

# War and Relatedness\*

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## Abstract

We develop a theory of interstate conflict in which the degree of genealogical relatedness between populations has a positive effect on their conflict propensities because more closely related populations, on average, tend to interact more and develop more disputes over sets of common issues. We examine the empirical relationship between the occurrence of interstate conflicts and the degree of relatedness between countries, showing that populations that are genetically closer are more prone to go to war with each other, even after controlling for a wide set of measures of geographic distance and other factors that affect conflict, including measures of trade and democracy.

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# 1 Introduction

Militarized conflicts have been among the most dramatic and costly events in human history, and at the center of an enormous historical and political literature for centuries.<sup>1</sup> In recent years, economists and political scientists have started to use formal theoretical tools and systematic empirical analyses to provide insights into the determinants of conflicts and wars.<sup>2</sup> Great progress has been made in our understanding of the effects of economic and political factors - such as trade and democracy - on the likelihood of international conflict.<sup>3</sup> Nonetheless, wars continue to be elusive phenomena, and fundamental questions about their roots remain open. A key question, which has not yet received a satisfactory empirical answer, is whether armed conflicts are more or less likely to emerge between populations that differ along cultural and historical dimensions, such as ethnicity, language, and religion.

In this paper we present a new theoretical approach, new data and new empirical findings shedding light on the determinants of international conflict. We use information about human genetic distance - a summary statistic of very long-run historical and cultural relatedness between populations - to explore the relationship between kinship and conflict.<sup>4</sup> Genetic distance measures

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<sup>1</sup>For recent salient examples, see Blainey (1988), Keegan (1984), Ferguson (2006) and Nye (2008).

<sup>2</sup>Classic contributions are Schelling (1960) and Boulding (1962). More recent economic formalizations of conflict and wars include, for example, Garfinkel (1990), Hirshleifer (1991, 1995), Skaperdas (1992), Hess and Orphanides (1995, 2001), Jackson and Morelli (2009). Garfinkel and Skaperdas (2006) provide an overview of the economics literature on conflict. Influential contributions by political scientists on the formal theory of conflict include Bueno de Mesquita and Lalman (1992), Fearon (1995) and Powell (1999). Systematic empirical work on interstate conflict was pioneered by Wright (1942), Richardson (1960) and Singer (1972). For discussions of the recent empirical literature on the correlates of war see Vasquez (2000) and Schneider, Barbieri and Gleditsch (2003).

<sup>3</sup>The liberal peace view that trade and democracy should reduce the risk of war goes back to Montesquieu (1748) and Kant (1795), and has been the subject of a vast literature (e.g., see Oneal and Russett, 1999a and Russett and Oneal, 2001). Contributions on the empirics of trade and conflict include Polacheck (1980), Oneal and Russett (1999b), Barbieri (2002), and Martin, Mayer and Thoenig (2008), among many others. On the democratic peace hypothesis see, for example, Maoz and Russett (1993), Bueno de Mesquita et al. (1999), Gowa (2000), and Levy and Razin (2004).

<sup>4</sup>Specifically, we use measures of  $F_{ST}$  distance between human populations from Cavalli-Sforza et al. (1994). The measure  $F_{ST}$  was first suggested by the great geneticist and statistician Sewall Wright (1950). Interestingly, Sewall was the older brother of Quincy Wright, the professor of international law who pioneered empirical research on conflict (Wright, 1942). According to Singer (2000): "The story has it that [Sewall] admired Quincy's scholarship and his preoccupation with the scourge of war but lamented the lack of methodological rigor in his work and thus

the difference in gene distributions between two populations, where the genes under considerations are neutral: they change randomly and independently of selection pressure, and thus do not affect traits that directly matter for survival and fitness. Most random genetic change takes place regularly over time, as in a molecular clock (Kimura, 1968). Consequently, genetic distance measures the time since two populations have shared common ancestors - i.e., since they were the same population. In other words, divergence in neutral genes provides information about *lines of descent*: genetic distance is a summary measure of general relatedness between populations. Heuristically, the concept is analogous to 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. Since a very large number of characteristics - including cultural traits - are transmitted across generations over the long run, genetic distance provides a comprehensive measure of long-term cultural and historical distance across populations.

This paper's main result is that, surprisingly, genetic distance reduces the risk of conflict. Populations that are more closely related are more likely to engage in interstate conflict and wars, even after controlling for a wide range of geographic measures, measures of linguistic and religious distance, and other factors that affect interstate conflict including trade and democracy. These findings are consistent with a simple theoretical framework in which the degree of genealogical relatedness between populations has a positive effect on their conflict propensities, because closely related populations, on average, tend to share common traits and preferences, to interact with each other more, and to care about a larger set of common issues. In principle, such a conflict-generating effect could be offset by countervailing forces. More closely related populations could also have closer ideal points or could be better at coordinating on peaceful equilibria. However, in the data these other forces, if they exist, do not seem to be strong enough to counteract the main effect stemming from the greater set of common issues arising among genetically related populations. In a nutshell, from a long-term world-wide perspective, issues of war and peace are (unhappy) family matters.<sup>5</sup>

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introduced him to the scientific method - hence the fifteen-year project that culminated in the monumental *Study of War* (1942)." We hope that the Wright brothers would appreciate our joining their two lines of research in a study titled "War and Relatedness." The Wrights were a truly remarkable family. As explained in Stock and Trebbi (2003), Sewall and Quincy's father Philip Wright was the inventor of instrumental variable regression (and Sewall might have contributed to that discovery as well).

<sup>5</sup>We apologize to Leo Tolstoy for the double plagiarism.

This paper builds on a large and diverse literature. Broad questions about cultural distance, relatedness and conflict are probably as old as wars themselves, but have received increasing attention following the recent debate over the clash of civilizations (Huntington, 1993) and surging concerns about ethnic conflict within and across countries. For instance, Maynes (1993, p. 5) writes: "Animosity among ethnic groups is beginning to rival the spread of nuclear weapons as the most serious threat to peace that the world faces". Several commentators have wondered whether there may be a general tendency towards violent confrontation between populations that are culturally and ethnically distant. For example, Bremer (2000, p. 27), referring to evidence from social psychology, wonders whether "cultural differences [...] should lead to misunderstandings, stereotyping, clashes of values, and so forth, which in turn promote intercultural fights". This debate can partly be traced back to the sociologist William G. Sumner (1906), who formulated the primordialist view that ethnic dissimilarity between groups should be associated with war and plunder, while societies that are culturally related would tend to fight less with each other. In contrast, others have emphasized instrumentalist views of ethnicity, implying that such differences should not be closely correlated with inter-group conflict (e.g., Merton, 1957). A related hypothesis, proposed but not tested by Gleditsch and Singer (1975), is that the paramount force in conflict is geographical contiguity, and that, controlling for contiguity, one would not find a significant correlation between cultural relatedness and interstate conflict (see Henderson, 1997, for a review of this debate). At the same time, the few scholars who have attempted to estimate the effects of common culture, language or religion on international conflict have found little or no evidence that such variables are systematically associated with a lower probability of conflict.<sup>6</sup> In their influential study on conflict within states, Fearon and Laitin (2003) also found no evidence that ethnically diverse states would be more likely to experience civil conflict.

Our results go further in casting doubts over primordialist theories, as we show not only that their predictions are falsified when applied to interstate conflict, but that the effect goes into the opposite direction. The negative effect of genetic distance holds when controlling for a vast range of geographic measures (contiguity, geodesic distance, latitudinal and longitudinal differences, and other measures of geographic barriers), contrary to Gleditsch and Singer's (1975) hypothesis that

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<sup>6</sup>For example, see Richardson (1960, p. 296), who found no general pacifying effect for either common language or common religion, and Henderson (1997), who, controlling only for contiguity, found a negative association between a measure of religious similarity and interstate conflict, and a positive (but insignificant) correlation between a measure of ethnic similarity and conflict. See also the more recent contribution of Gartzke and Gleditsch (2006).

geographic proximity should be the predominant force in international conflict. It seems that the paramount effect attributed by some scholars to geographic proximity may in part be due to its correlation with cultural and historical relatedness. Once genetic distance is taken into account, geographic variables have smaller effects (although they remain significant). The effect of genetic distance is even higher - and the effects of geography smaller - when we instrument for modern genetic distance using genetic distance between ancestor populations of current countries as of 1500, to account for measurement error and possible endogeneity issues due to post-1500 migrations. The effect of genetic distance is also robust when accounting for other measures of cultural similarity, such as religious and linguistic distance, and for differences in income per capita across countries. Interestingly, religious distance also reduces the likelihood of conflict. This would be hard to rationalize within a clash-of-civilizations view, but is consistent with the predictions of our common-issues model.

Interesting results also emerge when adding measures of trade and democracy, to capture the central predictions of liberal peace theory: extensive bilateral trade links and the extent of democracy among countries in a pair should reduce their propensity to go to war. Not only are the effect of relatedness robust to controlling for trade and democracy variables, but the effects of trade and democracy on conflict hold even after controlling for relatedness. We are therefore able to address one of the most important criticisms of the empirical work on this subject: observers who believe that culturally related countries fight less with each other have often questioned whether there is a direct causal link going from trade and democracy to lower conflict, on the ground that culturally more similar societies also tend to trade more with each other and to share more similar political arrangements (such as democratic regimes). Following this reasoning, the observed low level of conflict might not be the direct effect of trade and democracy, but rather the outcome of deeper cultural similarities (for discussions of this debate see, for example, Schneider, Barbieri and Gleditsch, 2003). In contrast, our estimates provide strong evidence that the premise that closely related populations fight less with each other is incorrect, and hence cannot account for the pacifying effects of bilateral trade and democracy. In sum, our findings validate the liberal view concerning the pacifying effects of trade and democracy.

This paper is the first, to our knowledge, to study the relationship between genetic distance and the likelihood of international conflict and wars.<sup>7</sup> It is part of a small but growing empirical

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<sup>7</sup>In general, there are few formal or empirical analyses of the relations between war and genetic variables. Con-

literature on the connections between long-term relatedness and societal outcomes. In particular, while human genetic distance is not commonly used in the social sciences, recent work has pointed out to its usefulness and predictive power in economics and related areas. Spolaore and Wacziarg (2009) document the relation between genetic distance and differences in income per capita across countries, and provide an economic interpretation in terms of diffusion of economic development from the world technological frontier. Desmet et al. (2007) find a close relationship between genetic distance and cultural differences measured by the World Values Survey, which supports our interpretation of genetic distance as a broad measure of differences in intergenerationally-transmitted traits, including cultural characteristics.<sup>8</sup> More broadly, our paper is related to the evolutionary literature on cultural transmission of traits and preferences (e.g., Cavalli-Sforza and Feldman, 1981; Boyd and Richerson, 1985; Richerson and Boyd, 2004; for economic analyses of cultural transmission, see for instance Bisin and Verdier, 2000, 2001).

The rest of the paper is organized as follows. Section 2 presents a stylized model of conflict and relatedness (an extension is included in Appendix 1). Section 3 introduces our data and methodology. Section 4 discusses the empirical findings. Section 5 concludes.

## 2 A Model of Conflict and Relatedness

War is a very complex and multi-faceted phenomenon, and the relationship between conflict and long-term relatedness is also likely to be quite complex. That's exactly why it is useful to address this topic with the simplest possible framework we can design, keeping in mind that the main goal of our theoretical exercise is *not* to provide a complete and realistic description of actual interstate wars, but to obtain clear, testable implications that can shed light on the facts we will document in our empirical section. Therefore, in this section we present a stylized model

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tributions by economists are Hirshleifer (1998), who provided a theoretical discussion of the evolutionary motives for warfare, including the "affiliative instinct" (partially related to the primordialist view), and, more recently, Bowles (2009), who studies whether warfare among ancestral hunters-gathers may have affected the evolution of group-beneficial behavior.

<sup>8</sup>Desmet et al. (2007) find that European populations that are genetically closer give more similar answers to a broad set of 430 questions about norms, values and cultural characteristics, included in the 2005 World Values Survey sections on perceptions of life, family, religion and morals. They also find that the correlation between genetic distance and differences in cultural values remains positive and significant after controlling for linguistic and geographic distances.

of conflict, which captures the interrelations among international disputes, probability of violent conflict and relatedness in a crude but direct way, abstracting from unnecessary complications while highlighting the simple logic of the main mechanisms. In 2.1 we specify states' preferences over sets of issues, and define the concepts of common issues and disputes between states. In 2.2 we model states' choices over war and peace, and derive the equilibrium conditions under which disputes are resolved peacefully or violently. In 2.3 we link current preferences over issues to intergenerational transmissions of characteristics, and derive the relation between probability of conflict and relatedness.

## 2.1 Preferences and Common Issues

Consider two sovereign states (1 and 2), facing a set of issues  $M$ .<sup>9</sup> Each issue  $k \in M$  can take values  $x(k) \in X(k)$ , where  $M$  and  $X(k)$  are sets of real numbers. Each state  $i$ 's utility function is:

$$U_i = - \int_{k \in M} \alpha_i(k) |x(k) - x_i^*(k)| dk - c_i \quad (1)$$

where  $x(k)$  is the actual outcome for issue  $k$ ,  $x_i^*(k)$  is state  $i$ 's most preferred outcome,  $\alpha_i(k) \geq 0$  is the weight that state  $i$  attributes to issue  $k$ , and  $c_i$  denotes net costs from conflict (which are zero if disputes are solved peacefully, positive otherwise). We introduce the following straightforward definitions:

### Definition 1

Issue  $k$  is a *common issue* between the two states if both states care about issue  $k$  - that is, if and only if  $\alpha_1(k) > 0$  and  $\alpha_2(k) > 0$ .

### Definition 2

A common issue  $k$  is *disputed* when the two states prefer different outcomes  $x_1^*(k) \neq x_2^*(k)$ , where  $\Delta(k) \equiv |x_1^*(k) - x_2^*(k)|$  denotes the difference between ideal outcomes. We say that the two states face a dispute when one or more common issues are disputed.

## 2.2 The Resolution of Disputes

Disputes between the two states are resolved either peacefully or violently. When a dispute is resolved peacefully, either state bears conflict costs ( $c_i = 0$ ,  $i = 1, 2$ ), and the outcome for each

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<sup>9</sup>For simplicity we treat a state - or, equivalently, its government - as a unitary agent.

disputed issue  $k$  is:

$$x(k) = \beta x_1^*(k) + (1 - \beta)x_2^*(k) \quad (2)$$

where  $\beta$  denotes state 1's bargaining power in a peaceful dispute, with  $0 \leq \beta \leq 1$ . In contrast, if a violent conflict occurs the winner sets all disputed issues according to its preferences. Let  $P$  denote the probability that state 1 will win in a violent conflict and set  $x(k) = x_1^*(k)$  for all  $k \in M$ , while with probability  $1 - P$  state 2 will win and set  $x(k) = x_2^*(k)$ .<sup>10</sup> Therefore, the expected outcome of a violent dispute for each  $k$  is:

$$x(k) = Px_1^*(k) + (1 - P)x_2^*(k) \quad (3)$$

Each state can choose whether to "start a conflict" (strategy  $C$ ) or "not to start a conflict" (strategy  $NC$ ). Peace results if and only if both states choose  $NC$ , in which case all issues are settled peacefully, and the payoffs are:

$$U_1(NC, NC) = - \int_{k \in M} \alpha_1(k)(1 - \beta)\Delta(k)dk \quad (4)$$

$$U_2(NC, NC) = - \int_{k \in M} \alpha_2(k)\beta\Delta(k)dk \quad (5)$$

If both states choose  $C$ ,  $P = \pi$ , with  $0 \leq \pi \leq 1$ , and  $c_i = \psi_i > 0$ , and payoffs are:

$$U_1(C, C) = - \int_{k \in M} \alpha_1(k)(1 - \pi)\Delta(k)dk - \psi_1 \quad (6)$$

$$U_2(C, C) = - \int_{k \in M} \alpha_2(k)\pi\Delta(k)dk - \psi_2 \quad (7)$$

If state 1 chooses  $C$  while state 2 chooses  $NC$ , we assume  $P = \pi + \sigma_1$  with  $0 < \sigma_1 \leq (1 - \pi)$ .  $\sigma_1$  captures the increased probability of winning that results from a first-mover's advantage, in the tradition of Schelling (1960). The costs of conflict are  $c_1 = \phi_1 \geq 0$  and  $c_2 = \phi'_2 \geq \psi_2$ ,<sup>11</sup> and payoffs are:

$$U_1(C, NC) = - \int_{k \in M} \alpha_1(k)(1 - \pi - \sigma_1)\Delta(k)dk - \phi_1 \quad (8)$$

$$U_2(C, NC) = - \int_{k \in M} \alpha_2(k)(\pi + \sigma_1)\Delta(k)dk - \phi'_2 \quad (9)$$

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<sup>10</sup>Since utility functions are linear, we will not distinguish between ex-ante (expected) outcomes and ex-post (actual) outcomes in our notation, and denote both with  $x(k)$ .

<sup>11</sup>This assumption means, quite reasonably, that when state 2 enters into a conflict "unwillingly," it will face conflict costs at least as high as if it had decided to start the conflict willingly (i.e., if it had selected  $C$  rather than  $NC$ ).

Analogous equations hold for  $U_1(NC, C)$  and  $U_2(NC, C)$ .<sup>12</sup>

If one state plays  $C$ , the other state is better off to play  $C$  rather than  $NC$ , given that  $\sigma_i > 0$  and  $\phi'_i \geq \psi_i$ , which implies:

**Remark 1**

$(C, C)$  is a Nash equilibrium for all values of the parameters.

However,  $(C, C)$  may or may not be the *unique* Nash equilibrium. If  $(C, C)$  is the unique Nash equilibrium, war occurs with certainty. If  $(NC, NC)$  is also a Nash equilibrium, war may be avoided if both states coordinate on such peaceful equilibrium. Therefore, our model is consistent with Fearon's (1995) discussion of war as emerging from an inability to commit to a Pareto-superior outcome. In our framework both states would be better off if each could commit to play  $NC$ , but they can do that credibly only if  $(NC, NC)$  is also a Nash equilibrium. By substituting  $U_1(NC, NC) \geq U_1(C, NC)$  and  $U_2(NC, NC) \geq U_2(NC, C)$  with the respective expressions above, we have:

**Remark 2**

The peaceful outcome  $(NC, NC)$  is a Nash equilibrium if and only if:

$$(\pi - \beta + \sigma_1) \int_{k \in M} \alpha_1(k) \Delta(k) dk \leq \phi_1 \tag{10}$$

$$(\beta - \pi + \sigma_2) \int_{k \in M} \alpha_2(k) \Delta(k) dk \leq \phi_2 \tag{11}$$

These conditions can be simplified by assuming:

(i) symmetry ( $\sigma_1 = \sigma_2$  and  $\phi_1 = \phi_2$ ).

(ii) peaceful bargaining "under the shadow of war," (that is, a state's bargaining power depends on its strength should negotiations break up), which implies  $\beta = \pi$ .<sup>13</sup>

To simplify notation, define  $\frac{\phi}{\sigma} \equiv \omega$ . The parameter  $\omega$  captures the relative cost of starting a war, increasing in the cost of going to war ( $\phi$ ) and decreasing in the temptation to start a war ( $\sigma$ ). Under (i) and (ii) the results in Remark 2 can be re-written as:

**Remark 3**

<sup>12</sup>When state 1 chooses  $NC$  and state 2 chooses  $C$ ,  $P = \pi - \sigma_2$ , with  $0 < \sigma_2 \leq \pi$ ,  $c_1 = \phi'_1$  and  $c_2 = \phi_2$ , and payoffs are  $U_1(NC, C) = - \int_{k \in M} \alpha_{2k} (1 - \pi + \sigma_2) \Delta(k) dk - \phi'_1$   $U_2(NC, C) = - \int_{k \in M} \alpha_{2k} (\pi - \sigma_2) \Delta(k) dk - \phi_2$

<sup>13</sup>This is a common assumption in the literature. For example, see Alesina and Spolaore (2005).

The peaceful outcome  $(NC, NC)$  is a Nash equilibrium if and only if:

$$\max_{i=1,2} \left\{ \int_{k \in M} \alpha_i(k) \Delta(k) dk - \omega \right\} \leq 0 \quad (12)$$

In contrast, if  $\max_i \left\{ \int_{k \in M} \alpha_i(k) \Delta(k) dk - \omega \right\} > 0$ , conflict  $(C, C)$  is the unique Nash equilibrium.

Therefore, for a given relative cost of starting a war (measured by  $\omega$ ), violent conflict is more likely to be the unique Nash equilibrium the larger are the set of common issues under dispute, and the extent the two states care about those issues. But what is the probability of observing actual conflict between states, and how does it depend on long-term relatedness? We will address these questions in the rest of this section.

### 2.3 Relatedness and the Probability of Conflict

So far we have taken the set of common issues under dispute as given. Now we will consider the relationship between common issues and long-term connections between populations. The general idea is that if preferences over issues are persistent across time, and current populations inherit such preferences with variation from their ancestors, on average populations that are more closely related will be more likely to share a larger range of common issues.

A first step is to assume that each state cares about a mass  $R$  of issues denoted by a compact set of points on the real line: specifically, state  $i$  cares about all issues between point  $a_i$  and point  $b_i > a_i$ , with  $b_i - a_i = R$ , but does not care about issues outside that range. In addition, assume that all relevant issues receive equal weight  $\alpha > 0$  - that is,  $\alpha_i(k) = \alpha > 0$  if and only if  $a_i \leq k \leq b_i$ , while  $\alpha_i(k) = 0$  otherwise. These assumptions allow to characterize the set of issues that state  $i$  cares about by a single real number  $v_i$  (to fix ideas, the mid-point in state  $i$ 's set of relevant issues), which we can interpret as that state's type or fundamental characteristics:

$$v_i = a_i + \frac{R}{2} = b_i - \frac{R}{2} \quad (13)$$

Therefore, a state of type  $v_i$  has the following preferences:<sup>14</sup>

$$U_i = - \int_{v_i - \frac{R}{2}}^{v_i + \frac{R}{2}} \alpha |x(k) - x_i^*(k)| dk - c_i \quad (14)$$

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<sup>14</sup>In this simplified analysis we assume that each state is a unified agent, formed by one population with homogeneous characteristics  $v_j$ . In principle, two states can be of the same type - that is, they may care about the identical set of issues. So we abstract from the possibility that states may include mixed populations with different preferences over issues (however, population heterogeneity within states will be taken into account in the empirical analysis).

Let  $V(i, j) \equiv |v_i - v_j|$  denote the distance between state  $i$  and state  $j$  in their fundamental characteristics.<sup>15</sup> We are now ready to consider conflicts between states over such common issues.

### 2.3.1 Basic Setting

In what follows we derive the probability of conflict under two simplifying assumptions (we present an extension relaxing Assumption 1 at the end of this section, while Assumption 2 is relaxed in Appendix 1):

#### Assumption 1

*The extent of disagreement over all issues is constant and normalized to one - that is,  $\Delta(k) = 1$  for all  $k$ .*

#### Assumption 2

*When  $(NC, NC)$  is a Nash equilibrium, the two states will always coordinate on the peaceful equilibrium (no coordination failure).<sup>16</sup>*

An economic interpretation of Assumption 1 is in terms of conflict over *rival* issues. A good is rival when (a) any increase in a state's use of that good reduces the extent of the other state's use, and (b) each state's preferred outcome is to have full and exclusive use of the good. In such context, outcome  $x(k)$  can be conveniently defined as the extent to which state 1 can use the good once the dispute has been resolved, so that  $x_1^*(k) = 1$  denotes state 1's ideal outcome (state 1 has full and exclusive use), and  $x_2^*(k) = 0$  denotes state 2's ideal outcome (state 2 has full and exclusive use). Henceforth,  $\Delta(k) = 1$  for all rival issues. For instance, rival issues may arise when both states value the same rival good (say, a religious/cultural center or an offshore natural resource) because they have similar preferences over consumption and/or share similar production technologies. Rivalry may also emerge when the two states interact extensively with each other over an international

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<sup>15</sup>Our theoretical framework abstracts from explicit geographical considerations: we study the effects of relatedness on conflict taking geographical factors as given, i.e. when considering the comparative statics of genetic distance on conflict, we are implicitly looking at states that are at a constant geographic distance from each other. However, empirically, geography and genetic distance are connected, and both have effects on the probability of conflict. We explicitly address these points in the empirical section by controlling for a vast range of geographical distance measures.

<sup>16</sup>This assumption is equivalent to limiting the analysis to Coalition-Proof Nash Equilibria, as defined in Bernheim, Peleg and Whinston (1987).

policy issue (e.g., labor flows), and each state wants to impose its exclusive control over that issue. States may also interact with each other over non-rival issues. For example, both states may care about a common set of international public goods (security against terrorist threats, regulation of pollution or other externalities), where the use by one state would not reduce the other's ability to use the same public good, but may disagree about the ideal features of the public good, captured by  $x(k)$  in our simplified setting. Such more general case where  $\Delta(k)$  may differ from 1 is analyzed at the end of this section, while right now we focus on the simpler case  $\Delta(k) = 1$ .

How does the probability of violent conflict depend on the distance in fundamental characteristics  $V(i, j)$ ? First of all, conflict will never occur if  $V(i, j) > R$ . This captures the obvious but important point that two states which are very distant in the set of issues they care about will have no reason to fight. In contrast, if  $V(i, j) < R$  they will share a range of common issues, and we have the following:

**Remark 4**

*Violent conflict  $(C, C)$  is the unique equilibrium if and only if:*<sup>17</sup>

$$\alpha[R - V(i, j)] > \omega \tag{15}$$

This simple inequality illustrates a key result: for a given range  $R$  of common issues, populations which are more distant in preferences over relevant issues are *less* likely to go to war with each other. In particular, if  $\omega$  is a random variable distributed uniformly between 0 and  $\bar{\omega}$ , we have <sup>18</sup>

**Proposition 1**

*The probability of conflict between state  $i$  and state  $j$  is:*<sup>19</sup>

$$\text{Prob}(\text{Conflict}) = \frac{\alpha}{\bar{\omega}}[R - V(i, j)] \tag{16}$$

<sup>17</sup>For  $v_i \leq v_j$ , the common range includes all points between  $v_j - \frac{R}{2}$  and  $v_i + \frac{R}{2}$ , and  $(C, C)$  is the unique equilibrium for  $\int_{v_j - \frac{R}{2}}^{v_i + \frac{R}{2}} \alpha dk > \omega$ , (an immediate application of Remark 3). By the same token, if  $v_i \geq v_j$ ,  $(C, C)$  is the unique equilibrium for  $\int_{v_i - \frac{R}{2}}^{v_j + \frac{R}{2}} \alpha dk > \omega$ .

<sup>18</sup>Without loss of generality, we assume values of the parameters such that  $\frac{\alpha}{\bar{\omega}}[R - V(i, j)] \leq 1$ .

<sup>19</sup>That is, conflict is increasing in the extent states care about specific common issues ( $\alpha$ ) and the range of common issues each state cares about ( $R$ ), decreasing in the relative costs to start a conflict ( $\bar{\omega}$ ), and decreasing in the distance between the two states' fundamental characteristics  $V(i, j)$ .

We now go a step further and derive the relation between probability of conflict and explicit measures of long-term relatedness (genetic distance). If preferences are transmitted intergenerationally across populations (biologically and/or culturally) with variation, populations that are more closely related will be more likely to care about the same issues. This can be illustrated with a simple model of vertical transmission of characteristics. Assume that in period  $t$  a population  $i$  inherits its type  $v_{it}$  from an ancestor population with type  $v_{it-1}$ , with variation captured by a random shock  $\varepsilon_{it}$ :

$$v_{it} = v_{it-1} + \varepsilon_{it} \quad (17)$$

Without loss of generality, consider only two periods, and assume that  $\varepsilon_{it}$  follow a simple random walk, taking value  $\varepsilon > 0$  with probability 1/2 and  $-\varepsilon$  with probability 1/2 (with shocks independently distributed across different populations). Let  $g(i, j)$  ("genetic distance") denote the number of periods since two populations have shared common ancestors (in the empirical analysis, we use  $F_{ST}$  genetic distance, a measure that is approximately linear in the time since two populations shared their last common ancestors). Populations at  $g(i, j) = 1$  will be at  $V(i, j) = 0$  with probability 1/2 and  $V(i, j) = 2\varepsilon$  with probability 1/2, and hence at expected distance  $E\{V(i, j) \mid g(i, j) = 1\} = \varepsilon$ . By contrast, two populations at  $g(i, j) = 2$  (that is, sharing a two-period-old last-common-ancestor population) will be at a higher expected distance  $E\{V(i, j) \mid g(i, j) = 2\} = \frac{1}{2}2\varepsilon + \frac{1}{8}4\varepsilon = \frac{3}{2}\varepsilon$ . Hence:

**Remark 5**

*Expected distance in inherited characteristics  $V(i, j)$  is increasing in genetic distance  $g(i, j)$ :*

$$E\{V(i, j) \mid g(i, j) = 2\} - E\{V(i, j) \mid g(i, j) = 1\} = \frac{\varepsilon}{2} > 0 \quad (18)$$

An immediate implication of Proposition 1 and Remark 5 is that genetic distance  $g(i, j)$  is inversely related to their expected probability of conflict:<sup>20</sup>

**Corollary 1**

*The expected probability of conflict between state  $i$  and state  $j$  is decreasing in genetic distance  $g(i, j)$ :*

$$E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 2] - E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 1] = -\frac{\varepsilon\alpha}{2\bar{\omega}} < 0 \quad (19)$$

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<sup>20</sup>The equation in Corollary 1 is derived under the assumption that the parameters are such that  $V(i, j) < R$  for all possible realizations of the shocks. The effect of genetic distance  $g(i, j)$  on the probability of conflict could be even higher if  $V(i, j) > R$  - and hence no conflict were to occur - for some realizations of the shocks.

Corollary 1 is our central theoretical result, which we test directly in the empirical section. Even though this result is obtained under a series of simplifications and abstractions, it highlights the general logic of the relation among common issues, interactions across states, long-term relatedness, and probability of conflict. As we will see, this result is indeed consistent with the empirical evidence.

### 2.3.2 Extension

We now relax Assumption 1 and extend the analysis to the more general case in which the extent of disagreement  $\Delta_{ij}(k) = |x_i^*(k) - x_j^*(k)|$  is not necessarily equal to 1 for all issues, but may vary in functions of the inherited characteristics of the two states.<sup>21</sup> A priori, the relationship between inherited characteristics and extent of disagreement can go either way. On the one hand, it is possible that culturally closer population may face less disagreement over non-rival common issues (e.g., about the characteristics of specific international public goods), which, other things being equal, would reduce the probability of conflict. On the other hand, two closely related populations who care a lot about the *same* non-rival issue may also have strongly divergent preferences over the details of *how* the issue should be settled, and hence be farther away in their ideal points (for example, two closely related population that care about the same religious or cultural issue may also greatly diverge in their ideal outcomes). In what follows we present a simple and direct formalization linking the extent of disagreement to the distance in inherited characteristics, and study the relation between probability of conflict and genetic distance in this more general setting (in Section 4 we will present some evidence on voting patterns at the United Nations that empirically sheds some light on the relation between relatedness and the extent of agreement or disagreement over international issues).

Assume that for any set of issues between any two points on the real line, a fraction  $\rho$  is rival and a fraction  $(1 - \rho)$  is non-rival, and that the extent of disagreement over non-rival common issues between state  $i$  and state  $j$  may depend on the distance in inherited characteristics  $V(i, j)$ :

$$\Delta_{ij}(k) = \Delta_0 + \delta V(i, j) \tag{20}$$

where  $\Delta_0 \geq 0$  and  $\delta$  is a parameter measuring the relation between distance  $V(i, j)$  and disagreement  $\Delta_{ij}(k)$ , and  $k$  is a non-rival issue. The other assumptions of our model are maintained. In particular,

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<sup>21</sup>Clearly if  $\Delta_{ij}(k)$  is independent of  $V(i, j)$  for all issues, the qualitative results from the basic setting will not be affected.

it is still the case that all states at a distance  $V(i, j) > R$  share no common issues, and hence face no conflict. For states at a distance  $V(i, j) \leq R$ , violent conflict is the only equilibrium if and only if  $\alpha[\rho + (1 - \rho)\Delta_0][R - V(i, j)] > \omega$ . To simplify notation, we assume that all relevant issues share the same  $\alpha$  (the results would not change qualitatively if we assume that relevant rival issues enter the utility function with parameter  $\alpha_r > 0$  while non-rival issues enter with parameter  $\alpha_{nr} > 0$ ). Assuming again that  $\omega$  is a random variable distributed uniformly between 0 and  $\bar{\omega}$ , we now have:

**Proposition 2**

*The probability of conflict between the two states is given by:*

$$\text{Prob}(\text{Conflict}) = \frac{\alpha}{\bar{\omega}} \{[\rho + (1 - \rho)\Delta_0]R - [\rho + (1 - \rho)(\Delta_0 - \delta)]V(i, j) - (1 - \rho)\delta[V(i, j)]^2\} \quad (21)$$

*A negative relationship between probability of conflict and distance  $V(i, j)$  holds (i.e.,  $\frac{d\text{Prob}(\text{Conflict})}{dV(i, j)} < 0$ ) if  $\delta$  is small enough:*

$$\delta < \frac{\rho + (1 - \rho)\Delta_0}{(1 - \rho)[1 - 2V(i, j)]} \quad (22)$$

The above inequality is always satisfied if  $\delta \leq 0$ . If  $\delta > 0$ , the inequality is more easily satisfied the larger the fraction of rival issues  $\rho$ , and the larger the extent of disagreement which is independent of distance  $\Delta_0$ . An analogous condition can be stated in terms of expected probability of conflict and genetic distance. By taking expectations of the above  $\text{Prob}(\text{Conflict})$ , using the facts that  $E\{V(i, j) \mid g(i, j) = 1\} = \varepsilon$ ,  $E\{V(i, j)^2 \mid g(i, j) = 1\} = 2\varepsilon^2$ ,  $E\{V(i, j) \mid g(i, j) = 2\} = \frac{3}{2}\varepsilon$  and  $E\{V(i, j)^2 \mid g(i, j) = 2\} = 4\varepsilon^2$ , we have:

$$\begin{aligned} E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 2] - E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 1] = & \quad (23) \\ -\frac{\alpha}{\bar{\omega}}\{[\rho + (1 - \rho)(\Delta_0 - \delta)]\varepsilon + 2(1 - \rho)\delta\varepsilon^2\} & \end{aligned}$$

which immediately implies:

**Corollary 2**

*Expected conflict is decreasing in genetic distance (i.e.,  $E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 2] < E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 1]$ ) if:*

$$\delta < \frac{\rho + (1 - \rho)\Delta_0}{(1 - \rho)\varepsilon(1 - 2\varepsilon)} \quad (24)$$

Consequently, an inverse relationship between conflict and genetic distance is consistent with a small or negative effect of distance  $V(i, j)$  on the extent of disagreement over non-rival issues, and/or with a predominance of rival issues in international disputes.

In general, the net effect of relatedness on conflict depends on the relative size of the different effects, and is therefore an empirical question. As we will see, our empirical findings document a strong and robust *negative* effect of genetic distance on the probability of conflict. In other words, empirically we find that more closely related states fight more with each other, which is the implication of our basic setting. These findings are therefore consistent with a predominant role for the common-issue effect, which prevails over possible countervailing effects (such as the "extent of disagreement" effect presented above or the "coordination failure" effect discussed in Appendix 1).

The basic results presented in this section could be viewed as the reduced forms of more detailed and micro-founded settings in which specific interactions and common issues emerge from more complex dynamic processes and decisions. For example, societies with more similar long-term characteristics might endogenously end up with more similar production systems and/or consumption patterns, which may induce them to compete over a similar set of resources. Another (non-mutually exclusive) channel would emerge if genealogically more similar populations face lower fixed costs to interacting with each other, and therefore have more incentives and opportunities to interact over all sorts of common issues, multiplying the likelihood that some of those issues will be disputed. These interpretations are consistent with our simplified framework, as they predict a negative relationship between genetic distance and the probability of conflict.

### **3 Data and Methodology**

Our model shows that the degree of relatedness between populations has a positive effect on their conflict propensities due to a larger set of common issues (corollary 1). Genealogical relatedness may also affect differences in ideal points (corollary 2) and may affect the likelihood of reaching peaceful conflict resolution by facilitating coordination (corollary 3 in Appendix 1). Thus, the net effect of relatedness on conflict is a priori ambiguous. In the remainder of this paper we examine empirically the determinants of bilateral conflict across states, focusing on the degree of relatedness between the populations of each pair of countries. We control for other determinants of bilateral conflict, in particular a wide range of measures of geographic distance.

### 3.1 Measuring Conflict

We use panel data on interstate conflict between 1816 and 2001 from the Correlates of War Project ([www.correlatesofwar.org](http://www.correlatesofwar.org)).<sup>22</sup> We start from a discrete indicator of the intensity of a bilateral conflict between countries  $i$  and  $j$  in year  $t$ . The indicator takes on a value from 0 for no militarized conflict to 5 for an interstate war involving more than 1,000 total battle deaths. Following the convention in the literature, we define dummy variable taking a value of 1 if the intensity of militarized conflict is equal to or greater than 3. Our main dependent variable is this binary indicator of conflict, denoted  $C_{ijt}$ . We separately examine the determinants of the intensity of conflict, as well as the determinants of war (corresponding to a conflict intensity of 5). The database includes several other useful bilateral variables such as war casualties, an indicator of whether a pair is linked by an active military alliance, the number of other wars occurring in a given year and the number of peaceful years in a country pair  $(i, j)$  at each time  $t$ . We make use of these variables in the analysis below.

### 3.2 Measuring Relatedness

To capture genealogical relatedness, we use genetic distance. Since the interpretation and construction of this measure was discussed in detail in Spolaore and Wacziarg (2009), we provide only a short overview. Genetic distance is a summary measure of differences in allele frequencies across a range of neutral genes (or *chromosomal loci*). The measure we use mostly,  $F_{ST}$  genetic distance, captures the length of time since two populations became separated from each other. 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. In other words,  $F_{ST}$  genetic distance is a direct measure of genealogical relatedness, resulting from a molecular clock. The specific source for our data is Cavalli-Sforza et al. (1994), pp. 75-76.<sup>23</sup>

Our focus is on a set of 42 world populations for which there is data on bilateral genetic distance, computed from 120 neutral alleles. Among the set of 42 world populations, the maximum genetic distance is between Mbuti Pygmies and Papua New-Guineans ( $F_{ST} = 0.4573$ ), and the minimum

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<sup>22</sup>See also Jones et. al. (1996) and Faten et al. (2004).

<sup>23</sup>Cavalli-Sforza et al. (1994) also provide data on Nei genetic distance, a measure that is different but highly correlated with  $F_{ST}$  distance. Our results are robust to using Nei distance rather than  $F_{ST}$  distance. Corresponding estimates are available upon request.

is between the Danish and the English ( $F_{ST} = 0.0021$ ). The mean genetic distance among the 861 available pairs is 0.1338.

While the data on genetic distance is available at the level of populations, the rest of our data is at the country-pair level. It was therefore necessary to match genetic groups to countries. The procedure to match populations to countries is described in detail in Spolaore and Wacziarg (2009). To summarize, each of the 42 groups was matched to almost all of the 1,120 ethnic groups in Alesina et al. (2003). The same source provides the distribution of these ethnic groups across virtually all the countries in the world. Thus, we could construct measures of genetic distance between countries, rather than groups. We constructed two such measures. The first was the distance between the plurality ethnic groups of each country in a pair, i.e. the groups with the largest shares of each country’s population. The second was a measure of weighted genetic distance, constructed as follows: assume that country  $i$  is composed of populations  $m = 1 \dots M$  and country  $j$  is composed of populations  $n = 1 \dots N$ . Denote by  $s_{im}$  the share of population  $m$  in country  $i$  (similarly for country  $j$ ) and  $d_{mn}$  the genetic distance between populations  $m$  and  $n$ . The weighted  $F_{ST}$  genetic distance between countries  $i$  and  $j$  is then:

$$FST_{ij}^W = \sum_{m=1}^M \sum_{n=1}^N (s_{im} \times s_{jn} \times d_{mn}) \quad (25)$$

where  $s_{km}$  is the share of group  $m$  in country  $k$ ,  $d_{mn}$  is the  $F_{ST}$  genetic distance between groups  $m$  and  $n$ . This represents the expected genetic distance between two randomly selected individuals, one from each country. Weighted genetic distance is very highly correlated with genetic distance based on plurality groups (the correlation is 91.9%), so for practical purposes it does not make a big difference which one we use. We will use the weighted  $F_{ST}$  distance as the baseline measure throughout this study, as it is a more precise measure of average genetic distance between countries.<sup>24</sup>

The match of populations to countries pertains to the contemporary period, after the great migrations that followed the conquest of the New World. Hence, for instance, for the current period the plurality population in Australia is the English population. To address bias resulting from errors in the match populations to countries for the current period, as well as concerns that current genetic distance may be endogenous with respect to past wars, we also matched countries

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<sup>24</sup> All our results are robust to using genetic distance between plurality groups rather than weighted genetic distance. The corresponding estimates are available upon request.

to their 1500 AD populations. Hence, for instance, in the 1500 match, Australia is matched to Aborigines. Genetic distance between countries using the 1500 match can be used as an instrument for current genetic distance.<sup>25</sup>

### 3.3 Summary Statistics

Table 1 and 2 provide summary statistics that can help to give a sense of the data and provide clues concerning the relationship between conflict and relatedness.<sup>26</sup> The baseline sample is an unbalanced panel of 517,251 observations covering 13,575 country pairs, based on 176 underlying countries, from 1816 to 2000. Table 1 displays the means of genetic distance, geodesic distance and a dummy variable for contiguity between the two countries in a pair, conditional on the intensity of conflict. The mean of genetic distance when there is no militarized conflict (0.102) is greater than at any other level of the conflict intensity indicator (for hostility levels ranging from 2 to 5, the mean of genetic distance ranges from 0.050 to 0.063), consistent with Corollary 1. Somewhat to our surprise, a relatively small portion of full fledged-wars occur between contiguous countries (18.2%), and the mean geodesic distance separating countries at war is relatively high (5,562 km).

Table 2 shows the conditional frequency of both wars and conflicts. Wars are a relatively rare occurrence, as only 1,010 pair-year observations are characterized as wars, out of more than half a million observations. Over a quarter of these wars occurred between countries in the bottom decile of genetic distance, and almost half of all wars occurred in pairs in the bottom quartile. Only 44 wars were observed in pairs in the top quartile, of which 32 involved South Africa as one of the combatants. While South Africa is characterized as genetically distant from European populations due to the large African majority, a historical examination of wars involving South Africa reveals that the wars were spurred mainly by conflicts over issues separating European powers and South Africa's European power elite. In sum, there are very few wars between genetically distant populations in our sample. Even wars occurring across large geographic distances typically

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<sup>25</sup>Since we do not have detailed data on ethnic composition going back to 1500, the corresponding match only refers to plurality groups. The matching of countries to populations for 1500 is more straightforward than for the current period, since Cavalli-Sforza et al. (1994) attempted to sample populations as they were in 1500, likely reducing the extent of measurement error. The correlation between weighted genetic distance matched using current period populations and genetic distance between plurality groups as of 1500 is 0.714 in our baseline sample.

<sup>26</sup>Appendix 2 provides further summary statistics for the main variables in our study, in the form of means and correlations, to aid in the interpretation of our empirical results.

involve mostly genetically similar participants - for instance it is still the case that almost half of the wars occurring between non-contiguous countries involved country pairs in the bottom quartile of genetic distance. Similar observations hold when we consider more broadly militarized conflicts rather than wars per se: while there are vastly more of these conflicts (3,728 versus 1,010), the relative frequency by quartile of genetic distance is roughly preserved. Similarly, the proportions do not change very much when conditioning on geographic distance being large between the countries in a pair - countries not sharing a common sea or ocean, non-contiguous countries, or countries that are more than 1,000 kilometers apart.

### 3.4 Empirical Specification

While these summary statistics are an informative starting point, we turn to a more formal regression setup, allowing us to control for a wide range of determinants of interstate militarized conflicts. As a starting point for our empirical specification, we follow the practice in the existing literature (for instance Bremer, 1992, Martin, Mayer and Thoenig, 2008) of regressing a binary indicator of interstate conflict on a set of bilateral determinants. The baseline regression equation is:

$$C_{ijt} = \beta X_{ijt} + \gamma FST_{ij}^W + \varepsilon_{ijt} \quad (26)$$

The vector  $X_{ijt}$  contains a series of controls such as a contiguity dummy, log geodesic distance, log longitudinal and latitudinal distance, several other indicators of geographic isolation, as well as a set of dummy variables representing whether both countries in the pair are democracies, whether they were ever in a colonial relationship, whether they belong to an active military alliance, among other controls. The choice of controls follows the existing literature closely, particularly the contribution of Martin, Mayer and Thoenig (2008). A major difference is that we greatly augment the list of geographic controls compared to existing contributions, in an effort to identify separately the effects of geographic proximity from those of genealogical relatedness. It is important for our purposes to adequately control for geographic isolation as genetic distance and geographic isolation tend to be correlated (for instance the correlation between  $F_{ST}$  genetic distance and log geodesic distance in our baseline sample is 0.404). Equation (26) is estimated using probit, clustering standard errors at the country-pair level. Throughout, we report marginal effects evaluated at the mean of the independent variables, providing a quantitative assessment of the magnitude of the effects. Because the proportion of pair-year observations with conflicts is only 0.721%, to improve the readability of the marginal effects we multiplied all of them by 100 in all tables.

## 4 Empirical Results

### 4.1 Baseline Estimates

Table 3 presents baseline estimates of the coefficients in equation (26). We start with a univariate regression (column 1), showing a very strong negative relationship between genetic distance and the incidence of militarized conflict. The magnitude of this effect is large, with a one standard deviation change in genetic distance (0.066) associated with a 0.492 decline in the percentage probability of conflict (the mean of this variable, again, is 0.721). Obviously, this estimate is tainted by omitted variables bias, stemming mainly from the omission of geographic factors. Column (2) introduces eight measures of geographic distance. These measures usually bear the expected signs, and their inclusion greatly reduces the effect of genetic distance.<sup>27</sup> However, this effect remains negative and highly significant statistically. Its magnitude is still substantial - a one standard deviation shift in genetic distance is associated with a reduction in the probability of conflict of 12.15% of that variable's mean.

Several other factors have been proposed as correlates of war. Chief among them is the central tenet of liberal peace theory, namely the idea that democracies tend not to go to war with each other. A dummy variable equal to 1 if both countries are democracies (defined as a combined Polity score greater than 5) has a negative and highly significant marginal effect, with roughly the same magnitude as that of genetic distance. Column 3 includes other controls such as whether countries in a pair ever had colonial ties, the number of peaceful years prior to the current year, the number of wars taking place globally at time  $t$ , and whether the two countries are members of the same alliance. All of these bear coefficients with the expected signs. Once all these controls are included, the coefficient on genetic distance falls further, but remains negative and significant at the 1% level. The effect of a one standard deviation shift in genetic distance, with the full set of controls, remains equal to 8.52% of the mean probability of conflict. We continue to condition on this full set of controls in all the regressions that follow.

None of these observations change very much when using a logit estimator rather than a probit estimator (column 4). We continue to use a probit estimator in the rest of this paper. Finally,

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<sup>27</sup>Similarly, excluding genetic distance from the baseline specification generally raises the magnitude of the geographic effects, particularly that of log geodesic distance (results are available upon request). Thus, the exclusion of relatedness from past empirical specifications seeking to explain conflict likely led to overstating the quantitative impact of geographic factors.

in column 5, we instrument for genetic distance using genetic distance between populations as they were in 1500. The results are very close to those previously reported, but the effect of genetic distance rises by over 50% relative to the estimates of column 3, suggesting that the latter understated the effect. It is likely that the higher effect of genetic distance under IV reflects the fact that measurement error is less prevalent, since arguments about reverse causality or omitted variables bias would suggest that instrumenting should reduce the effect of genetic distance. To adopt a conservative approach, we refrain from instrumenting for genetic distance in the bulk of our analysis, keeping in mind that our reported effect is likely an understatement of the true magnitude.

## 4.2 Estimates Across Time and Space

To examine if specific periods or regions account for the finding of a negative effect of relatedness on conflict, we broke down the sample by time period and region. Results are presented in Tables 4 and 5. We find that results are remarkably robust within regions and periods. Table 4 shows that the coefficient on genetic distance is negative and roughly of the same magnitude whether considering the pre- or post-1900 periods. The coefficient for the pre-1900 period is not statistically significant, perhaps because there are many fewer observations in the early periods (only 799 country pairs as opposed to 13,175 for the broader sample), and few observations with conflict (436 out of a total of 3,728 conflicts in the broader sample). Focusing on the 20th century, the effect is particularly pronounced and significant for the post 1946 period - in other words our finding is not simply an artifact of the Second World War, which pitted a lot of European populations against each other.<sup>28</sup> In fact, our finding holds even after the end of the Cold War (column 7). The coefficient is negative whatever the subperiod under consideration.

Turning to the regional breakdown in Table 5, we again uncover a negative effect of genetic distance on conflict whatever the region under consideration. Column (2) starts by including a dummy variable taking on a value of one if both countries in a pair are part of the same continent (continents are defined as Africa, Americas, Asia, Europe, and Oceania). The concern is that conflicts occur predominantly among countries located on the same continent (this was the case for 2,086 out of a total of 3,728 conflicts in our baseline sample), and that populations located on the same continent tend to be genetically close (the mean of  $F_{ST}$  genetic distance for pairs on the

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<sup>28</sup>2,053 observations involve militarized conflicts in the post 1946 period, while the 1939-1946 period involved 634 bilateral conflict-years, or 17% of the total number of observations with conflicts between 1816 and 2001.

same continent is 0.066 versus a sample-wide mean of 0.102). However, the inclusion of the same continent dummy hardly changes the coefficient on genetic distance at all.

Column (3) presents results for Europe. For this continent, we observe a separate matrix of  $F_{ST}$  genetic distances, available for almost all the countries in Europe.<sup>29</sup> Despite the paucity of observations (only 291 country pairs), the effect of genetic distance remains negative and significant at the 5% level. A one standard deviation change in genetic distance reduces the probability of conflict by 12.531% of its mean, a magnitude slightly larger than, but roughly in line with, the results found in the World sample. Columns (4) through (6) provide estimates for Asia, Africa and the Americas (there were no conflicts within Oceania in our baseline sample, so this category is missing). The coefficient on genetic distance is consistently negative, and significant at the 10% level for Asia and Africa, but small and insignificant for the Americas.<sup>30</sup> Overall, the regional breakdown suggests that the negative effect of relatedness on war is remarkably consistent across space, the results within Europe, where genetic distance is small, being particularly striking.

### 4.3 Adding Linguistic and Religious Distance

While genetic distance is a precise and continuous measure of the degree of relatedness between populations and countries, alternative measures exist. The existing literature on interstate conflict has examined linguistic and religious ties in an effort to tell apart primordialist theories of conflict from instrumentalist theories (Richardson, 1960, Henderson, 1997). Thus, it is important to evaluate whether these variables trump genetic distance, and more generally how their inclusion affects our main coefficient of interest. Linguistic relatedness is associated with genetic relatedness because, like genes, languages are transmitted intergenerationally: populations speaking similar languages are likely to be more related than linguistically distinct populations (Cavalli-Sforza et al., 1994).<sup>31</sup> Religious beliefs, also transmitted intergenerationally, are one type of difference in

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<sup>29</sup>Details concerning the  $F_{ST}$  genetic distance matrix for the European continent can be found in Spolaore and Wacziarg (2009). There are only 5 distinct European populations in the worldwide matrix, so estimates using the European matrix, where there are 26 distinct genetic groups, are likely to be much more reliable.

<sup>30</sup>The number of intracontinental interstate conflicts experienced by these continents were 787 (Asia), 252 (Africa) and 433 (Americas).

<sup>31</sup>On the other hand, there are many reasons why genetic and linguistic distance are imperfectly correlated. Rates of genetic and linguistic mutations may differ; populations of a certain genetic make-up may adopt a foreign language as the results of the edict of foreign rulers, as happened when the Magyar rulers imposed their language on the

human traits that can lead to conflict. In what follows, we evaluate whether the effect of genetic distance is reduced or eliminated when controlling for linguistic and religious distance, and whether these variables have an independent effect on the incidence of interstate conflict.<sup>32</sup>

Prior to showing the results, we briefly discuss how these measures were constructed. To capture linguistic distance, we used the data and approach in Fearon (2003), making use of linguistic trees from Ethnologue to compute the number of common linguistic nodes between languages in the world, a measure of their linguistic similarity (the linguistic tree in this dataset involves up to 15 nested classifications, so two countries with populations speaking the same language will share 15 common nodes).<sup>33</sup> Using data on the distribution of each linguistic group within and across countries, from the same source, we again computed a measure of the number of common nodes shared by languages spoken by plurality groups within each country in a pair. We also computed a weighted measure of linguistic similarity, representing the expected number of common linguistic nodes between two randomly chosen individuals, one from each country in a pair (the formula is analogous to that of equation 25).<sup>34</sup> Following Fearon (2003), we transformed these measures so that they reflect linguistic distance (LD) rather than similarity, and are bounded by 0 and 1:

$$LD = \sqrt{\frac{(15 - \# \text{ Common Nodes})}{15}} \quad (27)$$

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Hungarian population. Other salient examples include countries were colonized by European powers, adopting their language (English, French, Portuguese or Spanish), while maintaining very distinct populations genetically. See Spolaore and Wacziarg (2009) for an in-depth discussion of these points.

<sup>32</sup>Pairwise correlations between measures of genetic, linguistic and religious distances appear in Appendix 2, panel b. These correlations are generally positive, as expected, but not very large. For instance, the correlation between  $F_{ST}$  genetic distance and weighted linguistic distance is 0.164. Religious distance bears a correlation of 0.544 with linguistic distance, and 0.210 with genetic distance.

<sup>33</sup>As an alternative, we used a separate measure of linguistic distance, based on lexicostatistics, from Dyen, Kruskal and Black (1992). This is a more continuous measure than the one based on common nodes, but it is only available for countries speaking Indo-European languages. It captures the number of common meanings, out of a list of 200, that are conveyed using "cognate" or related words. Summing over the 200 meanings, a measure of linguistic distance is the percentage of non-cognate words. Using the expected (weighted) measure of cognate distance led to effects of genetic distance very similar to those obtained when controlling for the Fearon measure, albeit on a much smaller sample of countries speaking Indo-European languages. These results are available upon request.

<sup>34</sup>The two measures deviate from each other whenever a country includes populations speaking different languages. Using the measure based on the plurality language or the weighed measure did not make any difference for our results. As we did for genetic distance, we focus on weighted measures.

To measure religious distance we followed an approach based on religious trees, similar to that used for linguistic distance, using a nomenclature of world religions obtained from Meham, Fearon and Laitin (2006). This nomenclature provides a family tree of World religions, first distinguishing between monotheistic religions of Middle-Eastern origin, Asian religions and "others", and further subdividing these categories into finer groups (such as Christians, Muslims and Jews, etc.). The number of common classifications (up to 5 in this dataset) is a measure of religious similarity. We matched religions to countries using Meham, Fearon and Laitin's (2006) data on the prevalence of religions by country and transformed the data in a manner similar to that in equation (27), again computing plurality and weighted distances separately.

Table 6 presents estimates of the effect of genetic distance on the propensity for interstate conflict when linguistic and religious distance are included. Since the use of these variables constrains the sample (a loss of some 77,081 observations, or almost 15% of the sample), we start in column (1) with the baseline estimates for this new sample: they are in line with those reported above. When adding linguistic distance and religious distance either alone or together (columns 2-4), interesting results emerge. First, the coefficient on genetic distance is barely affected. Second, linguistic distance exerts a null effect when controlling for genetic distance. Third, religious distance is negatively related with conflict, though the effect is only significant at the 7.6% level, and its significance level drops to 13% when including linguistic distance along with religious distance.<sup>35</sup> This latter finding, while weak, is consistent with the view that religion is one of the vertically transmitted traits that make populations more or less related to each other, and its effect on conflict goes in the same direction as that of genetic distance, a broader measure of relatedness.

#### 4.4 Nonlinearities and Determinants of Conflict Intensity

In this subsection, we consider several extensions of our baseline specification. Our goal is to characterize whether relatedness may operate differently for different pairs of countries, and to investigate its effect on the intensity of conflict. To do so, we first look for interactive and nonlinear effects of genetic distance (Table 7). We then seek to evaluate the effect of genetic distance on the intensity of conflict, rather than on a binary indicator of conflict incidence (Table 8).

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<sup>35</sup>This result contrasts with that in Henderson (1997), who found evidence that religious *similarity* was negatively related to conflict. The difference may stem from a much bigger sample in our work, as well as our inclusion of a much broader set of controls (Henderson only controlled for contiguity).

We first isolate countries that are non contiguous. In the baseline sample, 34% of conflicts occur between contiguous countries, and isolating pairs composed of non-contiguous countries is a further way to control for geographic proximity. The standardized effect of genetic distance actually *rises* modestly, as a one standard deviation increase in genetic distance is associated with a 9.41% decrease in the mean probability of conflict (versus 8.52% in the baseline regression). This reinforces our confidence that the effect is not driven by geographic distance or other possibly omitted factors specific to contiguous countries.

In columns (3) through (5) of Table 7 we add several interaction terms to the baseline specification. The effect of genetic distance does not appear quantitatively more or less pronounced for pairs that are contiguous, for pairs that are geographically proximate (i.e. countries are either contiguous or separated by a distance less than 2,500 km), or for pairs that include a major power. We then allow for a linear spline, i.e. a different slope for the effect of genetic distance whether it is greater than the sample median of 0.095, or lower. Column (6) shows no evidence of such a differential effect (varying the spline threshold did not matter greatly). Finally, introducing a squared term in genetic distance (column 7) does not reveal much evidence of a nonlinear effect. In sum, we find no evidence that the effect of genetic distance depends on some characteristic of the pairs, or that it is nonlinear.

Table 8 seeks to explain the intensity of militarized conflict as opposed to its incidence only. To do so, we modified the dependent variable in several ways. Column (1) simply uses the measure of the intensity of conflict from the Correlates of War dataset, rather than the binary transform of this variable we have been using so far. With least squares estimation, there is evidence that genetic distance bears a negative relationship with conflict intensity. However, column (2), which limits the sample to pairs having experienced conflict, demonstrates that genetic distance does not affect the intensity of conflict (among levels 3, 4 and 5) once we condition on the subsample with conflict. This result rationalizes our focus on a bilateral measure of conflict rather than on the continuous measure. In line with results in Table 3, instrumenting for genetic distance based on the current match of populations to countries using genetic distance based on the 1500 match increases the estimated magnitude of the effect by 64% (column 3).

In columns (4) and (5) we consider the determinants of war casualties. We find that genetic distance reduces war casualties, but again this effect is almost entirely driven by the extensive margin, since genetic distance has a statistically insignificant effect on war casualties for observations

with nonzero casualties. Our last test is to redefine the dependent variable as a binary indicator of war, i.e. a dummy variable taking on a value of one if conflict intensity is 5 (corresponding to conflicts with more than 1,000 total battle deaths). Genetic distance reduces the propensity for war in a statistically significant way: a standard deviation increase in genetic distance reduces the probability of full-blown war by 2.956% of this variable's mean, an effect quantitatively smaller than that on conflict more broadly (the underlying probability of a country pair-year being at war in our baseline sample is relatively low, on the order of 0.195%).

To summarize, the effect of genetic distance is very robust to using alternative measures of conflict, but we uncover little evidence that genetic distance affects the intensity of conflict conditional on a conflict occurring.

#### 4.5 Analysis for the 1950-2000 period

Several important correlates of war, such as measures of trade intensity and differences in income, are missing from our specification due to their lack of availability over the long time period covered by the baseline specification (1816-2001). In order to incorporate these additional controls, we focus on the 1950-2000 period for which various measures of trade and income are available.

A long tradition associated with liberal peace theory, going back to Montesquieu (1748) and Kant (1795), holds that extensive bilateral commercial links between countries reduces the probability of conflict, essentially by raising its cost, since valuable trade links would be lost in a militarized conflict. In an important paper, Martin, Mayer and Thoenig (2008, henceforth MMT) added an additional hypothesis: if the countries in a pair trade a lot with third parties, their bilateral trading link matters less, so controlling for bilateral trade, multilateral trade intensity should increase the probability of conflict among the countries in a pair. The issue we face is that the omission of these trade terms may bias the coefficient estimate on genetic distance, to the extent that genetic distance and trade are correlated.

We obtained the same data on bilateral and multilateral trade openness used in MMT's paper, and included their measures of trade in our baseline specification.<sup>36</sup> These measures include a metric of bilateral trade openness (the ratio of bilateral imports to GDP, averaged across the two countries in a pair), a metric of multilateral trade intensity (defined as the ratio of the sum of all bilateral imports from third countries to GDP, averaged between the two countries in a pair),

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<sup>36</sup>The data was obtained from <http://team.univ-paris1.fr/teamperso/mayer/data/data.htm>

and the interaction of each of these metrics with log geodesic distance. All of these measures were lagged by 4 years to limit the incidence of reverse causality running from conflict to trade, exactly as was done in MMT.

Results appear in Table 9. In column (1), we replicate the baseline specification for the smaller sample covering 1950-2000. We are able to exactly recover the pattern of coefficients on the trade terms as the one reported in MMT: bilateral openness reduces conflict, multilateral openness raises conflict, and these effects are more pronounced quantitatively for pairs that are closer to each other. Our findings lend further support to liberal peace theory, as recently amended by MMT. The effect of genetic distance in this sample is slightly smaller than in the 1816-2001 sample: a standard deviation increase in genetic distance reduces the probability of conflict by 6.612% of this variable's mean. Adding the trade terms in column (2), this effect falls further, but remains negative and highly significant statistically. In column (3), we include additional trade-related variables, a dummy for whether the two countries in a pair belong to a free trade area, and the number of GATT members in the pair. The coefficient on genetic distance is barely affected.

Another omitted variable concern stems from the results in Spolaore and Wacziarg (2009), where genetic distance was found to be robustly correlated with absolute differences in per capita income across pairs of countries. To the extent that differences in income capture power imbalances, or the extent of possible spoils of war, they may influence the probability of conflict (this could go in either direction: power imbalances may make a weaker prey easier to capture militarily, but also more willing to surrender peacefully). In column (5), we add the absolute value of log income differences (the same variable used as a dependent variable in Spolaore and Wacziarg, 2009) to the specification that includes the broadest set of controls (including trade controls from MMT).<sup>37</sup> The coefficient on income differences is positive and significant, indicating that heterogeneity in income levels across the countries in a pair is conducive to conflict, but its inclusion does not affect the coefficient on genetic distance. Finally, column (6) substitutes the absolute difference in total GDP instead of differences in per capita GDP. Heterogeneity in total GDP does not affect conflict propensity, and its inclusion does not affect the coefficient on genetic distance.

To summarize, the inclusion of a wide set of trade-related controls and of income differences, while confirming past results in MMT, does not change the basic message that relatedness has a positive effect on conflict.

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<sup>37</sup>The source for the income data is the Penn World Tables, version 6.1 (Heston, Summers and Aten, 2002).

## 4.6 Analysis of UN voting patterns

In our theoretical framework, Corollary 2 suggests that one way relatedness could affect conflict is through its effect on the degree of similarity in countries' ideal points over non rival issues. Stated simply, related populations may have more or less similar preferences over sets of international issues, quite apart from the effect of relatedness on the range of issues relevant to the pair, stemming from past interactions. In the theory section, we remained agnostic as to the possible direction of this relationship. In this subsection we seek to uncover empirically the direction of the effect by analyzing the degree of countries' similarity in stated preferences over global diplomatic issues. To do so, we use data on their voting patterns at the UN General Assembly. The data comes from Gartzke (2006), who states that "dozens or hundreds of resolutions appear in each session of the General Assembly." Most of these votes constitute symbolic position taking by UN members, who usually do not have a direct stake in the issue they vote on. Another advantage of this data is that all UN members take positions (including abstaining) on a constant set of issues.

Based on data on votes themselves, Gartzke constructed an index of the "affinity of nations", which is simply the bilateral correlation of votes for each country pair in a given year. The measure ranges from  $-1$  to  $1$  and is available from 1946 to 2002. Two separate indices are available depending on whether abstentions are considered a form of position taking, or excluded. We use both indices as dependent variables to examine the effect of genetic distance on the degree of similarity in preferences over diplomatic issues considered at the UN General Assembly. We maintain the same baseline specification used to estimate the determinants of conflicts (Table 3, column 3), regressing UN vote correlation indices on genetic distance, geographic distance and other controls.

Estimates suggest that genetic distance is positively associated with UN vote correlations. That is, countries that are more related have more *different* preferences over issues arising at the UN Assembly. Column (2) of Table 10 shows this is the case unconditionally. The effect remains positive and significant when including a set of geographic and historical controls (columns 2 and 3). The effect remains when considering only the 1990-2000 time period where votes were less likely to be aligned with the major geopolitical blocs of the Cold War era. The effect is also robust to excluding abstentions from the calculation of UN vote correlations. In terms of magnitude, using the baseline regression of column (3), a one standard deviation increase in genetic distance is associated with an increase in the UN vote correlation equal to 10.10% of this variables standard deviation, i.e. the standardized beta is 10.10%. This standardized measure of magnitude rises to

11.49% when excluding abstentions.

To summarize, this evidence suggests that any positive effect of relatedness on conflict arising from the role of past interactions in generating grievances is likely to be reinforced by the negative effect of relatedness on preference similarity (in the parlance of our model,  $\delta$  is negative).

## 5 Conclusion

In this paper, we examined the empirical relationship between the occurrence of international conflicts and the degree of relatedness between countries. We found that populations that are genetically closer are more prone to engage in militarized conflicts with each other, even after controlling for a wide set of measures of geographic distance, income differences, and other factors affecting conflict, including measures of bilateral and multilateral trade and differences in democracy levels. We also provided a theoretical model of conflict and relatedness that is consistent with these results. In the simplest version of our model, populations that share a more recent common history have had less time to diverge in preferences and characteristics that determine the set of common issues they care about, and over which they are prone to fight.

To our knowledge, this is the first paper that documents a link between genetic distance and international conflict, and provides an interpretation in terms of cultural and historical relatedness. As we have discussed in the introduction, our results provide strong evidence against the primordialist view that cultural and ethnic dissimilarity should breed war and plunder.

More broadly, this paper is part of a growing literature in political economy focusing on the effects of long-term cultural and historical variables on political, economic and institutional outcomes, both theoretically and empirically. It would be interesting to link our approach to the extensive literature on ethnic fractionalization and polarization within countries (see Alesina et al. 2003, Fearon, 2003) and to study the effects of long-term genealogical relatedness across groups on civil conflicts and other intrastate outcomes. A positive relationship between relatedness and conflict within states would be consistent, for example, with the finding in Fearon and Laitin (2003) that ethnic fractionalization and civil wars are unrelated. Further research on this question should focus on reliable subnational data on inter-group relatedness.<sup>38</sup>

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<sup>38</sup>Another area of research where our approach could be fruitful is the study of national formation and breakup, and their connections with international conflict (Spolaore, 2004; Alesina and Spolaore, 2005, 2006) and civil conflict

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## Appendix 1: Coordination Failure

We can further extend our basic framework by relaxing Assumption 2 (that is, by allowing for the possibility of coordination failure). As we have noted in Section 2,  $(C, C)$  is always a Nash equilibrium (Remark 1). Nonetheless, both states would be better off with a peaceful negotiation than with violent conflict  $(C, C)$ , because of the costs of war, which are not borne in a peaceful outcome. As we have seen, if  $(NC, NC)$  is a Nash equilibrium, it is the unique coalition-proof Nash equilibrium, as defined by Bernheim, Peleg and Whinston (1987). But what if states fail to coordinate on such superior  $(NC, NC)$  equilibrium, and end up in the inferior  $(C, C)$  equilibrium, even when the conditions for a peaceful equilibrium are satisfied? And what if such coordination failure were to be more likely across populations that are genealogically more distant, since their norms, habits, languages etc. are likely to be more different, and they may therefore find communication and coordination more difficult? If that were the case, such "coordination failure effect"

would reduce the negative correlation between genetic distance and probability of conflict (in contrast, if coordination failure were more likely between more closely related populations, the effect of relatedness on conflict would be strengthened).

A formalization of these ideas can be provided as follows. Let  $\chi(i, j)$  denote the probability that state  $i$  and state  $j$  would fail to coordinate on the peaceful outcome when it is an equilibrium, and assume that such coordination failure is more likely if the states are distant in their preferences and characteristics, measured by  $v_i$  and  $v_j$ . Specifically, assume that:

$$\chi(i, j) = \chi_0 + \theta V(i, j) \quad (\text{A1})$$

with  $\chi_0 \geq 0$  and  $\theta$  is a parameter measuring the relation between distance  $V(i, j)$  and probability of coordination failure  $\chi(i, j)$ . We also assume that all parameters satisfy the appropriate restrictions to ensure that  $0 \leq \chi(i, j) \leq 1$ . Therefore, for  $V(i, j) \leq R$ , and assuming again that  $\omega$  is a random variable distributed uniformly between 0 and  $\bar{\omega}$ , we have:

### Proposition 3

*The probability of conflict between the two states when all common issues are rival ( $\rho = 1$ ) can be written as:*

$$\begin{aligned} \text{Prob}\{\text{Conflict}\} &= \chi(i, j) \text{Prob}[\alpha[R - V(i, j)] \leq \omega] + \text{Prob}[\alpha[R - V(i, j)] > \omega] = \quad (\text{A2}) \\ &= \chi(i, j) + [1 - \chi(i, j)] \frac{\alpha}{\bar{\omega}} [R - V(i, j)] \end{aligned}$$

*The probability of conflict is decreasing in distance  $V(i, j)$  if:*

$$\theta < \frac{1 - \chi_0}{\frac{\bar{\omega}}{\alpha} - R - 2V(i, j)} \quad (\text{A3})$$

*An analogous condition holds for the more general case  $\rho \leq 1$  (see generalization below).*

The above inequality always holds for  $\theta < 0$ . For a positive  $\theta$ , it is more easily satisfied for smaller  $\chi_0$ , larger  $\alpha$  and  $R$ , and larger  $V(i, j)$ .

An analogous condition holds regarding the relation between expected probability of conflict and genetic distance:

### Corollary 3

*Expected conflict is decreasing in genetic distance (i.e.,  $E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 2] < E[\text{Prob}(\text{Conflict}) \mid g(i, j) = 1]$ ) if:*

$$\theta < \frac{1 - \chi_0}{\left[\frac{\bar{\omega}}{\alpha} - R - 2\varepsilon\right]\varepsilon} \quad (\text{A4})$$

Consequently, if observed conflict partly stems from coordination failure, an inverse relationship between conflict and genetic distance (as the one we actually observe in the data) is consistent with a small (or even negative) effect of relatedness on the probability of coordination failure (low  $\theta$ ).

### Generalization of Proposition 3 for $\rho \leq 1$

For the more general case  $\rho \leq 1$ , we have:

$$\text{Prob}\{\text{Conflict}\} = \chi(i, j) + [1 - \chi(i, j)] \text{Prob}\{C, C \text{ Unique Eq}\} \quad (\text{A5})$$

where:

$$\text{Prob}\{C, C \text{ Unique Eq}\} = \frac{\alpha}{\bar{\omega}} \{[\rho + (1 - \rho)\Delta_0]R - [\rho + (1 - \rho)(\Delta_0 - \delta)]V(i, j) - (1 - \rho)\delta[V(i, j)]^2\} \quad (\text{A6})$$

By substituting  $\chi(i, j) = \chi_0 + \theta V(i, j)$  and taking the derivative of the probability of conflict with respect to distance  $V(i, j)$ , we have the following generalization of Proposition 3:

*The effect of distance  $V(i, j)$  on the probability of conflict is negative if*

$$\theta < \frac{(1 - \chi_0) \{ \rho + (1 - \rho)(\Delta_0 - \delta) + 2(1 - \rho)\delta V(i, j) \}}{\frac{\bar{\omega}}{\alpha} - [\rho + (1 - \rho)\Delta_0]R - 2[\rho + (1 - \rho)(\Delta_0 - \delta)]V(i, j) - 3(1 - \rho)\delta[V(i, j)]^2} \quad (\text{A7})$$

which reduces to the condition  $\theta < \frac{1 - \chi_0}{\frac{\bar{\omega}}{\alpha} - R - 2V(i, j)}$  for  $\rho = 1$  (an analogous condition can be obtained for the relation between expected probability of conflict and genetic distance, along the lines illustrated above).

**Appendix 2 – Summary statistics and correlations for the main variables in the analysis**

**Panel a – Summary Statistics**

<b>Variable</b>	<b># Obs.</b>	<b>Mean</b>	<b>Std. Dev.</b>	<b>Min</b>	<b>Max</b>
Conflict (%)	517,251	0.721	8.459	0	100
War (%)	517,251	0.195	4.415	0	100
Fst genetic distance, weighted	517,251	0.102	0.066	0	0.355
Log geodesic distance	517,251	8.690	0.816	2.349	9.899
Dummy for contiguity	517,251	0.026	0.159	0	1
Religious Distance Index, weighted	443,472	0.811	0.186	.089	1
Linguistic Distance Index, weighted	440,170	0.944	0.160	0	1
1 - % cognate measure of linguistic distance, weighted	76,330	0.531	0.292	0	0.918

**Panel b – Pairwise Correlations**

	Conflict (%)	War (%)	FST genetic distance	Log geodesic distance	Contiguity	Religious distance	Linguistic distance
War (%)	0.519* (517,251)	1 (517,251)					
Fst genetic distance, weighted	-0.058* (517,251)	-0.026* (517,251)	1 (517,251)				
Log geodesic distance	-0.101* (517,251)	-0.033* (517,251)	0.404* (517,251)	1 (517,251)			
Dummy for contiguity	0.168* (517,251)	0.043* (517,251)	-0.148* (517,251)	-0.391* (517,251)	1 (517,251)		
Religious Distance Index, weighted	-0.020* (443,472)	0.001 (443,472)	0.210* (443,472)	0.243* (443,472)	-0.175* (443,472)	1 (443,472)	
Linguistic Distance Index, weighted	-0.035* (440,170)	-0.001 (440,170)	0.164* (440,170)	0.255* (440,170)	-0.193* (440,170)	0.544* (440,170)	1 (440,170)
1 - % cognate, weighted	0.003 (76,330)	0.008* (76,330)	-0.104* (76,330)	0.160* (76,330)	-0.177* (76,330)	0.632* (67,657)	0.823* (67,657)

(# of observations in parentheses)

**Table 1 – Means of Genetic Distance, Geodesic Distance and Contiguity  
Conditional on the Overall Level of Hostility \***

	<b>Fst Genetic Distance, weighted</b>	<b>Geodesic Distance, km</b>	<b>Contiguity dummy</b>
Overall Hostility Level = 0 (# of observations = 513,407)	0.102	7,635	0.024
Overall Hostility Level = 2 (# of observations = 116)	0.050	3,455	0.284
Overall Hostility Level = 3 (# of observations = 626)	0.054	3,495	0.372
Overall Hostility Level = 4 (# of observations = 2,092)	0.055	3,695	0.408
Overall Hostility Level = 5 (# of observations = 1,010)	0.063	5,562	0.182

517,251 pair-year observations from 13,575 country pairs.

\* No observations involved an overall hostility level equal to 1 in the sample.

The overall hostility level is defined by COW as the maximum of each country's hostility level within a pair.

Hostility levels are defined in COW as follows: 0=No hostility, 1=No militarized action, 2=Threat to use force, 3=Display of force, 4=Use of Force, 5=War.

**Table 2 – Conditional Frequency of War (number of pair-year observations  
by quartile of genetic distance)**

<b>Conditioning statement:</b>	<b>Bottom decile of genetic distance</b>	<b>Bottom quartile of genetic distance</b>	<b>Third quartile of genetic distance</b>	<b>Second quartile of genetic distance</b>	<b>Top quartile of genetic distance*</b>	<b>Total</b>
	<b>Hostility level = 5 (War)</b>					
None	277	487	178	301	44	1,010
Common sea / ocean = 0	170	329	129	269	44	771
Contiguity = 0	175	368	123	291	44	826
Distance > 1000 km	163	349	155	289	44	837
	<b>Hostility Level &gt; 3 (Conflict)</b>					
None	1,076	1,937	940	717	134	3,728
Common sea / ocean = 0	582	1,128	569	553	114	2,364
Contiguity = 0	537	1,202	520	616	119	2,457
Distance > 1000 km	512	1,210	780	684	134	2,808

Based on 517,251 pair-year observations from 13,575 country pairs.

\* 32 of the 44 cases in rows 3-6 involve South Africa as a combatant.

**Table 3: Baseline analysis, 1816-2000**  
(dependent variable: dichotomous indicator of conflict)

	(1)	(2)	(3)	(4)	(5)
	Univariate, probit	Geography controls, probit	Baseline, probit	Baseline, logit	IV probit, instrument- ing with 1500 GD
<b>Fst genetic distance, weighted</b>	<b>-7.4543</b> (12.297)**	<b>-1.3275</b> (5.837)**	<b>-0.9313</b> (8.922)**	<b>-0.7389</b> (-6.224)**	<b>-1.4414</b> (-6.511)**
Log geodesic distance		-0.1577 (4.842)**	-0.0735 (4.487)**	-0.0435 (-2.964)**	-0.0531 (-2.787)**
Log absolute difference in longitudes		-0.0120 (0.579)	-0.0003 (0.029)	-0.0089 (-1.189)	-0.0085 (-0.812)
Log absolute difference in latitudes		-0.0607 (3.276)**	-0.0250 (2.927)**	-0.0249 (-3.909)**	-0.0284 (-3.166)**
1 for contiguity		0.8897 (7.713)**	0.4227 (7.760)**	0.1617 (3.675)**	0.4346 (3.716)**
Number of landlocked countries in the pair		-0.2088 (6.219)**	-0.1197 (7.553)**	-0.0875 (-6.392)**	-0.1219 (-7.012)**
Number of island countries in the pair		0.1712 (4.312)**	0.0551 (2.969)**	0.0468 (3.240)**	0.0616 (3.255)**
1 if pair shares at least one sea or ocean		0.0782 (1.900)	0.1029 (4.501)**	0.0657 (3.281)**	0.1049 (3.264)**
Log product of land areas in square km		0.0986 (13.263)**	0.0511 (15.762)**	0.0398 (12.889)**	0.0532 (11.687)**
1 if both countries are democracies (polity2>5)			-0.0935 (8.670)**	-0.0816 (-8.614)**	-0.1012 (-8.989)**
1 for pairs ever in colonial relationship			0.1478 (3.413)**	0.0708 (2.096)*	0.1541 (2.272)*
1 if countries were or are the same country			0.0444 (1.021)	0.0344 (1.031)	0.0526 (0.948)
Number of peaceful years			-0.0066 (13.545)**	-0.0074 (-14.131)**	-0.0069 (-11.182)**
Number of other wars in year t			0.0035 (16.748)**	0.0025 (9.447)**	0.0039 (9.666)**
Dummy for alliance active in year t			-0.0593 (4.686)**	-0.0450 (-5.063)**	-0.0537 (-4.591)**
Pseudo-R2	0.047	0.208	0.300	0.309	-

Robust t statistics in parentheses (clustering at the country pair level);

\* significant at 5%; \*\* significant at 1%.

All columns estimated with 517,251 observations from 13,175 country pairs.

Probit marginal effects reported in columns (1)-(3). Logit marginal effects reported in column (4).

For dummy variables, marginal effects are for discrete changes from 0 to 1.

All marginal effects were multiplied by 100 for readability (underlying average probability of conflict is 0.72%)

Table 4: Sample breakdown by historical subperiod  
(dependent variable: dichotomous indicator of conflict; estimator: probit)

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	1816-2001 baseline	1816-1900	1901-2001	1914-1945	1946-2001	1919-1989	1990-2001
<b>Fst genetic distance, weighted</b>	<b>-0.9313 (8.922)**</b>	<b>-0.8059 (0.526)</b>	<b>-0.7590 (8.668)**</b>	<b>-0.6467 (0.684)</b>	<b>-0.3915 (7.293)**</b>	<b>-0.7591 (7.372)**</b>	<b>-0.3555 (5.317)**</b>
Log geodesic distance	-0.0735 (4.487)**	-0.3183 (2.887)**	-0.0608 (4.247)**	-0.5597 (5.745)**	-0.0216 (2.919)**	-0.0717 (4.225)**	-0.0081 (1.449)
1 for contiguity	0.4227 (7.760)**	0.8359 (3.759)**	0.3893 (7.645)**	0.6932 (2.585)**	0.2395 (7.411)**	0.5238 (7.235)**	0.1203 (4.851)**
# observations	517,251	32,292	484,959	50,281	423,790	330,365	139,159
# of pairs	13,175	799	13,175	2,027	13,175	10,397	13,175
Pseudo-R2	0.300	0.186	0.319	0.292	0.346	0.321	0.353

Robust t statistics in parentheses (clustering at the country pair level); \* significant at 5%; \*\* significant at 1%.

Probit marginal effects reported in all columns. For dummy variables, marginal effects are for discrete changes from 0 to 1. All marginal effects were multiplied by 100 for readability.

**Controls:** In addition to reported coefficients, every column includes controls for: Log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy=1 if pair shares at least one sea or ocean, log product of land areas in square km, dummy=1 if both countries are democracies ( $polity2 > 5$ ), dummy=1 for pairs ever in colonial relationship, dummy=1 if countries were or are the same country, number of peaceful years, number of other wars in year t, dummy for alliance active in year t.

**Table 5 - Regional analysis**  
 (dependent variable: dichotomous indicator of conflict; estimator: probit)

	(1)	(2)	(3)	(4)	(5)	(6)
	Baseline specification	Same continent dummy	Europe, with Europe FST Gen. Dist.	Asia	Africa	America
Fst genetic distance <sup>a</sup>	-0.9313 (8.922)**	-0.9711 (9.438)**	-49.5053 (1.976)*	-2.1541 (1.824)	-0.6891 (1.755)	-0.2466 (0.383)
Log geodesic distance	-0.0735 (4.487)**	-0.0788 (4.694)**	-0.2775 (1.878)	-0.2850 (4.087)**	-0.0199 (1.488)	-0.0478 (0.865)
1 for contiguity	0.4227 (7.760)**	0.4377 (7.875)**	-0.0090 (0.051)	0.6151 (3.885)**	0.5354 (4.252)**	0.5270 (3.911)**
1 of both countries are on the same continent		-0.0358 (2.380)*				
# of observations	517,251	517,251	22,006	28,738	31,017	35,398
# of pairs	13,175	13,175	291	866	848	581
Pseudo-R2	0.300	0.301	0.266	0.430	0.316	0.296

Robust t statistics in parentheses (clustering at the country pair level); \* significant at 5%; \*\* significant at 1%.

Probit marginal effects reported in all columns. For dummy variables, marginal effects are for discrete changes from 0 to 1. All marginal effects were multiplied by 100 for readability.

<sup>a</sup> : Weighted genetic distance in all columns except column (4), where FST genetic distance between plurality groups from the European genetic distance matrix is entered instead.

**Controls:** In addition to reported coefficients, every column includes controls for: Log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy=1 if pair shares at least one sea or ocean, log product of land areas in square km, dummy=1 if both countries are democracies (polity2>5), dummy=1 for pairs ever in colonial relationship, dummy=1 if countries were or are the same country, number of peaceful years, number of other wars in year t, dummy for alliance active in year t.

**Table 6 - Alternative measures of historical distance, including GD (dependent variable: dichotomous indicator of conflict; estimator: probit)**

	(1)	(2)	(3)	(4)
	Baseline specification	Add linguistic distance	Add religious distance	Add religious and linguistic distances
<b>Fst genetic distance, weighted</b>	<b>-1.1697 (8.613)**</b>	<b>-1.1717 (8.608)**</b>	<b>-1.1466 (8.501)**</b>	<b>-1.1461 (8.495)**</b>
Log geodesic distance	-0.0920 (4.301)**	-0.0921 (4.284)**	-0.0936 (4.390)**	-0.0936 (4.390)**
1 for contiguity	0.5621 (7.894)**	0.5516 (7.853)**	0.5219 (7.676)**	0.5224 (7.719)**
Linguistic Distance Index, weighted		-0.0298 (0.539)		0.0028 (0.043)
Religious Distance Index, weighted, Fearon			-0.0872 (1.777)	-0.0882 (1.518)
1 - % cognate measure of linguistic similarity, weighted				
# of observations	440,170	440,170	440,170	440,170
# of pairs	10,021	10,021	10,021	10,021
Pseudo-R2	0.292	0.292	0.293	0.293

Robust t statistics in parentheses; \* significant at 5%; \*\* significant at 1%

All coefficients multiplied by 100 for readability. The table reports marginal effects from probit estimates.

In addition to reported coefficients, all regressions include controls for log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy for pair shares at least one sea or ocean, log product of land areas in square km, dummy for both countries are democracies (polity2>5), dummy for pairs ever in colonial relationship, dummy for countries were or are the same country, number of peaceful years, number of other wars in year t, dummy for alliance active in year t.

**Table 7 - Nonlinearities and sample splits**  
(dependent variable: dichotomous indicator of conflict; estimator: probit)

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	Baseline	Excluding contiguous pairs	Contiguity interaction	Proximity interaction	Major power interaction	Spline	Quadratic
<b>Fst genetic distance, weighted</b>	<b>-0.9313</b> <b>(8.922)**</b>	<b>-0.6978</b> <b>(8.332)**</b>	<b>-0.9706</b> <b>(8.982)**</b>	<b>-0.9852</b> <b>(8.858)**</b>	<b>-0.9319</b> <b>(8.882)**</b>	<b>-1.0774</b> <b>(3.882)**</b>	<b>-0.3287</b> <b>(0.965)</b>
Log geodesic distance	-0.0735 (4.487)**	-0.0865 (6.131)**	-0.0750 (4.703)**	-0.0700 (4.269)**	-0.0592 (4.171)**	-0.0731 (4.414)**	-0.0743 (4.652)**
1 for contiguity	0.4227 (7.760)**		0.3232 (4.976)**	0.4030 (7.639)**	0.4536 (8.202)**	0.4261 (7.733)**	0.4064 (7.742)**
Fst Gen.Dist * contiguity			0.5419 (1.177)				
Fst Gen.Dist * proximity				0.3511 (1.309)			
Fst Gen. Dist * major power dummy					0.1382 (0.625)		
1 if at least one country is a major power					0.3043 (6.256)**		
Fst Gen.Dist * dummy for FST GD > median						0.1325 (0.586)	
Squared Fst genetic distance, weighted							-2.9895 (1.915)
# observations	517,251	503,748	517,251	517,251	517,251	517,251	517,251
# of pairs	13,175	12,928	13,175	13,175	13,175	13,175	13,175
Pseudo-R2	0.300	0.250	0.301	0.301	0.311	0.300	0.301

Robust t statistics in parentheses (clustering at the country pair level); \* significant at 5%; \*\* significant at 1%. Probit marginal effects reported in all columns. For dummy variables, marginal effects are for discrete changes from 0 to 1. All marginal effects were multiplied by 100 for readability.

**Controls:** In addition to reported coefficients, every column includes controls for: Log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy=1 if pair shares at least one sea or ocean, log product of land areas in square km, dummy=1 if both countries are democracies (polity2>5), dummy=1 for pairs ever in colonial relationship, dummy=1 if countries were or are the same country, number of peaceful years, number of other wars in year t, dummy for alliance active in year

**Table 8 – Regressions explaining the intensity of conflict  
(dependent variable and estimator as described in the second row)**

	(1)	(2)	(3)	(4)	(5)	(6)
	OLS on conflict intensity variable	OLS on conflict intensity in subsample with conflict	IV on conflict intensity using 1500 GD as IV	OLS on number of war casualties	OLS on number of war casualties, sample with positive casualties	Probit on War dummy variable (conflict intensity=5)
<b>Fst genetic distance, weighted</b>	<b>-0.1685 (8.290)**</b>	<b>0.2536 (0.613)</b>	<b>-0.2757 (7.413)**</b>	<b>-0.1153 (8.055)**</b>	<b>-0.9103 (0.611)</b>	<b>-0.0875 (6.001)**</b>
Log geodesic distance	-0.0330 (4.245)**	0.0032 (0.090)	-0.0263 (3.126)**	-0.0161 (3.549)**	-0.1013 (0.463)	-0.0061 (2.663)**
1 for contiguity	0.2983 (7.693)**	-0.0785 (1.403)	0.2983 (7.696)**	0.0881 (4.982)**	-1.2939 (5.105)**	0.0051 (1.221)
1 if both countries are democracies (polity2>5)	-0.0297 (10.703)**	-0.1377 (1.954)	-0.0317 (10.918)**	-0.0187 (11.204)**	-0.9759 (1.586)	-0.0113 (5.838)**
Number of peaceful years	-0.0008 (9.996)**	-0.0041 (5.990)**	-0.0008 (9.987)**	-0.0004 (9.438)**	-0.0021 (0.641)	-0.0011 (7.190)**
Number of other wars in year t	0.0011 (12.483)**	0.0063 (11.912)**	0.0011 (12.785)**	0.0009 (10.544)**	0.0075 (3.950)**	0.0005 (16.540)**
Dummy for alliance active in year t	-0.0418 (4.955)**	-0.2373 (6.096)**	-0.0414 (4.906)**	-0.0279 (5.994)**	-0.3757 (1.331)	-0.0082 (5.337)**
# observations	517,251	3,844	517,251	516,758	1,531	517,251
# of pairs	13,175	741	13,175	13,175	394	13,175
Adjusted R-squared <sup>a</sup>	0.042	0.135	0.042	0.013	0.252	0.311

Robust t statistics in parentheses (clustering at the country pair level); \* significant at 5%; \*\* significant at 1%.

<sup>a</sup>. Pseudo R-squared in column 6.

Probit marginal effects reported in column (6), where: for dummy variables, marginal effects are for discrete changes from 0 to 1; all marginal effects were multiplied by 100 for readability.

**Controls:** In addition to reported coefficients, every column includes controls for log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy=1 if pair shares at least one sea or ocean, log product of land areas in square km, dummy=1 for pairs ever in colonial relationship, dummy=1 if countries were or are the same country.

**Table 9: Post-1950 analysis, controlling for trade variables and absolute income differences  
(dependent variable: dichotomous indicator of conflict; estimator: probit)**

	(1)	(2)	(3)	(4)	(5)	(6)
	Baseline with common sample	Control for trade terms	Additional trade terms	Baseline with common sample	Add per capita income difference	Add total income difference
<b>Fst genetic distance, weighted</b>	<b>-0.5223</b> (7.181)**	<b>-0.3247</b> (5.810)**	<b>-0.3098</b> (5.485)**	<b>-0.3119</b> (4.974)**	<b>-0.3531</b> (5.386)**	<b>-0.3240</b> (4.673)**
Log geodesic distance	-0.0154 (2.107)*	0.0047 (0.721)	0.0043 (0.652)	0.0034 (0.509)	0.0018 (0.269)	0.0032 (0.477)
1 for contiguity	0.2528 (6.638)**	0.2186 (7.349)**	0.2134 (7.326)**	0.2313 (7.098)**	0.2762 (7.520)**	0.2326 (7.160)**
Log bilateral openness, t-4		-0.0414 (4.813)**	-0.0395 (4.546)**	-0.0403 (4.327)**	-0.0360 (4.145)**	-0.0400 (4.306)**
Log multilateral openness, t-4		0.0552 (1.993)*	0.0595 (2.191)*	0.0327 (1.032)	0.0158 (0.527)	0.0306 (0.962)
Log distance * log mult. openness		-0.0093 (2.656)**	-0.0098 (2.854)**	-0.0071 (1.789)	-0.0048 (1.289)	-0.0068 (1.700)
Log distance * log bilateral openness		0.0054 (5.095)**	0.0053 (4.883)**	0.0053 (4.627)**	0.0047 (4.398)**	0.0052 (4.490)**
Dummy for zero trade, t-4		-0.0159 (2.382)*	-0.0159 (2.431)*	-0.0137 (1.898)	-0.0127 (1.748)	-0.0149 (2.034)*
Free trade area (full set)			-0.0236 (2.859)**	-0.0226 (2.576)*	-0.0214 (2.310)*	-0.0221 (2.526)*
# of GATT members			-0.0147 (3.768)**	-0.0172 (4.158)**	-0.0162 (3.888)**	-0.0170 (4.134)**
Absolute difference in log per capita income					1.6297 (4.790)**	
Absolute difference in total GDP						0.1909 (0.773)
# of observations	226,357	226,357	226,357	202,523	202,523	202,523
# of pairs	9,127	9,127	9,127	9,127	9,127	9,127
Pseudo-R2	0.336	0.350	0.353	0.351	0.356	0.351

Robust t statistics in parentheses (clustering at the country pair level);

\* significant at 5%; \*\* significant at 1%.

Probit marginal effects reported in all columns. For dummy variables, marginal effects are for discrete changes from 0 to 1. All marginal effects were multiplied by 100 for readability.

**Controls:** In addition to reported coefficients, every column includes controls for: Log absolute difference in longitudes, log absolute difference in latitudes, number of landlocked countries in the pair, number of island countries in the pair, dummy=1 if pair shares at least one sea or ocean, log product of land areas in square km, dummy=1 if both countries are democracies (polity2>5), dummy=1 for pairs ever in colonial relationship, dummy=1 if countries were or are the same country, number of peaceful years, number of other wars in year t, dummy for alliance active in year t.

**Table 10: OLS Analysis of UN Vote Correlations Data, 1946-2000**

	(1)	(2)	(3)	(4)	(5)
	Univariate	Add geography controls	Full specification	1990-2000	Excluding abstentions
Fst genetic distance, weighted	0.2657 (13.356)**	0.2852 (14.140)**	0.2923 (14.363)**	0.1500 (8.033)**	0.4709 (15.590)**
Log geodesic distance		0.0240 (5.764)**	0.0276 (6.654)**	0.0143 (4.006)**	0.0435 (7.406)**
Log absolute difference in longitudes		-0.0199 (8.052)**	-0.0186 (7.841)**	-0.0081 (3.856)**	-0.0282 (8.251)**
Log absolute difference in latitudes		-0.0387 (26.599)**	-0.0370 (25.206)**	-0.0355 (24.698)**	-0.0694 (31.779)**
1 for contiguity		0.0535 (5.271)**	0.0539 (5.617)**	0.0300 (2.962)**	0.0806 (5.835)**
Number of landlocked countries in the pair		0.0171 (6.661)**	0.0177 (6.861)**	0.0205 (9.460)**	0.0177 (4.561)**
Number of island countries in the pair		0.0298 (10.593)**	0.0301 (10.909)**	0.0300 (11.194)**	0.0408 (9.562)**
1 if pair shares at least one sea or ocean		-0.0183 (3.456)**	-0.0294 (5.643)**	-0.0325 (5.344)**	-0.0470 (6.701)**
Log product of land areas in square km		-0.0061 (10.591)**	-0.0063 (10.759)**	0.0001 (0.234)	-0.0097 (11.683)**
1 if both countries are democracies (polity2>5)			-0.0071 (2.100)*	-0.0338 (9.939)**	-0.0437 (9.332)**
1 for pairs ever in colonial relationship			-0.1224 (9.184)**	-0.1451 (10.500)**	-0.2133 (11.464)**
Number of peaceful years			0.0005 (7.853)**	-0.0001 (2.111)*	0.0007 (7.992)**
Number of other conflicts in year t			0.0013 (32.156)**	-0.0004 (33.041)**	0.0023 (46.343)**
Dummy for alliance active in year t			0.0614 (12.096)**	0.0442 (6.785)**	0.1078 (14.887)**
Constant	0.8347 (278.491)**	0.9436 (31.987)**	0.8311 (26.381)**	0.9103 (32.921)**	0.6499 (14.837)**
Adjusted R-squared	0.008	0.074	0.100	0.101	0.147

Robust t statistics in parentheses; \* significant at 5%; \*\* significant at 1%; All regressions run on 385,783 observations from 12,655 country pairs; Note: Ever the same country dummy excluded as regressor as no pair in the sample with UN vote correlations data was made up of countries that were ever a single country.