-migration in the diffusion of farming (see Richards [60] for a detailed review of genetic traces of population movements in Europe. Richards [60] suggests that movement of ideas were more important than movements of people).

human populations were larger (or older) in what now is the poorest region of the world. Whereas these broad patterns may just be historical coincidence, they are also consistent with a view in which past technologies and past population size are a ‘barrier’ for radical technological changes.

Technological leadership is determined by a multiplicity of factors. In models of endogenous growth, past technology and population size always reinforce leadership, see (1). Many of the implications of differences in past demography and technological conditions have been studied in past technological transitions with mixed success. For example, archaeologists and prehistorians have debated the role of ‘population pressure’ in agricultural origins. Assessments of a population pressure are less favorable nowadays, see, e.g., Harlan [26]. Instead, alternative views suggest that climatic change was important for agricultural origins, see, e.g., Harlan [26]. (This view would be consistent with the high degree of synchronization in the adoption of farming across separate regions of the world.)

Separately, past technological leadership would have failed to predict Europe’s industrialization. Among the many authors that favor this view, Diamond ([16], 409-410) argues:

A historian who had lived at anytime between 8500 B.C. and 1450 A.D., and who had tried then to predict future historical trajectories, would surely have labeled Europe’s eventual dominance as the least likely outcome, because Europe was the most backward of those three Old World regions for most of those 10,000 years.²⁶

An alternative view to models of endogenous growth are models that highlight the advantages of ‘backwardness.’ For instance, models in which advances in one technology

²⁶It continues with: “From 8500 B.C. until the rise of Greece and then Italy after 500 A.C., almost all major innovations in western Eurasia – animal domestication, plant domestication, writing, metallurgy, wheels, states, and so on – arose in or near the Fertile Crescent. Until the proliferation of water mills after about A.D. 900, Europe west or north of the Alps contributed nothing of significance to Old World technology or civilization; it was instead a recipient of developments from the eastern Mediterranean, Fertile Crescent, and China.”

reduce the profitability of alternative technologies.²⁷ One example of such view is Brezis et al. [5]. To highlight the difference with endogenous growth models, consider again equation (1). Integrating equation (1), also a Bernoulli differential equation, gives:

$$A(t; t_0) = A(t_0) [(1 - \phi)\theta]^{1/(1-\phi)} \left[\int_{t_0}^t N(s)^\gamma ds \right]^{1/(1-\phi)}. \quad (8)$$

In the previous equation $A(t; t_0)$ represents the level of technology at date $t \geq t_0$ for a technology introduced at date t_0 . Besides the role of exogenous determinants θ , technology $A(t; t_0)$ in equation (8) is determined by $A(t_0)$ and $\int_{t_0}^t N(s)^\gamma ds$. The first term is the initial level of this technology, e.g., $A(t_0; t_0)$, while the second measures the accumulated ‘experience’ with this technology.

In models of endogenous growth, a higher value of $A(t_0)$ or more experience reinforce leadership, i.e., $A(t; t_0)$ is an increasing function of $A(t_0)$ and $\int_{t_0}^t N(s)^\gamma ds$ (as long as $\phi < 1$). A leapfrogging view considers that past technologies and experience rather than generating an advantage, are a disadvantage when a major technological change takes place.²⁸ For example, assume that a new technology is made available at time $T > t_0$. Productivity in the old technology is given by $A(T; t_0)$ in equation (8). Productivity in the new technology is $\tilde{A}(T; T)$ as there is no experience in such a technology. As in Brezis et al. [5], there are advantages in $\tilde{A}(T)$ because $\tilde{A}(t; T) > A(t; T)$, for $t > T$. That is, if both technologies had the same experience, $\tilde{A}(t)$ would dominate. If a comparative advantage guides the adoption or the allocation of time between both technologies, economies without experience in $A(t)$ will first adopt or invest in technology

²⁷No other technological revolution has received more attention than agriculture and some inferences can be drawn from current hunter-gatherers. It is clear that present-day hunter-gatherers know how to cultivate crops. Agricultural systems, however, require more work for a unit of food and “neither agricultural nor industrial man has anything like the leisure time of hunters and gatherers,” see Harlan ([26], 40-43). One can argue that the accumulated experience in hunter-gathering would make technologies for permanent farming much less attractive. Mokyr ([49], chapter 6) presents an additional discussion of resistance to technology based on rigidities in the economic system, cultural, religious, and political factors. Abundant examples of barriers of adoption and innovation in economic history are also discussed in detail by Mokyr ([49], chapter 6).

²⁸A well-known study is Alexander Gerschenkron’s [25] theory of relative backwardness. Gerschenkron [25] argued that economic backwardness before industrialization in Europe (i.e., in Russia, Italy, and Germany) made their post-industrial growth faster.

$\tilde{A}(t)$ and, as time goes by, these economies will overtake advanced regions.

In the model, an early origin t_0 , a large initial population size $N(t_0)$, and a large initial technological advantage $A(t_0) [(1 - \phi)\theta]^{1/(1-\phi)}$, discourage the adoption of “radical” technologies. The specific mechanisms by which the adoption of radical forms of technological change is delayed have been only partially explained in this paper and they need further documentation and study, see, e.g., Mokyr [49]. These mechanisms are subsumed into adverse ‘external effects’ of past population and technological change. Yet, as in Kremer [38], population growth is beneficial for “normal” technological change. In addition to the previous distinction, a view that allows for changes in leadership provides transitional differences in economic and technological conditions as well as the possibility of ‘catching-up’ based on the receptivity to new technologies and social change.

5 Concluding remarks

In this paper, I re-examined the empirical relationship between population growth and long-term economic development to further the discussion initiated by Kremer [38]. My re-assessment of this existing literature has been stimulated partly by biases in current time series and cross-sectional assessments and partly by new findings derived from the anthropological analysis of human genetics. In particular, I showed that in current populations, physical, linguistic, and genetic diversity are higher in Africa than in any non-African region. I also argued that the high levels of African diversity signal a large population in the past or an earlier origin, see, e.g., Cavalli-Sforza et al. [9], Eswaran et al. [19], Jobling et al. [31], and Relethford [58].

The main theoretical implication that deserves mention here is the fact that demographic influences may play a role as ‘producers’ of diversity. That is, many individual and social attributes coevolve with genes or share a common mode of transmission and mutation. As these mutations are larger in larger populations, diversity may be linked to past demographic forces. The influence of diversity may be positive or negative as the preceding discussion has shown (see also Galor and Ashraf [24]). Yet, the current state

of empirical assessments points toward a negative role of diversity on modern economic outcomes, see, e.g., Alesina et al. [1], Easterly and Levine [17], Miguel and Gugerty [48], Montalvo and Reynal-Querol [50], and Spolaore and Wacziarg [69]. In part, these influences may reflect past demographic aspects which do not necessarily represent Malthusian considerations of resource scarcity.

In the paper, I also described a long-term pattern of changes in technological leadership and argued that such a pattern cannot be easily interpreted through models that predict persistence of leadership. The theoretical argument advanced in this paper can be summarized by looking at tool making, agriculture, and industrialization. Since Deevey [14], these technologies have been seen as the fundamental drivers of human population growth, see, e.g., Livi-Bacci [42].

The main highlights of the changes in technological leadership I described are the following: industrialization had a single origin in Europe and it diffused initially to regions that lacked indigenous agriculture, Australia and North America. Whereas Asia had several independent origins of agriculture (e.g., the Near East and China), agriculture did not originate in Europe. The hunter-gatherers in Europe acquired agriculture through the diffusion of ideas and populations from the Near East (Richards [60]). Agriculture had many other independent origins including the New World and sub-Saharan Africa. However, the typical advances of agriculture were not observed in sub-Saharan Africa. State formation and urbanization were far less prevalent in sub-Saharan Africa than in South and Central America or in Eurasia (Chandler [10]). It is also known that contact with the outside world was sufficient to expose African societies to Eurasian technologies (even more considering the geographic isolation of the New World). Not only did sub-Saharan Africa have repeated contact with the rest of the Old World, but Africa also had a larger/earlier population and perhaps earlier advances in stone tools technologies (Mellars [47]).²⁹

²⁹It is perhaps interesting to contemplate an alternative “natural experiment” to study the role of population on development. Holland [30] discusses a counterfactual as part of a series of “what if’s” in human history. She considers the fate of Europe if Ogadai Khan had not died on the eve of the Mongol siege of Vienna in 1242 and estimates the impact using Bagdad as a “control.” According to Holland [30], European cities would have replaced learning with religious prejudice and would have fallen

Further research is needed to clarify the possible links between the high levels of ethnic, linguistic, physical, and genetic diversity in Africa with past populations and with current economic outcomes.³⁰ Despite the qualifications, all of which seem irremediable in the short run, three key “facts” discussed in this paper seem to be of interest. First, that populations in sub-Saharan Africa were larger and/or had an earlier origin and that despite of this, current economic conditions in the continent are worse than in any other part of the world. Second, that a wide variety of measures of diversity which may be seen as a consequence of past demographic influences are higher for societies in sub-Saharan Africa. And third, that industrialization took place in and diffused into the few geographical areas where agriculture did not originate. In a broad generalization, these observed changes in economic leadership suggest a leapfrogging pattern in which “success breeds failure.”

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into the fundamentalism that the Islamic world experienced after the Mongol invasions. The inferences that can be drawn from this experiment, however, are somewhat limited. If Ogadai Khan’s death saved Europe, the Black Death visited only a century after the Mongol’s retreat. Since Europe faced a severe depopulation by the Black Death, the Mongol’s retreat only saved Europe temporarily.

³⁰On the question of why Europeans were the ones to colonize sub-Saharan Africa, Diamond ([16], 397-398) writes: “That it was not the other way around is especially surprising, because Africa was the sole cradle of human evolution for millions of years, as well as perhaps the homeland of anatomically modern *Homo sapiens*. To these advantages of Africa’s enormous head start were added those of highly diverse climates and habitats and of the world’s highest human diversity.”

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6 Appendix A: On increasingly increasing growth

Kremer [38] introduced a model of population growth whose solution is a nonlinear differential equation subject to a *blow-up* not commonly studied in economics. In this Appendix I provide additional remarks on the mathematical nature of increasingly increasing growth and blow-ups.

A blow-up occurs when a nonlinear differential equation escapes to infinity in finite time because the solution (or in some cases its derivatives) becomes infinite due to the cumulative effect of the nonlinearities. The simplest example of a blow-up occurs in a nonlinear (autonomous) differential equation given by:

$$\frac{dx(t)}{dt} = f(x(t)), \quad (9)$$

with $f(x) > 0$ for $x > 0$ and smooth; at least $\mathcal{C}^1([0, \infty))$. The necessary and sufficient conditions for the occurrence of blow-up for any solution of an autonomous differential equation above are described in the next Theorem (see Samarskii et al. [63] for further developments):

Theorem 1 *For any $x(t_0 = 0) > 0$, any solution of equation (9) is globally bounded (i.e., does not blow-up) if and only if the following (Osgood) condition*

$$\int_1^\infty \frac{ds}{f(s)} = \infty, \quad (10)$$

is satisfied.

Proof. Let $x(t_0 = 0) = M > 0$. $x(t)$ is determined by the following equation:

$$\int_M^{x(t)} \frac{ds}{f(s)} = t,$$

so if condition (10) is satisfied, $x(t)$ will be defined for all $t \in (0, \infty)$.

That the previous condition is necessary can be seen as follows. Assume that (10) is not satisfied. Then, there exists a t^* given by:

$$t^* = \int_M^\infty \frac{ds}{f(s)} < \infty,$$

such that $x(t) \rightarrow \infty$ as $t \rightarrow t^*$. ■

One can easily show that in Kremer [38], $t^* = N(t_0)^{1-\alpha}/\theta(\alpha - 1)$, see equation (5). Hence, if $\alpha \leq 1$ there is no blow-up. This is an alternative test for increasingly increasing growth made popular by Foerster et al. [20] in the 1960s.

Blow-ups are also featured in some endogenous growth models. As an example, consider the well-known Ak model of economic growth under positive productivity growth at a rate θ ; that is, $dA(t)/dt = \theta A(t)$. The production function is given by: $y(t) = A(t)k(t)$ and the evolution of capital, under simple Solow savings rules, is:

$$\frac{dk(t)}{dt} = sA(t)k(t) - nk(t) > 0,$$

with constant population growth n and savings rate s . Income per-capita $y(t)$ will be $y(t) = y(t_0) \exp\{(\theta - n)t + sA(t_0) (\exp\{\theta t\} - 1) \theta^{-1}\}$. This function is hyper-exponential so income will increase at increasing rates. The Taylor expansion of the exponential with high order members being neglected, gives the following dependence

$$y(t) \simeq \frac{y(t_0)}{1 - [sA(t_0) + \theta - n]t}, \text{ with } t^* = [sA(t_0) + \theta - n]^{-1}.$$

7 Appendix B: On genetic diversity

The findings regarding human genetic diversity, while still debated, have made extensive use of DNA sequences.³¹ A measure of gene diversity or heterozygosity that corresponds to the theoretical notion derived in (7) counts the differences in sites between any two DNA sequences by $H = 1 - \sum_i (n_i/n)^2$, in which (n_i/n) represents the frequency of copies of type i and $n = \sum_n n_i$ is the number of sites. For example, if a sequence has ten sites and one differs between the two sequences, $H = 1 - (0.9)^2 = 0.19$. When more than two sequences are being compared, genetic diversity employs mean pairwise differences. In that case, if there are m sequences, there will be $m(m - 1)/2$ potential comparisons. The mean pairwise difference is represented by: $\pi = m(m - 1) \sum_{i < j} d_{ij} (n_i/n) (n_j/n)$, with d_{ij} as the proportion of sites that differ between the i -th and j -th sequences, see Relethford [58]. For example, Table A1 presents a selection taken from Tishkoff and Verrelli [70] for two of the most common genetic locus: mtDNA and nuclear DNA (see also Relethford [58], Figure 5.2).

The previous analyses are subject to caveats. The basis for the association between popula-

³¹DNA is a molecule genetically transmitted and composed of combinations of four chemical units or bases: A (adenine), T (thymine), G (guanine), and C (cytosine). A DNA sequence is a succession of letters that represent the structure of the DNA molecule or strand. Every individual can be identified with a DNA sequence so differences in sites serve to calculate differences between individuals or species. DNA sequences are very long so analyses break sequences into small pieces or locus such as mitochondrial DNA (mtDNA) and nuclear DNA.

tion and diversity assumes neutral mutations or changes not driven by natural selection. Support for population expansions has mostly been limited to mtDNA and Y-chromosome data.³² Moreover, for the purpose of this paper, it is important to notice that measures of effective population size N^e do not correspond exactly to census estimates of population levels so the inferences one can draw from genetic findings is limited (see Hawks et al. [29]). Effective population size varies with the number and gender ratio of parents (among other aspects). Variations predicted by effective size, however, are not inconsistent with census estimates of population (Relethford [59]).

Table 3. Genetic diversity (mean pairwise differences) in populations in the Old World.

Region	Mitochondrial DNA		Nuclear DNA	
	(<i>a</i>)	(<i>b</i>)	(<i>c</i>)	(<i>d</i>)
Africa	0.022	0.030	0.076	0.085
Europe	0.009	0.010	0.045	0.077
Asia	0.015	0.011	0.047	0.075

Source: Tishkoff and Verrelli ([70], Table 2). (*a*)-(*d*) denote different coding regions of DNA, (*a*) refers to marker system HVS-I, (*b*) to HVS-II, (*c*) to (1q24), and (*d*) to marker system (22q11). The number of chromosomes in mtDNA for Africa, Europe and Asia is: 72, 120, and 63 respectively. For nuclear DNA the number of chromosomes is 20 in all instances except for Europe in column (*c*) that has 21 chromosomes.

³²Since natural selection usually affects a single genetic locus, the variations in mtDNA consistent with population changes are often considered as outcomes of positive selection. For instance, nuclear DNA has weaker or no signals of population expansion (Hawks et al. [29] and Eswaran et al. [19]). In Table A1, diversity was higher for mtDNA than for nuclear DNA. Since nuclear DNA is the result of contributions of fathers and mothers, while the genetic transmission in mtDNA does not allow for recombination (as fathers have zero contribution to mtDNA), there could be selection effects responsible for the high diversity seen in Africa. In general, it is difficult to differentiate selective from demographic factors but evidence for selection is not definite. A size or an age difference in Africa is observed in selective-neutral sites and in fossil and archeological records from anatomically modern humans in Africa (see Reich and Goldstein [54], Mellars [47], and Tishkoff and Verrelli [70] for additional analyses).