

# Kin-based institutions and economic development

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How can we explain global differences in economic prosperity? While this is perhaps the oldest question in economics, a great deal of progress has been made in the last two decades as new data sources and fresh insights have accumulated. Researchers have argued for the importance of factors related to climate and geography (Diamond 1997; Hibbs & Olsson 2004), disease (Alsan 2015), political institutions (Acemoglu et al. 2002), colonialism (Acemoglu et al. 2009; Dell 2010), human capital (Glaeser et al. 2004), and culture (Alesina & Giuliano 2013; Landes; Tabellini 2010). While important roles for many factors have been demonstrated, these are likely part of complex causal networks in which aspects of climate, geography, ecology and endemic diseases impact cultural evolution, beliefs, preferences, social norms, institutions, and technologies (Enke 2019; Schulz et al. 2019; Spolaore & Wacziarg 2013). In this paper, we aim to contribute to mapping this causal web by examining whether the tightness and breadth of family organizations—what we'll call *kinship intensity*—can contribute to explaining differences in economic prosperity around the globe.

Focusing on the oldest and most fundamental of human institutions—those based on extended kinship and marriage—we argue that *kin-based institutions* shape people's ways of thinking, motivations, social networks and personal incentives (Schulz et al. 2019). These social and psychological differences induced by kin-based institutions, which vary substantially around the globe and back into history (Murdock 1967), then influence the formation and functioning of larger-scale political and economic institutions. Existing research indicates, for example, that greater kinship intensity is associated with lower levels of trust, individualism, and cooperation with strangers, but greater corruption, conformity and nepotism (Akbari et al. 2016; Bergeron 2020; Enke 2019; Schulz et al. 2019) as well as less well-functioning democratic institutions (Schulz 2017a).

Here, we focus narrowly on the reduced-form linkage between kinship intensity and economic prosperity. Combining pixel- and population-level data on satellite luminosity (a proxy for economic development), regional GDP, marriage practices and kin-based institutions, biogeographic variables, and genotypic data (from which we estimate inbreeding levels), we establish a tight empirical link between kinship intensity on the one hand and economic development at the other. Our results hold across countries, within country at both the regional and population (ethnicity) levels, and within country in regression-discontinuity design specifications (RDD). Below, we report a subset of these results, emphasizing results that involve genotypic data.

## Data

To measure economic prosperity, we rely primarily on satellite luminosity data, which has been shown to be a good proxy for economic development (Donaldson & Storeygard 2016;

Henderson et al. 2018). We supplement that data with more direct measures of economic growth (Gennaioli et al. 2014; results not presented here).

To measure kinship intensity, we employ two approaches. First, following Schulz et al. (2019), we compute a *kinship-intensity index* (KII). To do so, we combine data from the *Ethnographic Atlas*, a compilation of anthropological observations based on coding ethnographies from over 1,200 societies, and global language phylogenies from over 7,000 ethno-linguist communities (Lewis 2009).

Second, we analyze contemporary genotypic data from the Human Origins (HO) dataset (*Human Origins dataset*; Lazaridis et al. 2016) and compute each individual's coefficient of inbreeding—denoted  $F$ .  $F$  is a fundamental variable in population genetics that measures the probability that two alleles at a location in the genome are identical by descent. The expected value of an individual's  $F$  coefficient increases with the degree of relatedness of that individual's parents. Longer runs of homozygosity (ROH) are typically observed as a result of inbreeding (Ceballos et al. 2018), and have been shown to correlate well with pedigree-based estimates of inbreeding (McQuillan et al. 2008). Our goal is to infer consanguineous marriage practices from inbreeding coefficients estimated using ROH.

We estimate the inbreeding coefficient by using the ROHgen2 pipeline developed by Clark et al. (2019) to compute  $F_{ROH}$ , which is the fraction of an individual's genome that is located in ROH that are longer than 1.5 Mb.<sup>1</sup> Shorter ROH are more likely to arise from population structure or lack of genetic diversity whereas longer ROH tend to arise from inbreeding (Ceballos et al. 2018; Kang et al. 2017; Pemberton et al. 2012). We then compute the average  $F_{ROH}$  across the individuals in a population as our proxy for the level of consanguineous marriage practices in the population.

ROH can arise in individuals for a variety of reasons unrelated to marital practices and kinship systems. For example, ROH and inbreeding coefficients are inflated in genetically isolated populations, since low effective population sizes can increase homozygosity (Pemberton & Rosenberg 2014). In addition, inbreeding coefficients are highly correlated with distance from Africa, consistent with a migration model that predicts increased genetic drift and decreased heterozygosity with increased distance from Africa (Pemberton & Rosenberg 2014). We therefore compute several quantities that are correlated with ROH and unrelated to parental relatedness, and we include these quantities in our main regressions as controls. For each population, we use the HO genetic data to compute each population's mean regional pairwise  $F_{ST}$ , mean expected heterozygosity, and mean on each of the top 20 principal components of the genotype.

We emphasize that, though  $F$  is a *genetic* variable that can be measured from the genome, the relevant variation in  $F$  for our analyses captures *cultural* practices. The correlation we document below between  $F$  and marriage practices arises because when relatives mate and produce an offspring, that offspring will tend to have more ROH and thus a higher  $F$ . The arrow of causation runs from marriage practices to  $F$ , and not vice versa.

To measure population density and biogeographic factors (including temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake), we combine geocoded data from various sources.

<sup>1</sup> A megabase (Mb) is a unit of physical distance in the genome; the entire genome is ~3,100 Mb in length.

We match the different variables to *Ethnologue* populations based on language and using ArcGIS as needed.

## Analyses and preliminary results

Figure 1 shows the distribution of light density across the world and Figure 2 shows the distribution of the KII across the world. As can be seen, low-KII areas tend to have denser lights.

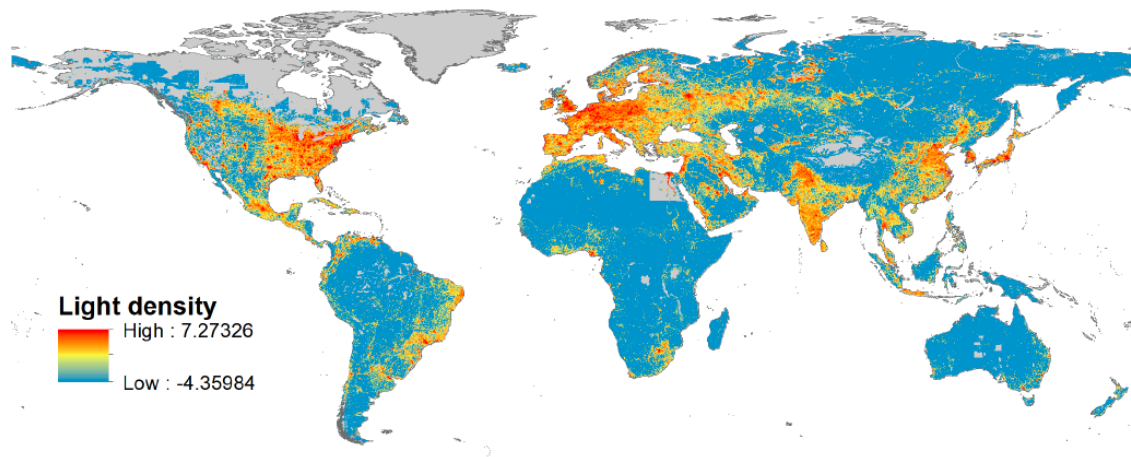


Figure 1: Log light density across the world. Unpopulated regions are in gray. Blue color indicates regions that have some population density but also the lowest light density. Note that in regions such as Egypt where GPW uses data at a finer scale, populated areas are separated from the surrounding uninhabited desert areas. This cannot be done in neighboring countries where data reports a low population number for larger areas with sparse settlements.

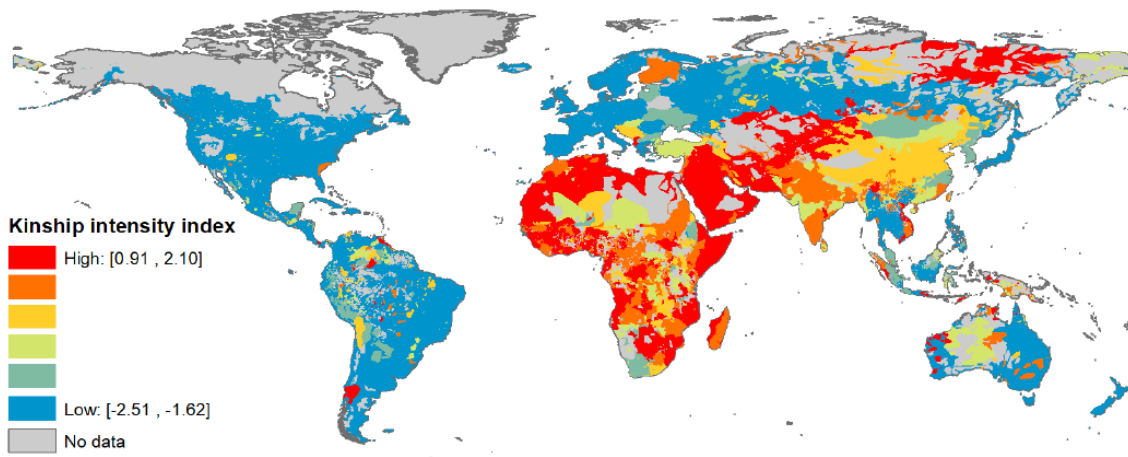


Figure 2: Kinship intensity index (KII) of 2,352 ethno-linguistic groups across the world. Regions with no population, no *Ethnologue* or *Ethnographic Atlas* data are in gray.

Table 1 shows the results of regressions of log light density on the KII and control variables (including log population density and biogeographic variables) across 377,656 geographic pixels that cover inhabited parts of the world. Even when country fixed effects (FEs) are

included (in Column 6), we estimate a negative and significant association between the KII and light density. Our estimate with country FEs suggests a one-standard-deviation increase in the KII is associated with a 5.2% increase in light density.

VARIABLES	Log light density				
	(2)	(3)	(4)	(5)	(6)
KII	-0.499*** (0.152)	-0.409*** (0.144)	-0.099** (0.046)	-0.109** (0.044)	-0.052** (0.023)
Log population density quadratic	yes	yes	yes	yes	yes
Geographic controls		yes	yes	yes	yes
Continent FE			yes		
Regions FE				yes	
Country FE					yes
Observations	377,656	377,656	377,656	377,656	377,656
R-squared	0.488	0.538	0.584	0.620	0.665
Number of clusters	138	138	138	138	138

**Table 1.** The unit of analysis is a pixel of 0.125 x 0.125 decimal degrees. The Sample of ethnicities with KII based on direct matching to the EA. Regression 4, 5, and 6 control for fixed effects of 5 continents, 15 sub-continent regions, and 138 countries respectively. Standard errors, clustered at country-level, are in parentheses. \*\*\* p<0.01, \*\* p<0.05, \* p<0.1

In Table 2, we regress light density on  $F_{ROH}$  and control variables. We again estimate a negative and significant association, even when country FEs are included.

VARIABLES	Log light density					
	(2)	(3)	(4)	(5)	(6)	(7)
mean_f_roh	-37.519* (19.645)	-31.875*** (12.115)	-30.590*** (11.557)	-26.126** (11.940)	-13.708 (12.652)	-20.615*** (7.427)
Log population density quadratic	yes	yes	yes	yes	yes	yes
Genetic controls		yes	yes	yes	yes	yes
Geographic controls			yes	yes	yes	yes
Continent FE				yes		
Region FE					yes	
Country FE						yes
Observations	280,974	280,974	280,974	280,974	280,974	280,974
R-squared	0.501	0.642	0.658	0.660	0.664	0.679
Number of clusters	98	98	98	98	98	98

**Table 2.** The unit of analysis is a pixel of 0.125 x 0.125 decimal degrees. Standard errors, clustered at country-level, are in parentheses. \*\*\* p<0.01, \*\* p<0.05, \* p<0.1

Finally, in Table 3, we regress a measure of cousin marriage preferences from the *Ethnographic Atlas* on  $F_{ROH}$  and controls, and in Table 4 we regress the KII on  $F_{ROH}$  and controls. We estimate positive and significant relationships, indicating that a higher  $F_{ROH}$  is associated with stronger preferences for cousin marriage and with a higher KII. With country FEs, including  $F_{ROH}$  in a regression of cousin marriage preferences on control variables increases the  $R^2$  of the regression by 0.117 versus a baseline  $R^2$  of 0.683 in the regression with only the controls, indicating that  $F_{ROH}$  accounts for more than a third of the variation left in cousin marriage preferences after controlling for the controls.

VARIABLES	Cousin marriage preference				
	(1)	(2)	(3)	(4)	(5)
(mean) mean_f_roh_HO	18.491*** (5.346)	45.744*** (5.653)	44.566*** (5.772)	41.839*** (5.772)	37.557*** (8.379)
Genetic controls		yes	yes	yes	yes
Continent FE			yes		
Region FE				yes	
Country FE					yes
Observations	398	397	397	397	397
R-squared	0.077	0.433	0.453	0.491	0.683
Number of clusters	127	127	127	127	127
dr2_r20	0.0775	0.144	0.174	0.127	0.117

**Table 3.** The unit of analysis is an ethnicity (a population). Standard errors, clustered at country-level, are in parentheses. Geographic controls include PCs.

\*\*\* p<0.01, \*\* p<0.05, \* p<0.1

VARIABLES	KII				
	(1)	(2)	(3)	(4)	(5)
mean_f_roh	11.641*** (3.067)	13.185*** (2.714)	13.319*** (2.761)	11.999*** (2.682)	14.549*** (4.033)
Genetic controls		yes	yes	yes	yes
Continent FE			yes		
Region FE				yes	
Country FE					yes
Observations	396	395	395	395	395
R-squared	0.066	0.717	0.720	0.743	0.843
Number of clusters	127	127	127	127	127
dr2_r20	0.0665	0.0570	0.0666	0.0487	0.0797

**Table 4.** The unit of analysis is an ethnicity (a population). Standard errors, clustered at country-level, are in parentheses. Geographic controls include PCs.

\*\*\* p<0.01, \*\* p<0.05, \* p<0.1

To conclude, we document a strong statistical relationship between measures of kinship intensity and a light density, a proxy for economic development. Possible mechanisms involve the impact of kinship intensity on psychology, cooperation, and corruption (Akbari et al. 2016; Bergeron 2020; Enke 2019; Schulz et al. 2019) and political institutions (Schulz 2017b; Woodley & Bell 2012) and their plausible impact on property rights, labor specialization and trade, and innovation. We caution, however, against concluding that intensive kin-based institutions are less desirable and that policy should seek to dismantle them: in many places, intensive kin-based institutions play a critical role in providing a safety net and maintaining social order. Tight family network may also foster happiness and life satisfaction (Alesina & Giuliano 2012).

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