# Ancestry, Place, and Belief in Witchcraft as a Cause of Illness: Evidence from Contemporary Africa*

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**Abstract**

Supernatural explanations of illness have deep historical roots and remain widespread around the world. This paper examines how beliefs in witchcraft as a cause of HIV/AIDS are structured in contemporary Sub-Saharan Africa. The analysis draws on multiple waves of the Demographic and Health Surveys conducted in 27 countries between 2000 and 2019, covering nearly one million respondents from 675 ethnolinguistic groups. Combined with global language phylogeny and geocoded survey locations, these data are used to estimate a generalized linear mixed model that partitions variation in witchcraft beliefs into components reflecting shared ancestry, spatial proximity, and national context, conditional on sociodemographic characteristics. Estimation results show that these three broad dimensions account for substantial and similar shares of variation once modeled jointly, with no single component emerging as dominant. These findings suggest that contemporary supernatural attributions of illness are simultaneously shaped by ancestry and place.

*Keywords*: ancestry, cultural evolution, phylogenetic comparative methods, Sub-Saharan Africa, supernatural, witchcraft beliefs.

*JEL Classification Numbers*: I12, Z10, Z12, Z13

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# 1 Introduction

Supernatural explanations of illness have long occupied a central place in anthropological research (Foster, 1976; Murdock, 1980). Societies around the globe maintain shared cultural frameworks that attribute suffering to forces beyond natural causes and shape how individuals and communities respond to misfortune and assign blame. The attribution of illness to witchcraft – intentional harm inflicted by other people through supernatural means – has received particular attention in both seminal studies (Evans-Pritchard, 1937) and recent quantitative research (Willard et al., 2025).

Witchcraft beliefs have been documented for centuries in historical and ethnographic sources and remain widespread in contemporary societies. Survey evidence shows that such beliefs cut across continents, countries, ethnic groups, and sociodemographic strata (Gershman, 2022, 2023). Sub-Saharan Africa in particular displays a high prevalence of witchcraft beliefs, both in general (Gershman, 2016, 2026) and in the context of explaining illness (Sievert, 2025). Attributing disease to witchcraft and other supernatural causes has been linked to greater reliance on traditional healers, lower use and perceived efficacy of modern medicine, and stigmatization of people with certain illnesses, with broad implications for individual well-being and public health across the continent (Lowes and Montero, 2019; Sievert, 2025). Witchcraft-based explanatory frameworks have also been adapted to relatively recent diseases, most notably HIV/AIDS, illustrating how traditional culture is mobilized in new epidemiological contexts (Liddell et al., 2005; Rödlach, 2006).

Even as witchcraft beliefs persist across communities in Africa and worldwide, their prevalence varies substantially, and recent studies document a range of correlates at the individual, ethnic group, and country levels (Gershman, 2023). Rather than focusing on specific factors, this paper examines how heterogeneity in contemporary witchcraft beliefs as a cause of illness is structured across three broad sources: shared ancestry, spatial proximity, and national context.

The analysis draws on multiple waves of the Demographic and Health Surveys (DHS) conducted in 27 African countries between 2000 and 2019, comprising nearly one million respondents. These surveys provide harmonized individual-level data on beliefs that HIV/AIDS can be caused by witchcraft or other supernatural forces, along with information on respondents' ethnic identity, residential location, and sociodemographic characteristics. We combine these data with global language trees and employ a spatio-phylogenetic mixed-effects modeling framework to partition the variation in witchcraft beliefs across the domains of interest.

Our dataset spans a vast geographic area and encompasses 675 distinct ethnolinguistic groups, providing extensive coverage of Africa's cultural diversity. Furthermore, given the continent's colonial history and the high mobility of contemporary populations, individuals of the same ethnolinguistic ancestry frequently live in different countries and regions, while local communities commonly comprise people from diverse ethnic and socioeconomic backgrounds (Gershman and Rivera, 2018; Gershman and Upadhyay, 2026). This combination of broad coverage and population mixing creates empirical leverage to jointly model the contributions of ancestry, spatial proximity, and national context. Our results indicate that each of these three sources accounts for a substantial share of observed heterogeneity in beliefs, with no single component emerging as dominant.

Although our analysis is descriptive, characterizing the structure of variation in witchcraft beliefs is directly relevant for understanding their diffusion and persistence. One way to interpret this structure is through the lens of standard social learning frameworks (Fogarty and Kandler, 2025). For example, clustering by shared ancestry is consistent with intergenerational transmission within groups, while clustering along spatial and national dimensions may reflect horizontal or oblique transmission operating through social interaction. However, such clustering need not reflect cultural transmission processes alone and may also capture adaptive responses to common epidemiological, ecological, or institutional conditions. This perspective builds on earlier empirical work linking cultural variation across African societies to linguistic affiliation, ecology, and geographic proximity, corresponding to distinct mechanisms of cultural transmission and adaptation (Guglielmino et al., 1995).

This paper contributes to a large literature on the cultural evolution and transmission of supernatural beliefs (Swanson, 1960; Gervais et al., 2011; White et al., 2021; Bisin et al., 2023; Lesage et al., 2025). While much of this literature has focused on doctrinal religions, there has been growing interest in witchcraft and related beliefs, including their social benefits and costs (Gershman, 2023). Recent work has highlighted a range of functions that witchcraft beliefs may perform at the group or individual levels. One strand of the literature emphasizes their role in supporting in-group cohesion and self-governance through the enforcement of normative conformity in settings with weak formal institutions (Leeson, 2021; Gershman, 2022). Other research points to distributional functions, whereby witchcraft beliefs sustain leveling norms, discourage conspicuous accumulation, and facilitate redistributive transfers in the presence of social comparisons and economic inequality (Platteau, 2014; Gershman, 2015). Relatedly, such beliefs may limit excessive competition in zero-sum environments (Bergeron et al., 2025), while witchcraft accusations may be deployed strategically to sanction or eliminate rivals under conditions of resource scarcity (Peacey et al., 2022). Finally, witchcraft beliefs have long been argued to provide intuitive frameworks for explaining and responding to adverse events (Gershman, 2020; Boyer, 2021, 2022; Singh, 2021; Planer and Sterelny, 2024). At the same time, these functions may come with substantial costs: witchcraft beliefs have been linked to reduced cooperation and trust, elevated anxiety and lower life satisfaction, pessimistic worldviews, and weaker innovative activity (Gershman, 2016, 2022, 2026; Mace et al., 2018; Le Rossignol et al., 2022).

Despite this growing research agenda, evidence on the cultural transmission and the overall structure of variation in witchcraft beliefs across populations remains limited. Case studies from Sub-Saharan Africa reveal diverse patterns in the spread and persistence of witchcraft beliefs across social groups. In a classic comparative analysis of two neighboring but linguistically distinct societies of the Nuba Mountains of Sudan, Nadel (1952) documents a striking contrast despite their spatial proximity, shared environments, and frequent interaction: while the Korongo are described as having "no witchcraft beliefs at all," the Mesakin are "literally obsessed" with fears of witchcraft and accusations. By contrast, McElreath (2004) shows that individuals migrating between farming and pastoralist regions in rural Tanzania tend to adjust their beliefs toward those prevalent in their community of residence, highlighting horizontal learning. Finally, Adinkrah (2015) explores a range of national-scale socialization channels in contemporary Ghana – such as formal schooling, mass media, and religious institutions – through which witchcraft beliefs are reinforced and transmitted beyond the family and local community.

Quantitative research exploring the correlates of contemporary witchcraft beliefs also points to distinct channels of transmission and persistence. Gershman (2020) shows that in Sub-Saharan Africa, witchcraft beliefs are more prevalent among members of ethnic groups historically more exposed to the Atlantic slave trade, consistent with long-term intergenerational persistence. In Latin America, witchcraft beliefs are more widespread among Afro-descendants and residents of regions historically more reliant on slave labor, in line with both vertical and horizontal cultural transmission. Other empirical findings highlight the role of nationwide factors. For example, Gershman (2022) shows a strong negative association between the prevalence of witchcraft beliefs and the quality of government institutions in a global sample, while Sievert (2025) finds that the availability of antiretroviral therapy at the country level is associated with lower rates of attributing HIV/AIDS to supernatural forces in Sub-Saharan Africa. Together, these findings point to multiple dimensions of variation in witchcraft beliefs, underscoring the need for an approach that considers them jointly.

On the methodological side, this paper contributes to a growing body of research using phylogenetic comparative methods to study the distribution and dynamics of cultural traits, including supernatural beliefs (Mace and Pagel, 1994; Peoples et al., 2016; Mace and Zhang, 2025; Watts, 2025; Gershman and Mumladze, 2025). Most closely related is the recent study by Peacey et al. (2024), which uses ethnographic data on Bantoid societies of Sub-Saharan Africa to examine the cultural evolution of the "witchcraft phenotype." They show that some features, such as poison ordeals, exhibit strong phylogenetic signal, while others appear more labile. Their analysis operates at the ethnographic society level and focuses on the configuration of witchcraft-related traits rather than on variation in belief prevalence. In contrast, this study draws on individual-level survey data from contemporary populations to characterize how variation in witchcraft beliefs is structured across multiple dimensions.

The remainder of the paper is organized as follows. Section 2 describes the data and ethnicity-level patterns. Section 3 outlines the modeling framework, presents the main results, and discusses their implications. Section 4 concludes.

# 2 Data and ethnicity-level patterns

## 2.1 Main dataset and descriptive statistics

The main data for this study come from multiple waves of the Demographic and Health Surveys. The DHS are large-scale nationally representative household surveys, administered in low- and middle-income countries since the 1980s and containing comparable data on numerous indicators related to health, education, and material well-being. The surveys were implemented by the consulting and research firm ICF and its local partners, with primary funding from the United States Agency for International Development (USAID), the main sponsor of the program until 2025.

We focus on Sub-Saharan Africa and pool the data for 27 countries spanning the period between 2000 and 2019.[1] Our master sample is based on simultaneous availability

[1]These countries and survey waves (in parentheses) are, in alphabetical order, Benin (2006, 2011, 2017), Burkina Faso (2003, 2010), Cameroon (2004, 2011, 2018), Chad (2004, 2014), Côte d'Ivoire (2011), Democratic Republic of the Congo (2007, 2013), Eswatini (2006), Ethiopia (2005, 2011, 2016), Gabon (2000, 2012), Gambia (2013, 2019), Ghana (2003, 2008, 2014), Guinea (2005, 2012, 2018), Kenya (2008,

of the main survey question of interest and self-reported ethnicity identifiers of respondents required for investigating the role of ancestry.[2] Specifically, the survey question asks, "Can people get HIV/AIDS because of witchcraft or other supernatural means?", with response options "yes," "no," and "don't know." For brevity, in what follows we call it the "witchcraft question" and refer to "yes" respondents as "witchcraft believers."

The DHS cover all eligible women of reproductive age (15-49) in sampled households, but only a subset of men, resulting in a substantially larger number of female respondents. This reflects the program's focus on maternal and child health, with men's interviews included mainly for comparative and contextual purposes. We combine women's and men's samples to maximize the number of observations per ethnolinguistic group and improve the reliability of estimates. Overall, women constitute about 70% of the combined sample of close to a million individuals.[3] All surveys contain at least some information on the spatial location of households, as discussed in greater detail in section 3.

We rely on recent estimates of global time-calibrated language trees from Bouckaert et al. (2022) to approximate ancestral relationships between ethnolinguistic groups in our sample. These trees cover most extant languages and are derived using Bayesian inference techniques applied to multiple sources of information. These include the *Glottolog* database (Hammarström et al., 2019) for primary family classifications, language locations, existing phylogenies for nine major groups, and a wealth of historical, linguistic, genetic, and archaeological evidence. The posterior sample contains 902 global trees reflecting a substantial degree of phylogenetic uncertainty. All trees are rooted, ultrametric, and bifurcating, with

2014), Lesotho (2004), Liberia (2007, 2013, 2019), Malawi (2004, 2010, 2016), Mali (2006, 2012, 2018), Mozambique (2011), Namibia (2006, 2013), Niger (2006), Nigeria (2003, 2008, 2013, 2018), Republic of the Congo (2005, 2011), Senegal (2005, 2010, 2014, 2015, 2016, 2017), Sierra Leone (2008, 2013, 2019), Togo (2013), Uganda (2011, 2016), and Zambia (2007, 2013). The surveys were accessed through DHS (`https://dhsprogram.com`) and the IPUMS-DHS project (`https://www.idhsdata.org/idhs`).

[2]In two highly ethnically homogeneous countries, Eswatini and Lesotho, home language of respondents was used as a proxy for their ethnic identity. The Democratic Republic of the Congo surveys provide a classification largely based on geography rather than ethnicity, and we only have a reliable identifier for a single group, the Lunda.

[3]Existing evidence suggests that, both in Sub-Saharan Africa and globally, there is no systematic gender difference in witchcraft beliefs once other sociodemographic characteristics are taken into account (Gershman, 2020, 2022). In this sense, the overrepresentation of women in the DHS sample is unlikely to be a major concern. Furthermore, the main analysis in section 3 controls for gender across specifications. Interestingly, in the baseline model women are estimated to be somewhat more likely than men to attribute HIV/AIDS to witchcraft or other supernatural causes (figure 7), in contrast to earlier results on witchcraft beliefs in general.

tree height ranging from 75,000 to 120,000 years. Most diversification events are estimated to be fairly recent, with the vast majority of language splits occurring within the last 5,000 years. Our baseline analysis relies on the maximum clade credibility (MCC) summary tree, but we also conduct robustness checks using the entire available posterior sample.

The list of original ethnicity identifiers reported in the DHS data was thoroughly inspected and matched to the global language trees based on glottocodes, unique identifiers from the *Glottolog* database used by Bouckaert et al. (2022) to label tree tips. This matching standardizes the notion of an ethnolinguistic group as corresponding to a unique glottocode, which is important given the variety of classifications used in the DHS. In some cases, multiple groups were matched to the same glottocode, which happened for two reasons. First, many African ethnic groups have alternative names and spellings, often listed as separate identifiers in the original data. Second, some of the more detailed surveys differentiated between subgroups of the same ethnicity that either speak the same language or its dialects that do not have separate glottocodes.[4] The final dataset covers 675 ethnolinguistic groups belonging to 22 primary language families and one classified as an isolate, according to *Glottolog* 4.0. The two largest families are Atlantic-Congo and Afro-Asiatic, including 454 and 106 languages, respectively. Other sizable families are Mande, Nilotic, and Ta-Ne-Omotic, with the remaining ones consisting of less than 10 languages each.

Although our matching yields a large number of standardized ethnolinguistic groups, many of them have a relatively small number of respondents. While this is not an issue for the main analysis of section 3, it matters for the preliminary ethnicity-level patterns presented in the remainder of this section. According to DHS guidelines, any statistics based on fewer than 25 cases are suppressed and those based on 25 to 49 cases are marked as unreliable in final reports (Croft et al., 2023). Following these guidelines, in the ethnicity-level analysis, we drop all groups with fewer than 50 combined observations across all survey years. This leaves 451 groups, most of which are still fairly small, with a median size of 455 respondents. The five largest groups are, in descending order, Hausa, Pulaar, Wolof, Nyanja, and Yoruba, each with roughly 30-40 thousand respondents.

As shown in table 1, 16% of individuals in the full sample are witchcraft believers, 74% are non-believers, and 10% give "don't know" responses, with substantial variation in prevalence across countries and ethnolinguistic groups. At the country level, the share of believers ranges from 4.5% in Eswatini to 53% in the Republic of the Congo, with an average of 18% across 27 countries in the sample. At the ethnicity level, belief prevalence

[4]Our sample excludes creole groups, a few native African languages not covered by the global phylogenies, and Indo-European languages.

Table 1: Witchcraft beliefs across individuals, countries, and ethnolinguistic groups.

| | Sample size | Mean | St. dev. | Min | Max |
|---|---|---|---|---|---|
| *Individuals* | 958,295 | | | | |
| Yes (binary) | | 0.16 | | | |
| No (binary) | | 0.74 | | | |
| Don't know (binary) | | 0.10 | | | |
| *Countries* | 27 | | | | |
| Yes (share) | | 0.18 | 0.13 | 0.04 | 0.53 |
| No (share) | | 0.72 | 0.16 | 0.35 | 0.92 |
| Don't know (share) | | 0.10 | 0.05 | 0.03 | 0.19 |
| *Ethnolinguistic groups* | 451 | | | | |
| Yes (share) | | 0.19 | 0.13 | 0.00 | 0.60 |
| No (share) | | 0.70 | 0.16 | 0.28 | 1.00 |
| Don't know (share) | | 0.11 | 0.07 | 0.00 | 0.37 |

*Notes.* Ethnolinguistic groups are limited to those with 50 or more individual observations. Standard deviation, minimum, and maximum are omitted for individual (binary) responses.

ranges from 0 to 60%, with an average of 19%. There is also substantial within-country heterogeneity by ethnicity: for example, across 109 groups observed in Nigeria, the share of believers varies between 4 and 51%.

Not surprisingly, these figures on the attribution of HIV/AIDS to witchcraft or other supernatural causes are substantially lower than the prevalence of witchcraft beliefs in general across Sub-Saharan Africa. For example, according to Pew Research Center surveys covering 19 countries in 2008–2009, the share of witchcraft believers ranges from 31 to 96%, with a country average of about 54% (Gershman, 2020). Similarly, Gallup World Poll data on general belief in witchcraft from 34 countries in 2009–2011 yield estimates ranging from 14 to 95%, with an average of 65%. However, in a subsample of 18 countries surveyed by Gallup, where respondents were asked specifically whether HIV/AIDS can be contracted through witchcraft, the share of "yes" responses was about 14% on average, with country-level estimates ranging from 4 to 33%. This is consistent with the tighter range and country average of 18% in the DHS sample, based on a very similar question. Overall, this comparison suggests that the relatively low prevalence of supernatural HIV/AIDS attribution primarily reflects the specificity of the question rather than reluctance to report witchcraft beliefs in DHS surveys: respondents may endorse witchcraft as a general possibility without believing that HIV/AIDS can be caused by it.

## 2.2 Short-term persistence of witchcraft beliefs

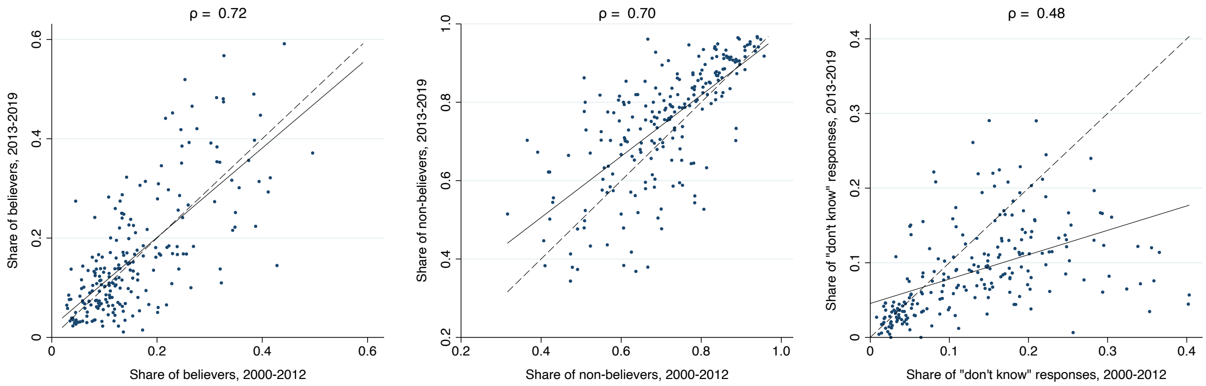
The availability of multiple survey waves allows us to examine the persistence of witchcraft beliefs at the ethnicity level in the very short run. Specifically, we split the master sample into two sub-periods, 2000–2012 and 2013–2019, each covering almost exactly 50% of all individuals. We then compare the shares of believers across 223 ethnic groups observed in both sub-periods, with at least 50 respondents in each of them.

Panel (a) of figure 1 shows three scatterplots illustrating how the shares of different responses to the witchcraft question change over time. The share of believers is highly persistent across sub-periods, with the raw correlation coefficient of 0.72. The best-fit line is very close to (and is not statistically different from) the 45-degree line, implying that, despite noticeable variation, the best prediction for the share of believers in 2013–2019 is their share in 2000–2012.[5]

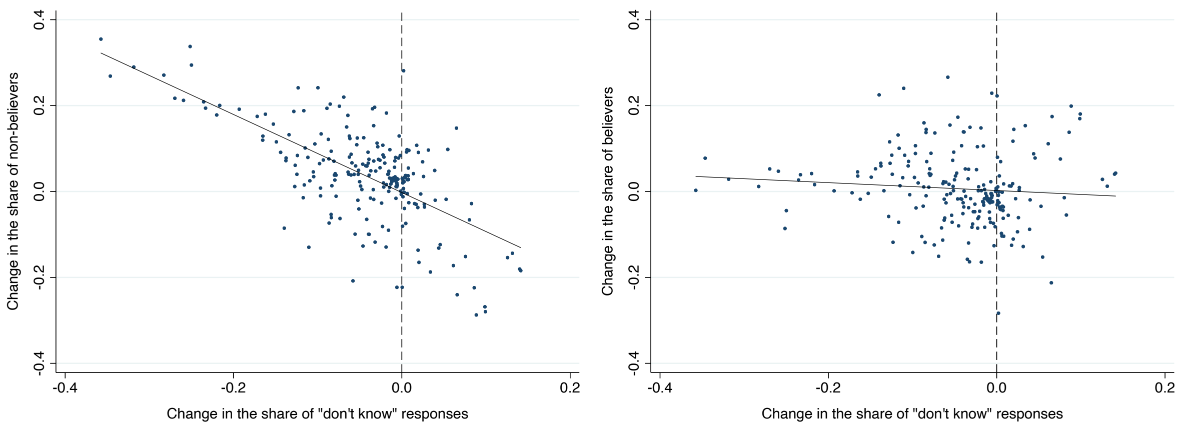
The share of non-believers is also persistent over time but shows a tendency to increase. This trend is largely accounted for by the decline of "don't know" responses apparent in the third plot of panel (a). This is further corroborated by figures in panel (b) showing that the change in the share of "don't know" responses is strongly negatively related to the change in the share of "no" but not "yes" responses.

Overall, this short-term analysis suggests that the share of believers is fairly stable over time, while uncertainty has markedly declined. Although such stability may not be too surprising considering the short time span, this particular period has seen widespread HIV education and prevention programs and a dramatic increase in the availability of treatment across Sub-Saharan Africa (Piot et al., 2015). Given the stability of the "yes" share, the following subsection focuses on this particular metric, based on observations pooled across all years, to capture group-level beliefs in witchcraft as a cause of HIV/AIDS in the first two decades of the 21st century.

[5]Imposing a higher minimum number of observations per group in each sub-period increases the correlation between response shares over time, reflecting reduced sampling noise. For example, the correlation for both "yes" and "no" shares is around 0.8 for thresholds of 200–500 individuals.




(a) Response shares over time.




(b) From uncertainty to disbelief.

Figure 1: Short-term persistence of witchcraft beliefs by ethnolinguistic group.

*Notes.* Each point (223 in total) corresponds to a unique ethnolinguistic group with 50 or more observations in each sub-period. Each plot in panel (a) shows a 45-degree line (dashed), the linear fit line (solid), and the raw correlation coefficient $\rho$.

## 2.3 Phylogenetic clustering and potential confounders

The short-term persistence of witchcraft beliefs across ethnolinguistic groups raises the question of whether their prevalence also displays continuity over much longer historical horizons. One common way to probe long-term persistence in cultural traits is to examine whether they exhibit phylogenetic signal, the tendency of more closely related ethnolinguistic groups to have more similar trait values. We quantify the strength of phylogenetic signal in the prevalence of witchcraft beliefs using Pagel's $\lambda$ (Pagel, 1999; Pearse et al., 2025). This statistic, commonly applied to continuous traits, measures the extent to which the observed covariance in trait values across groups corresponds to that expected under a

Table 2: Phylogenetic signal in the prevalence of witchcraft beliefs.

| | Full sample | | Atlantic-Congo | | Bantoid | | Narrow Bantu | |
|---|---|---|---|---|---|---|---|---|
| Threshold | $N$ | $\lambda$ | $N$ | $\lambda$ | $N$ | $\lambda$ | $N$ | $\lambda$ |
| 50 | 451 | 0.97 | 306 | 0.80 | 161 | 0.85 | 128 | 0.84 |
| 100 | 382 | 0.97 | 257 | 0.84 | 141 | 0.88 | 118 | 0.85 |
| 200 | 320 | 0.98 | 217 | 0.85 | 122 | 0.91 | 104 | 0.89 |
| 300 | 263 | 0.97 | 177 | 0.84 | 98 | 0.89 | 87 | 0.87 |
| 400 | 237 | 0.98 | 159 | 0.90 | 89 | 0.94 | 80 | 0.93 |
| 500 | 214 | 0.98 | 142 | 0.92 | 79 | 0.94 | 73 | 0.93 |

*Notes.* "Threshold" refers to the minimum number of individuals per group, $N$ is the number of groups, and $\lambda$ is the estimated value of Pagel's $\lambda$ in a given sample.

Brownian motion (BM) model of evolution on the language tree. A value of $\lambda = 1$ implies full conformity with BM, while $\lambda = 0$ indicates no phylogenetic structure.

Since $\lambda$ is benchmarked to standard (unbounded) BM model, and the proportion of believers is naturally constrained between 0 and 1, we apply a logit transformation to the original variable before evaluating phylogenetic signal, a common approach in the evolutionary ecology and biology literature (Warton and Hui, 2011; Humphreys et al., 2019).[6] As shown in appendix figure A.1, the logit transformation makes the prevalence variable approximately normally distributed, consistent with the BM model of evolution. The Shapiro-Wilk test cannot reject normality of the transformed variable (but not the original one) at the 5% significance level.

Table 2 provides the estimates of Pagel's $\lambda$ for different thresholds on the minimal number of observations per ethnolinguistic group. Specifically, it first reports signal values for the combined sample, based on the global MCC language tree, and then separately for the Atlantic-Congo family and the nested Bantoid and Narrow Bantu subfamilies, based on the pruned versions of the MCC tree. The $\lambda$ values are large across the board, implying strong phylogenetic signal.[7] Overall, it appears to be strongest in the full sample. There is also a tendency for phylogenetic signal to increase somewhat at higher thresholds on the

[6]The share of believers is equal to zero for only 1 society in the sample and we replace it with 0.009, which is just below the smallest positive proportion found in the dataset. Evaluating Pagel's $\lambda$ for raw untransformed values yields very similar results.

[7]Formal tests reject both phylogenetic independence and pure Brownian motion at conventional significance levels.

minimum number of observations, i.e., when focusing on a smaller number of better represented groups. As shown in appendix figure A.2, these patterns are broadly representative of estimates obtained across the full posterior sample of language trees.

Figure 2 visualizes the prevalence of witchcraft beliefs for ethnolinguistic groups in the Atlantic-Congo family with at least 200 surveyed individuals, mapped onto the pruned MCC language tree. As shown in table 2, this subsample comprises 217 distinct groups and yields $\lambda = 0.85$. Following the visualization approach for continuous traits proposed by Revell (2013, 2025), we reconstruct ancestral states under the BM model on the logit scale and back-transform the inferred node values to the original scale for display. The tree is then colored using a continuous gradient reflecting group-level belief prevalence, with colors varying smoothly along branches between node values. The resulting pattern highlights substantial clustering of belief prevalence along the language tree, reflecting strong phylogenetic signal.

Although this pattern is consistent with vertical cultural inheritance, there are alternative processes that could generate similar clustering. In our setting, two sources of confounding are particularly salient. First, closely related groups may be concentrated within the same country, where common factors such as institutions, educational systems, and public policies may shape beliefs in similar ways. Second, independently of national boundaries, related groups may occupy nearby geographic areas, creating scope for local cultural diffusion or for relevant spatially correlated ecological and socioeconomic conditions to generate resemblance in belief prevalence.

Figure 2 illustrates the first issue by highlighting the largest clades comprising at least three ethnolinguistic groups that are observed exclusively within a single country. Two large clades fall entirely within Nigeria, with smaller country-specific clades observed in Cameroon, Kenya, Namibia, Republic of the Congo, Uganda, and Zambia. In some cases, belief prevalence is similar across groups within these clades, consistent with clustering driven by shared national context. At the same time, the large Nigerian clades exhibit substantial within-clade variation, indicating that country-level factors alone are unlikely to account for the full extent of the observed phylogenetic clustering.

Visualizing potential spatial confounding at a finer scale is challenging, since subnational regions in contemporary African countries tend to be ethnically heterogeneous (Gershman and Rivera, 2018). Figure 3 provides an illustration for Nigeria and its geopolitical zones. We focus on a subset of 42 ethnolinguistic groups from figure 2 that are observed in Nigeria, and on three geopolitical zones: North East (NE), North Central (NC), and South South (SS). Although none of these groups are fully contained within a single zone,

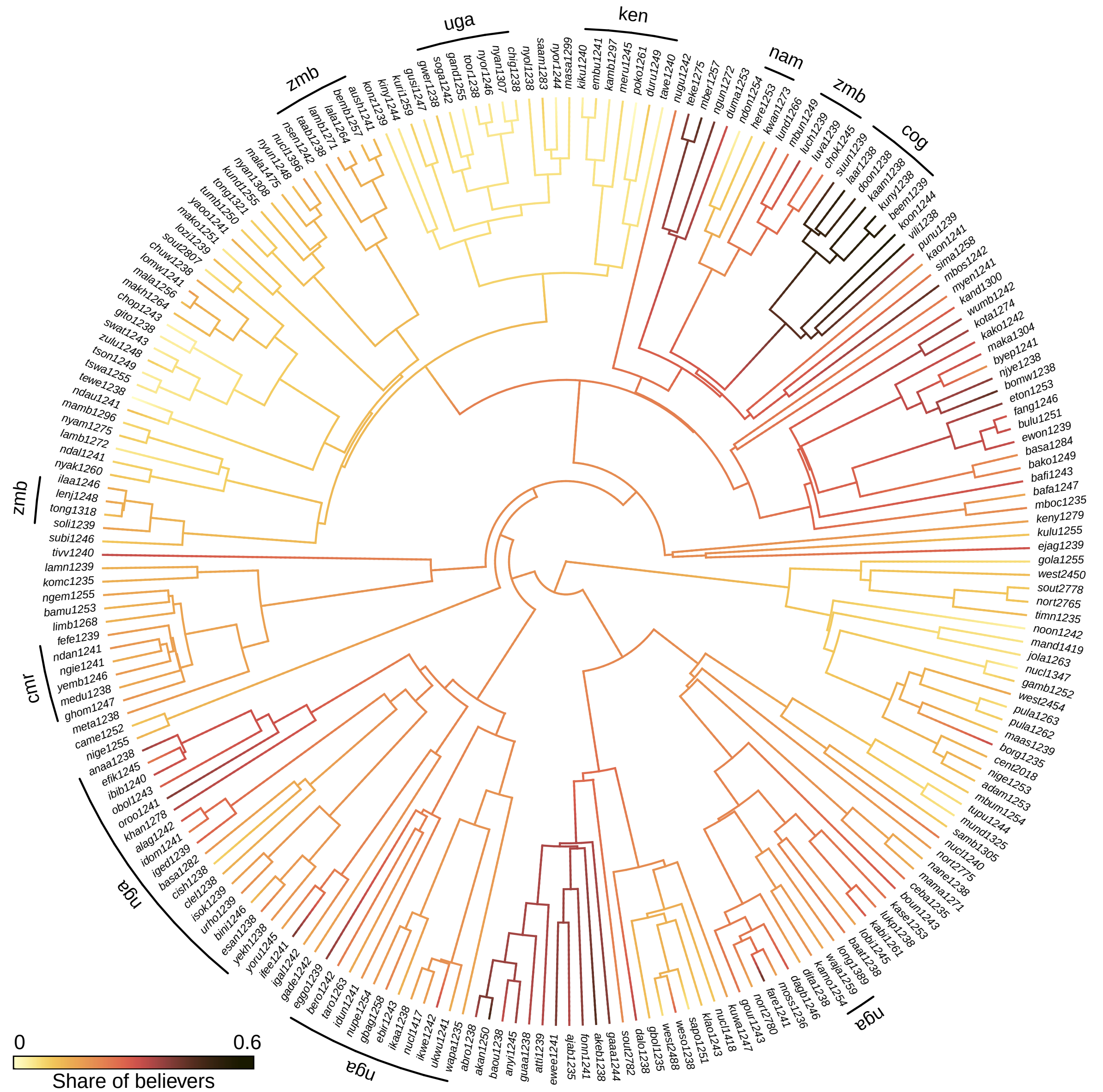



Figure 2: Witchcraft beliefs across the Atlantic-Congo language family.

*Notes.* The figure maps the prevalence of witchcraft beliefs by ethnolinguistic group on a pruned MCC language tree for the Atlantic-Congo family. Groups (217 in total) are only shown if they have at least 200 individual observations. Tips are labeled with glottocodes. Arks marked with country codes represent the largest clades containing at least three groups and only observed within those countries. The codes correspond to Cameroon [cmr], Kenya [ken], Namibia [nam], Nigeria [nga], Republic of the Congo [cog], Uganda [uga], and Zambia [zmb].

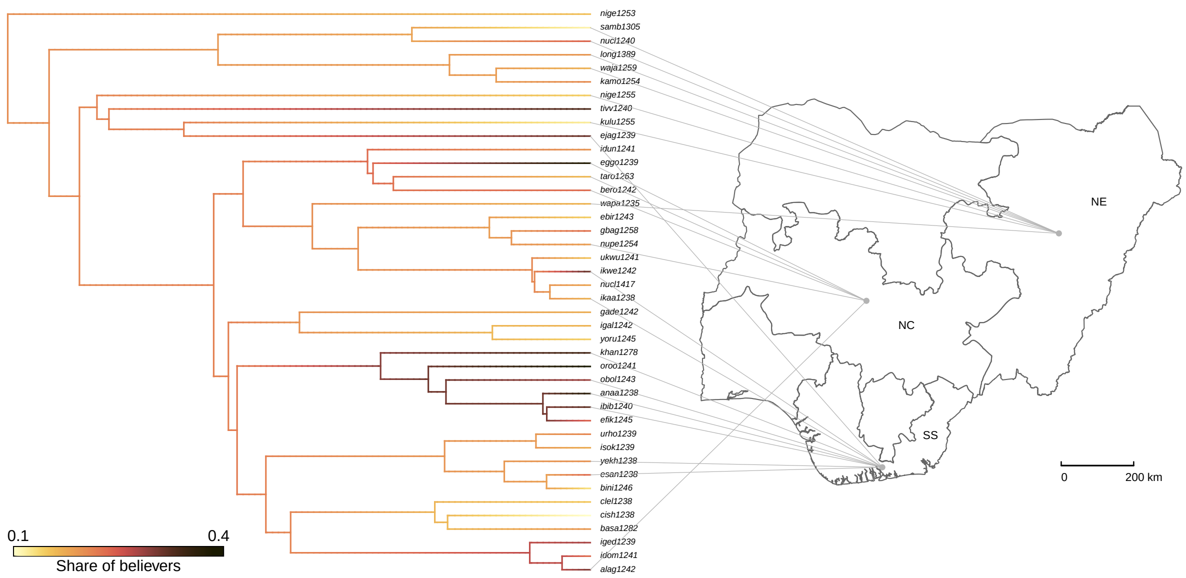



Figure 3: Witchcraft beliefs across the Atlantic-Congo language family in Nigeria.

*Notes.* The figure maps the prevalence of witchcraft beliefs by group on a pruned MCC language tree for the Atlantic-Congo family within Nigeria. Groups (42 in total) are only shown if they have at least 200 individual observations. Tips corresponding to groups residing predominantly (90% or more of respondents) in one of three Nigerian geopolitical zones are connected to the central points of those regions. NE, NC, and SS labels stand for North East, North Central, and South South zones, respectively.

for some, 90% or more of respondents reside in the same region. In these cases, we connect language tree tips to the corresponding regional centroids. The figure shows that spatial and phylogenetic clustering are sometimes – but not always – aligned, and that belief prevalence varies substantially within regions.

In sum, it is difficult to interpret the strong phylogenetic signal in the raw data in isolation, given potential confounding by country-level factors and local spatial correlation. The next section turns to a framework that jointly accommodates multiple sources of dependence.

# 3 Decomposing variation in witchcraft beliefs

We employ a spatio-phylogenetic generalized linear mixed modeling approach, which has become increasingly common in evolutionary biology and ecology for studying the sources of trait variation (Dinnage et al., 2020; Lancaster and Humphreys, 2020). Given data availability and computational constraints, most applications to date have relied either on species-level analysis or on relatively small-scale individual-level datasets. We leverage this general framework, together with recent advances in computational methods, to examine variation in a cultural rather than biological trait using large-scale survey data from contemporary Africa.

### 3.1 Estimation framework

In our setting, each surveyed individual $i$ belongs to an ethnolinguistic group $g$ (corresponding to a unique tip of the global language tree) and resides within a spatial unit $s$ of country $c$. Let $y_{igsc} \in \{0, 1\}$ denote whether respondent $i$ reports believing in witchcraft as a cause of HIV/AIDS or not.[8] The probability of a positive response is modeled using the following logistic mixed-effects model:

$$\mathrm{P}\{y_{igsc} = 1\} = \mathrm{logit}^{-1}\big(\mathbf{x}_{igsc}^{\top}\boldsymbol{\beta} + u_g + v_s + \varepsilon_c + \varepsilon_g\big)\,.$$

The vector $\mathbf{x}_{igsc}$ includes a set of observed covariates and $\boldsymbol{\beta}$ contains associated coefficients. The terms $u_g$ and $v_s$ denote structured phylogenetic and spatial random effects, respectively, while $\varepsilon_c$ and $\varepsilon_g$ denote i.i.d. random effects at the country and ethnolinguistic group levels. We follow the standard assumptions that $\varepsilon_j \sim \mathcal{N}(0, \sigma_j^2)$, $j \in \{c, g\}$, and all random effects are independent of each other.[9]

The structured components are defined as

$$\mathbf{u} \sim \mathcal{N}\big(\mathbf{0},\, \sigma^2_{\mathrm{phy}}\, \boldsymbol{\Sigma}_{\mathrm{phy}}\big)\,, \qquad \mathbf{v} \sim \mathcal{N}\big(\mathbf{0},\, \sigma^2_{\mathrm{spc}}\, \boldsymbol{\Sigma}_{\mathrm{spc}}(\theta)\big)\,,$$

where $\mathbf{u}$ is a vector of phylogenetic random effects indexed by ethnolinguistic groups and $\mathbf{v}$ is a vector of spatial random effects indexed by spatial units. As is common in the literature, the phylogenetic correlation matrix $\boldsymbol{\Sigma}_{\mathrm{phy}}$ is generated under the assumption of a Brownian-motion evolutionary process along the branches of the language tree. In this case, the covariance between the random effects for any two groups is proportional to the length of their shared evolutionary path from the tree root to the node representing their most recent common ancestor (Harmon, 2019). The spatial correlation matrix $\boldsymbol{\Sigma}_{\mathrm{spc}}(\theta)$ is

[8] We drop all "don't know" responses (about 10% of the original sample) and proceed with a binary outcome framework. This reduces the number of ethnolinguistic groups from 675 to 671. Recoding these responses as "no" yields results that are very similar to the baseline. Recoding them as "yes" makes a more notable difference, but does not alter the main qualitative conclusion.

[9] Given our focus on spatially correlated factors, and with country-level i.i.d. random effects already included, the baseline specification omits additional i.i.d. terms for finer-scale spatial units for parsimony. Robustness to their inclusion is examined in subsection 3.3 below.

assumed to have entries of the form $\exp(-d_{ss'}/\theta)$, where $d_{ss'}$ denotes the Euclidean distance between spatial units $s$ and $s'$, and $\theta > 0$ is an estimated range parameter governing the rate at which correlation decays with distance.

The key parameters of interest are the variance components, which provide a basis for statistically partitioning the latent-scale individual-level heterogeneity in witchcraft beliefs, conditional on observed covariates, across multiple sources: phylogenetic relatedness, spatial proximity, and idiosyncratic group differences at the country and ethnicity levels. This decomposition is performed using intraclass correlation coefficients (ICCs), or shares of latent-scale variance attributed to each component. For any random effect $k \in \{c, g, \text{phy}, \text{spc}\}$, its ICC is computed as

$$\text{ICC}_k = \frac{\sigma_k^2}{\sum_{m \in \mathcal{M}} \sigma_m^2 + \pi^2/3},$$

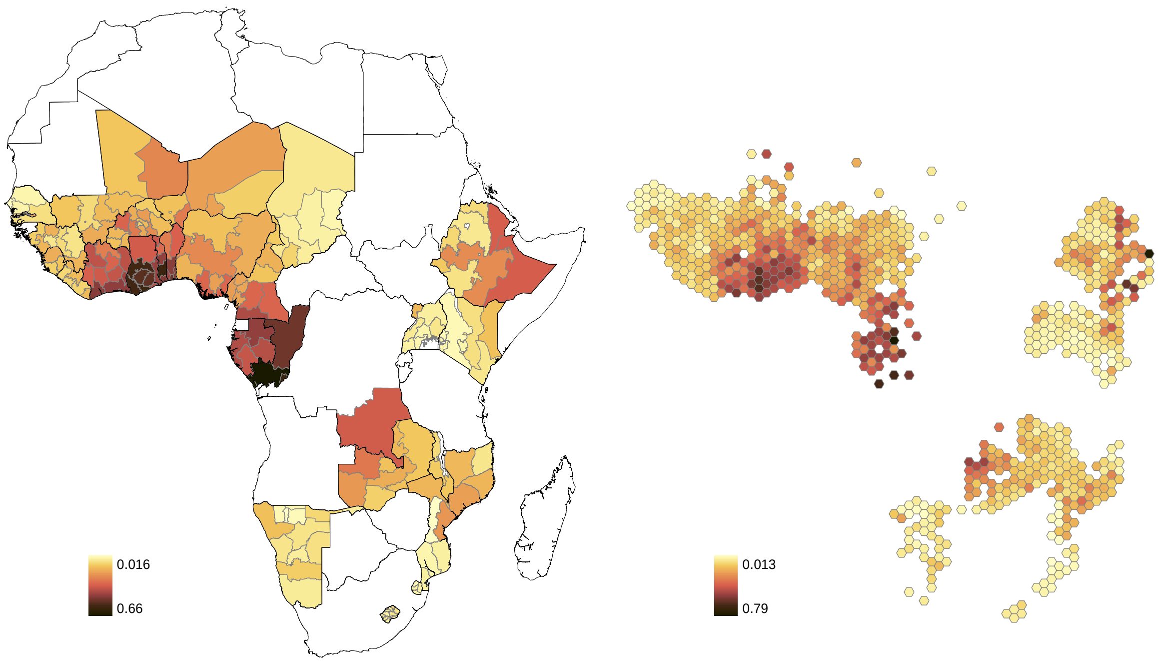
where $\mathcal{M}$ is the set of all random effects included in a given model specification and $\pi^2/3$ is the variance of the standard logistic distribution.[10] The model is estimated by maximum likelihood using the `glmmTMB` package in R, which allows fast estimation of generalized linear mixed models with multiple high-dimensional random effects, including those with spatial and phylogenetic covariance structures (Brooks et al., 2017; Williams et al., 2025).

We explore several definitions for spatial units under constraints imposed by data availability and computational feasibility. One option is to rely on subnational regions of residence recorded in the original surveys for each respondent.[11] In most cases, these roughly correspond to the official first-level administrative units, with some deviations caused by specifics of survey coverage across years and harmonization over time. The left panel of figure 4 maps the prevalence of witchcraft beliefs at this aggregation level. There are 201 regions in total and, for computing the $d_{ss'}$ elements in the spatial correlation matrix, each respondent's location is assumed to be the respective region's centroid.

The DHS data allow a more fine-grained spatial analysis, which is better suited for capturing local-level processes, especially considering the large size of many subnational regions. For almost 90% of individuals in our sample, we have approximate GPS coordi-

[10] In the biology literature, the ICC is also known as (latent-scale) repeatability (Nakagawa and Schielzeth, 2010).

[11] For countries surveyed multiple times within the relevant time frame, we make use of the harmonized subnational boundaries provided by IPUMS-DHS at `https://www.idhsdata.org/idhs/gis.shtml`.




(a) Harmonized subnational regions.    (b) Hexagonal cells, 10,000 km$^2$ each.

Figure 4: Spatial distribution of beliefs in witchcraft as a cause of HIV/AIDS.

*Notes.* Both panels map the shares of witchcraft believers in respective spatial units. Locations with fewer than 50 observations are not shown. "Don't know" responses have been omitted from the sample.

nates of survey clusters that respective households belong to.[12] These clusters represent primary sampling units that may correspond, for example, to a village in rural areas or city neighborhoods in urban context. Before public release the coordinates of cluster centroids are randomly displaced to protect respondent confidentiality, with the size of displacement up to 2 and 10 km in urban and rural areas, respectively (Burgert et al., 2013). Overall, there are over 25,000 georeferenced clusters.

Using raw survey clusters as unique spatial units is both computationally prohibitive and, given the random displacement of their locations, offers little additional information relative to coarser spatial aggregation. Therefore, we aggregate clusters to a regular hexagonal grid, with unit sizes between 2,500 and 40,000 square kilometers.[13] The right panel of

[12]The missing values are mostly, but not fully accounted for by the following complete survey waves without GPS coordinates: Benin (2006), Chad (2004, 2014), Gabon (2000), Gambia (2013, 2019), Niger (2006), and the Republic of the Congo (2005, 2011).

[13]These correspond to square grid cells between 50×50 km and 200×200 km. We prefer hexagonal tessellation because it produces more spatially balanced neighborhoods. In an etymological coincidence, "hex" also means a spell cast by a witch.

figure 4 maps the prevalence of witchcraft beliefs across 10,000-$\text{km}^2$ hexagons, which are the units employed in our baseline analysis (948 in total). Their centroid coordinates are used to construct the spatial correlation matrix. When cluster locations are unavailable, centroids of administrative regions are used instead.

All specifications include a set of individual-level sociodemographic characteristics: age, gender, place of residence (urban versus rural), educational attainment (none, primary, secondary, and higher), household wealth quintile, and religious affiliation (Christian, Muslim, traditional religion, other, and none). We also account for survey period fixed effects based on five-year intervals spanning 2000–2019 to account for common time shocks.

## 3.2 Baseline results

Figure 5 presents estimation results from a sequence of specifications that incorporate random effects of interest in various combinations (as captured by model labels on the vertical axis). The left panel of the figure reports estimated standard deviations for each included random effect, along with 95% confidence intervals, while the right panel displays stacked intraclass correlation coefficients.

The top portion of the figure reports estimates from models excluding the structured spatial term. In the simplest specification, ethnolinguistic group random effects account for a substantial share of the total latent variance, indicating strong within-group similarity in witchcraft beliefs when no additional structure is imposed. However, in the combined "$g$ + phy" model, the structured phylogenetic random effect clearly dominates, while the residual group-level variance shrinks substantially. Thus, what initially appeared as group-specific heterogeneity is largely systematic and aligned with shared ancestry. Including both components in this modeling framework, with multiple observations per group, is essential for isolating phylogenetic clustering as captured by $\text{ICC}_{\text{phy}}$, which is also commonly used as a measure of phylogenetic signal in mixed-effects settings (de Villemereuil and Nakagawa, 2014). According to this metric, in the "$g$ + phy" model, the estimated phylogenetic signal amounts to 0.7.

Adding country random effects further changes variance allocation across components. While country-level heterogeneity accounts for a meaningful share of variation, the phylogenetic effect remains quantitatively dominant, with $\text{ICC}_{\text{phy}} \approx 0.46$ in the "$g$ + phy + $c$" model. This result indicates that similarities in beliefs across more closely related ethnolinguistic groups are not simply a byproduct of shared national context and mechanical clustering of groups by country. Overall, the initial sequence of estimates documents a relatively strong phylogenetic structure.

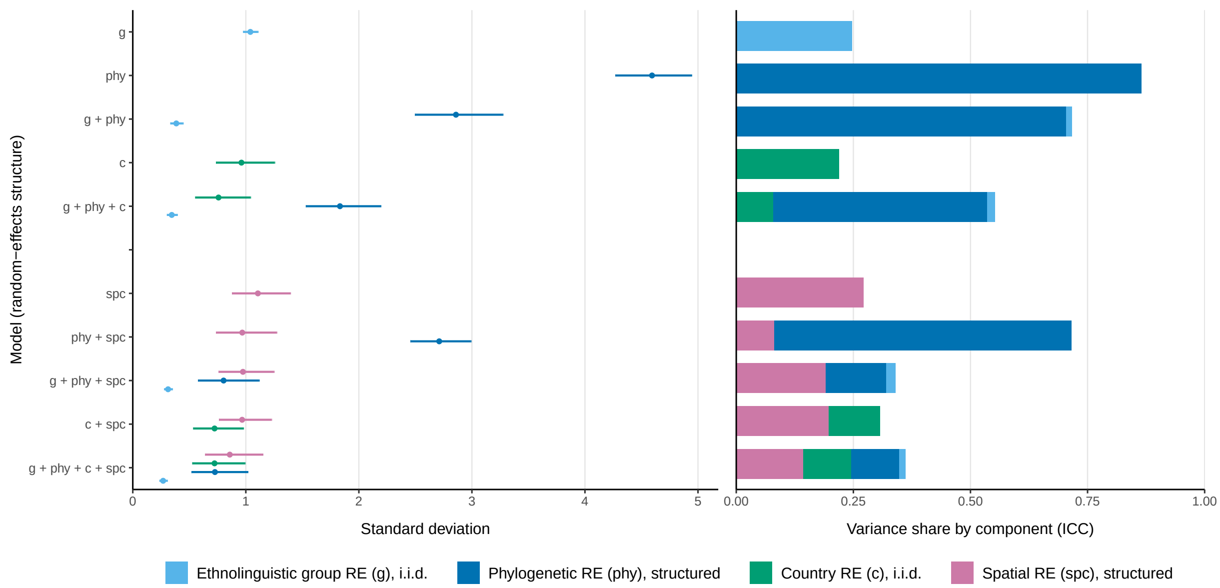



Figure 5: Estimation results: variance components and ICCs.

*Notes.* The figure displays estimates for alternative random-effects structures, listed along the vertical axis. Sample size is 852,335 individuals. Unlike the top five models, the bottom five include structured spatial random effects. The left panel reports estimated standard deviations, along with 95% confidence intervals, for each component across model variants, while the right panel shows the corresponding variance shares expressed as intraclass correlation coefficients (ICCs). Colored segments in the stacked bars indicate the contribution of each component to total latent-scale variance.

The lower portion of figure 5 reports estimation results from models including a structured spatial random effect. Across specifications, this component accounts for a meaningful share of variance, indicating the presence of local geographic clustering in witchcraft beliefs. Importantly, allowing for spatial dependence substantially reduces the phylogenetic variance component. However, although $\text{ICC}_{\text{phy}}$ declines relative to earlier specifications, reflecting partial overlap between geographic proximity and shared ancestry, it remains substantial. Likewise, the country-level component retains quantitative importance even after accounting for local spatial correlation.

The "baseline" specification at the very bottom of figure 5 includes all random effects simultaneously and illustrates how variance is partitioned across all domains of interest. Relative to the simple "$g$ + phy" model, both spatial and country components absorb part of the variation previously attributed to shared ancestry, while no single dimension dominates. Instead, variation is captured along complementary axes corresponding to deep historical relatedness, contemporary national context, and local spatial proximity.

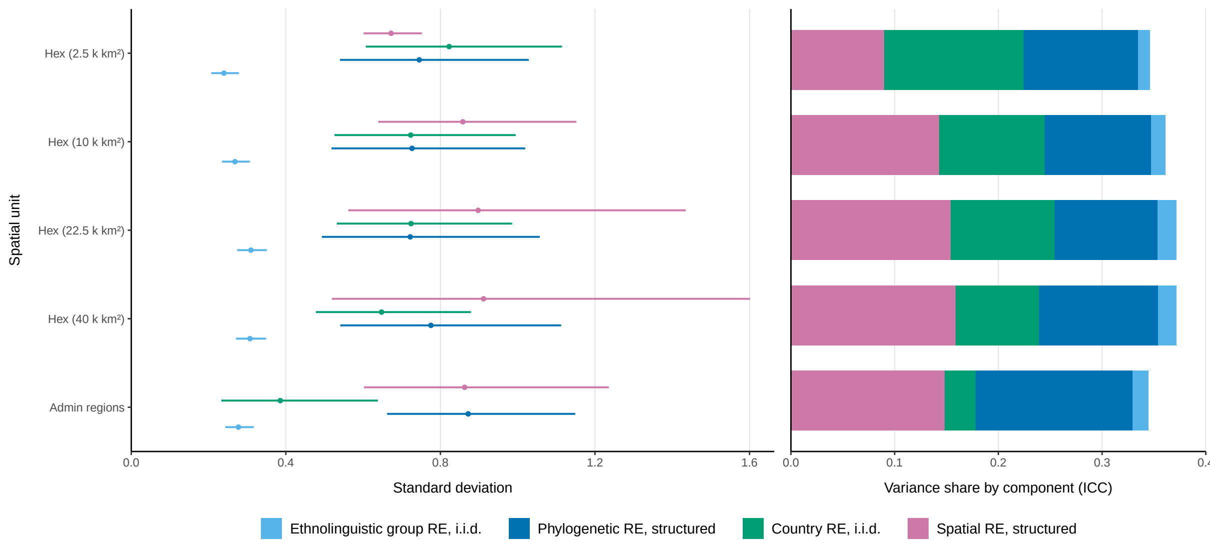



Figure 6: Estimation results for alternative spatial units.

*Notes.* The figure displays estimates of the baseline model for alternative definitions of spatial units used to construct the spatial correlation matrix. These are hexagonal grid cells ranging in size from 2,500 km$^2$ to 40,000 km$^2$ and subnational administrative regions. The corresponding numbers of spatial units are (from top to bottom) 2,753, 948, 495, 320, and 201. The left panel reports estimated standard deviations, along with 95% confidence intervals, for each component, while the right panel shows the corresponding variance shares expressed as intraclass correlation coefficients (ICCs).

The corresponding ICCs are of comparable magnitude, while the residual ethnolinguistic group component remains about an order of magnitude smaller.

Figure 6 examines the sensitivity of variance decomposition in the baseline model to alternative definitions of spatial units. We first consider regular hexagonal grid cells of decreasing resolution (from top to bottom), including the baseline choice of 10,000-km$^2$ hexagons, followed by harmonized administrative regions. Across all spatial definitions, the phylogenetic component remains quantitatively substantial and relatively stable, with $\text{ICC}_{\text{phy}}$ in the 0.1–0.15 range. It is roughly comparable in magnitude to the country and structured spatial components. $\text{ICC}_c$ shrinks substantially in the case of administrative regions, while $\text{ICC}_{\text{spc}}$ gets smaller when the finest hexagonal grid is used for spatial aggregation.[14] $\text{ICC}_g$ remains small and stable across specifications.

Although not the main object of interest, Figure 7 reports marginal effects for individual-level sociodemographic factors from the baseline model, expressed as differences in pre-

[14]The estimated range parameter $\theta$ increases monotonically from 160 to almost 2,000 km as the spatial grid resolution decreases, and it is close to 1,000 km for the case of administrative regions.

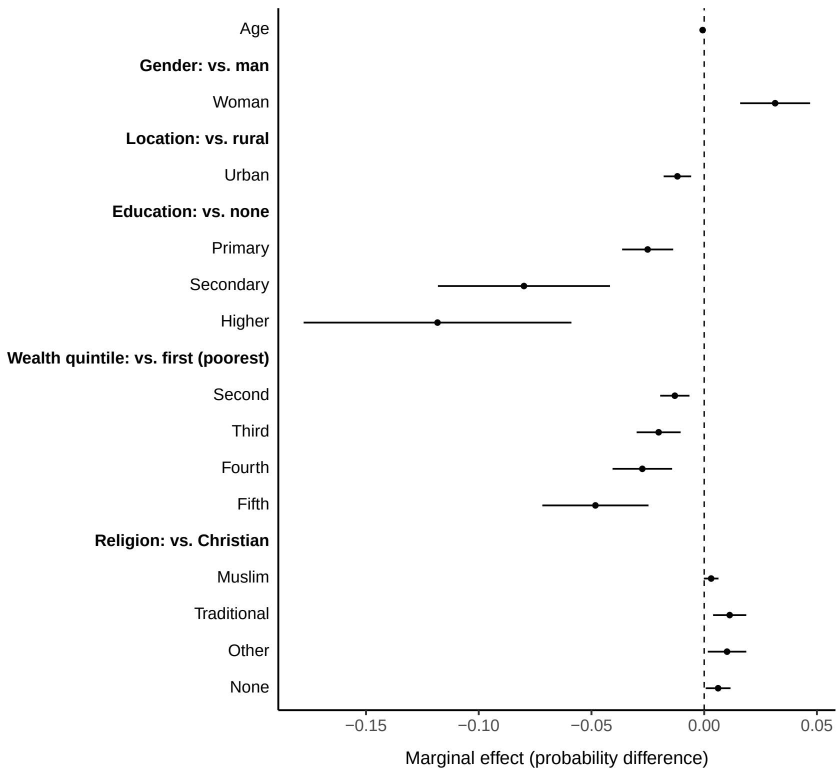



Figure 7: Marginal effects for sociodemographic factors in the baseline model.

*Notes.* Marginal effects are expressed as differences in predicted probabilities and reported alongside 95% confidence intervals. The age effect corresponds to a one-standard-deviation increase, while all other effects are defined relative to the indicated reference categories.

dicted probabilities and computed using the `emmeans` package in R (Lenth and Piaskowski, 2025). Most prominently, individuals with higher levels of education and material well-being are substantially less likely to believe in witchcraft as a cause of HIV/AIDS, consistent with previously documented associations for witchcraft beliefs in Sub-Saharan Africa and globally (Gershman, 2020, 2022). Women and rural residents are more likely to be believers, whereas age shows no statistically significant association with belief. Individuals reporting adherence to traditional, other, or no religion are slightly more likely to be believers than Christians. By contrast, there is no statistically significant difference between the two main religious affiliations, Muslims and Christians.

The latent-scale $R^2$ decomposition of the baseline model indicates that the marginal $R^2$, corresponding to individual-level covariates and period fixed effects, is approximately 5%,

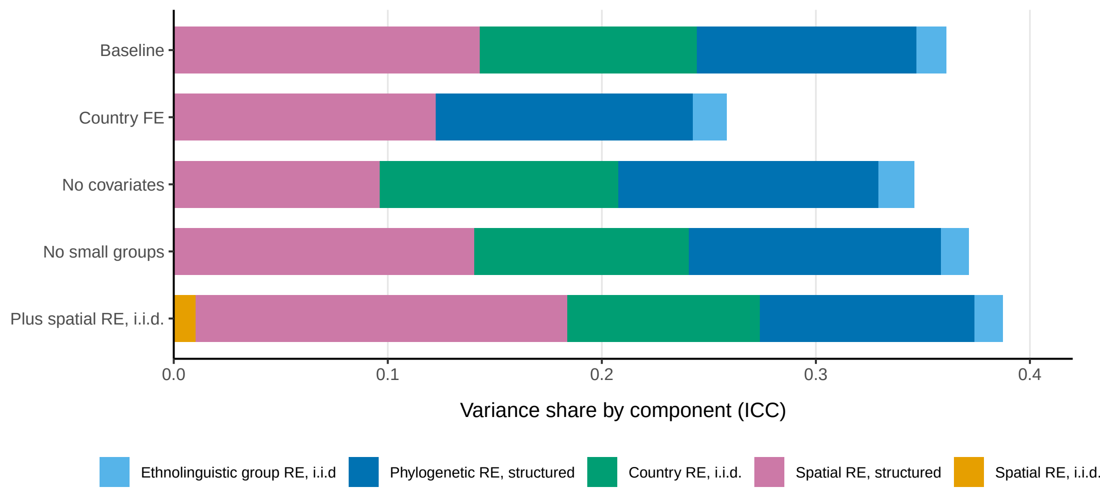



Figure 8: ICCs in alternative model specifications.

*Notes.* The figure reports stacked ICCs for several variations on the baseline model (shown at the top). From top to bottom, these modifications include: country fixed effects replacing country random effects; excluding all individual-level covariates and period fixed effects; restricting the sample to ethnolinguistic groups with at least 50 observations (451 in total); augmenting the model with an additional spatial unit i.i.d. random effect. Sample size is 862,178 in the "no covariates" model and 852,335 in the remaining cases (due to missing data on the sociodemographic characteristics of some respondents).

capturing a modest share of the overall variance.[15] The conditional $R^2$, which additionally incorporates all random effects, is close to 40%, reflecting the importance of higher-level structure in the baseline specification.

## 3.3 Robustness checks

We conduct a series of robustness checks to assess the stability of variance decomposition in the baseline model. Figure 8 reports stacked ICC estimates for each alternative specification, with the baseline shown at the top. First, replacing country random effects with fixed effects (absorbing all country-level differences in mean belief prevalence) shifts some variance toward the phylogenetic term while leaving the overall decomposition close to the baseline. Second, removing all individual-level covariates and period fixed effects yields a slight redistribution of variance from spatial to phylogenetic component. Third, restricting the sample to ethnolinguistic groups with at least 50 observations produces a pattern very

[15]In contrast to the ICC-based analysis, which is defined over random effects (plus the logit residual), the $R^2$ decomposition treats the variance associated with the linear predictor $\mathbf{x}_{igsc}^{\top}\boldsymbol{\beta}$ as an additional component of total latent-scale variance (Nakagawa and Schielzeth, 2013).

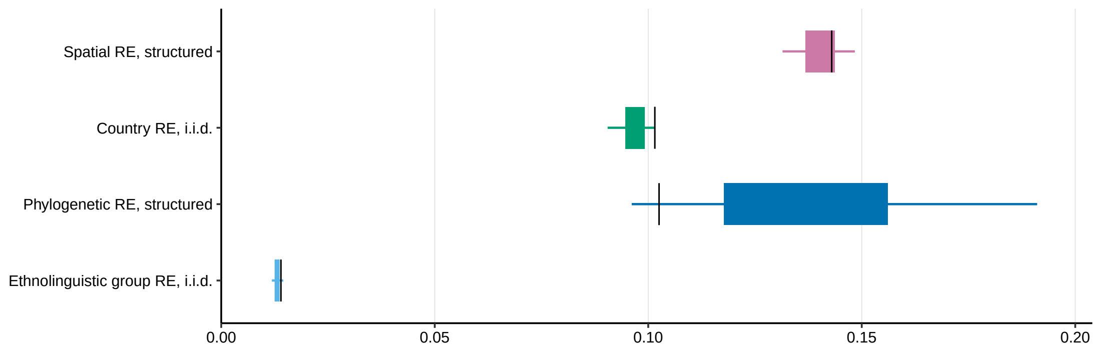



Figure 9: Distribution of ICC estimates across alternative language trees.

*Notes.* For each component, box-and-whisker plots summarize ICC estimates obtained across 902 language trees for the baseline specification. Whiskers indicate the 5th and 95th percentiles, while the box spans the interquartile range. Vertical black ticks mark the corresponding ICC estimates for the MCC tree.

similar to the baseline, suggesting that small groups are not disproportionately influencing the results. Finally, augmenting the model with an additional i.i.d. spatial term (10,000-km$^2$ hexagonal grid cell random effect) introduces a modest new variance component and is associated with a somewhat larger ICC for the structured spatial effect. Overall, the robustness checks indicate a fairly stable decomposition.

Finally, we assess robustness to phylogenetic uncertainty by re-estimating the baseline specification across all 902 available language trees. Figure 9 displays box-and-whisker plots of the resulting distributions for each ICC, with the corresponding MCC-tree-based estimates indicated by black vertical lines. For the spatially structured and ethnolinguistic group i.i.d. components, baseline ICCs fall within or close to the interquartile range of the tree-specific estimates. By contrast, the MCC-tree estimates for the country and phylogenetic components lie closer to the tails of their respective distributions, with baseline $\text{ICC}_{\text{phy}}$ relatively low and $\text{ICC}_c$ relatively high. As expected, the phylogenetic component exhibits the greatest dispersion. Taken together, the overall distribution of estimates across trees suggests a modestly larger $\text{ICC}_{\text{phy}}$ than implied by the MCC tree alone, without altering the qualitative conclusions.

## 3.4 Discussion

A central result of our analysis is that shared ancestry, spatial proximity, and national context all account for substantial and broadly comparable shares of variation in beliefs about witchcraft as a cause of HIV/AIDS. Each of these domains of belief similarity likely reflects multiple underlying processes.

Phylogenetic clustering is consistent with long-term intergenerational transmission of witchcraft beliefs within ethnolinguistic lineages. It may also arise because related groups inherit broader cultural, institutional, or socioeconomic features that make the adoption and persistence of these beliefs more likely. Such clustering may also reflect common historical shocks or past similarities in ecological environments faced by related groups, which may have shaped durable – and in some cases convergent – cultural responses. Diffusion or borrowing may also have been more likely among linguistically related groups, contributing to similarities along ancestral lines. In this sense, the phylogenetic structure reflects lineage-correlated processes, but does not by itself distinguish among the specific mechanisms through which it arises.

Spatial clustering is consistent with horizontal transmission through social interaction among nearby populations. Another plausible interpretation is that geographically proximate groups face similar contemporary environments that support witchcraft beliefs as explanations for illness and misfortune. Such environments may include disease ecology, local prevalence of HIV/AIDS, access to medical services, and broader economic conditions such as resource scarcity or inequality.

Notably, a substantial share of variation in witchcraft beliefs is attributed to national context even after accounting for shared ancestry and geographic proximity. This is consistent with evidence on the association between belief prevalence and nationwide factors, such as weak institutions (Gershman, 2022) or availability of HIV treatment (Sievert, 2025). At the same time, the importance of the country component may appear somewhat surprising in light of research emphasizing the limited reach of formal institutions and national policy regimes in much of Sub-Saharan Africa, given the recency and artificiality of most state borders (Herbst, 2000; Michalopoulos and Papaioannou, 2014). Nevertheless, qualitative research shows that there are many other channels operating nationwide that can support the spread of witchcraft beliefs.

A useful illustration is Ghana, which appears almost uniformly high-prevalence in panel (a) of figure 4. In his detailed case study, Adinkrah (2015) discusses how socialization into witchcraft beliefs in Ghana occurs at national scale. One relevant channel is the official school curriculum. For example, witchcraft is covered in Ghanaian social studies and religion curricula at the junior and senior secondary levels. Textbook material includes discussions of "the nature of witchcraft; how witchcraft is acquired, and how witches work," along with exercises asking students to identify the sources of witch power and describe some of the things that witches can do. Mass media and popular culture also play an important role: newspapers, television, movies, radio programs, internet news outlets, religious broadcasting, children's books, folk tales, adult fiction, and popular music all circulate stories about witchcraft. These channels reach audiences across the country and may help sustain shared witchcraft narratives across otherwise diverse local settings. Another example from popular culture relevant across Africa is sport: controversies over the use of witchcraft in soccer are often debated through national media, especially around national teams and major tournaments (Schatzberg, 2006).

National political context is another potential channel. Kohnert (1996) discusses how witchcraft beliefs have been instrumentalized for political purposes across postcolonial Africa. These uses range from accusations, threats, and violence against political rivals to efforts to discredit opponents or legitimize political authority through appeals to occult power. One set of examples concerns despotic rulers such as Mobutu in Zaire and Eyadéma in Togo, who leveraged witchcraft beliefs to bolster control over citizens. A more recent case is Yahya Jammeh's brutal state-orchestrated witch-hunts in the Gambia in 2008–2009, which were tied to his efforts to reinforce political power and cultivate a reputation as a defender of Islam (Agyemang et al., 2024). In democratizing Benin, Nicéphore Soglo's public embrace and official recognition of the Vodun religion has similarly been interpreted as a politically useful campaign against witchcraft and as an attempt to assert superiority in the realm of occult forces (Kohnert, 1996).

# 4 Conclusion

This paper examines how beliefs in witchcraft as a cause of HIV/AIDS are structured in contemporary Sub-Saharan Africa. While a growing literature documents the prevalence of witchcraft beliefs and their correlates, it has not systematically assessed the extent to which observed clustering reflects intergenerational transmission and persistence within groups, local environmental influences and cultural diffusion, and shared national contexts. The approach taken here provides a quantitative characterization of how these broadly construed domains jointly account for heterogeneity in beliefs.

The analysis draws on a large dataset of nearly one million respondents from the Demographic and Health Surveys conducted in 27 countries between 2000 and 2019, combined with global language phylogenies and information on household locations. Leveraging extensive population mixing in contemporary Africa to disentangle multiple dimensions of clustering, a spatio-phylogenetic logistic mixed-effects model partitions variation in individual beliefs into components associated with shared ancestry, spatial proximity, and country-level context, conditional on sociodemographic characteristics. The results show that these three broad domains account for meaningful and comparable shares of variation once considered jointly. This pattern is robust to alternative spatial units, model specifications, and uncertainty in the global language phylogeny.

The study has several limitations. First, while the analysis provides a decomposition of variation in witchcraft beliefs across ancestry and place, it does not pin down the specific mechanisms underlying these patterns. Some of these mechanisms could potentially be examined in future research by incorporating relevant proxy variables into the empirical framework. Second, the analysis is based on a single survey question capturing the attribution of HIV/AIDS to witchcraft or other supernatural means. This measure does not reflect the prevalence or complexity of witchcraft beliefs in general, and survey responses may also be influenced by context and framing. At the same time, the Demographic and Health Surveys provide uniquely rich data in terms of sample size, geographic coverage, and the number of ethnolinguistic groups represented, making it possible to study patterns of variation at a scale that would otherwise be infeasible.

Beyond the substantive case of witchcraft beliefs, this paper illustrates a general methodological approach for studying variation in cultural traits in contemporary populations. By combining large-scale survey microdata, global language trees, and spatio-phylogenetic mixed models, this framework provides a way to empirically engage with theories of cultural persistence and diffusion.

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# Appendix

## A Additional figures

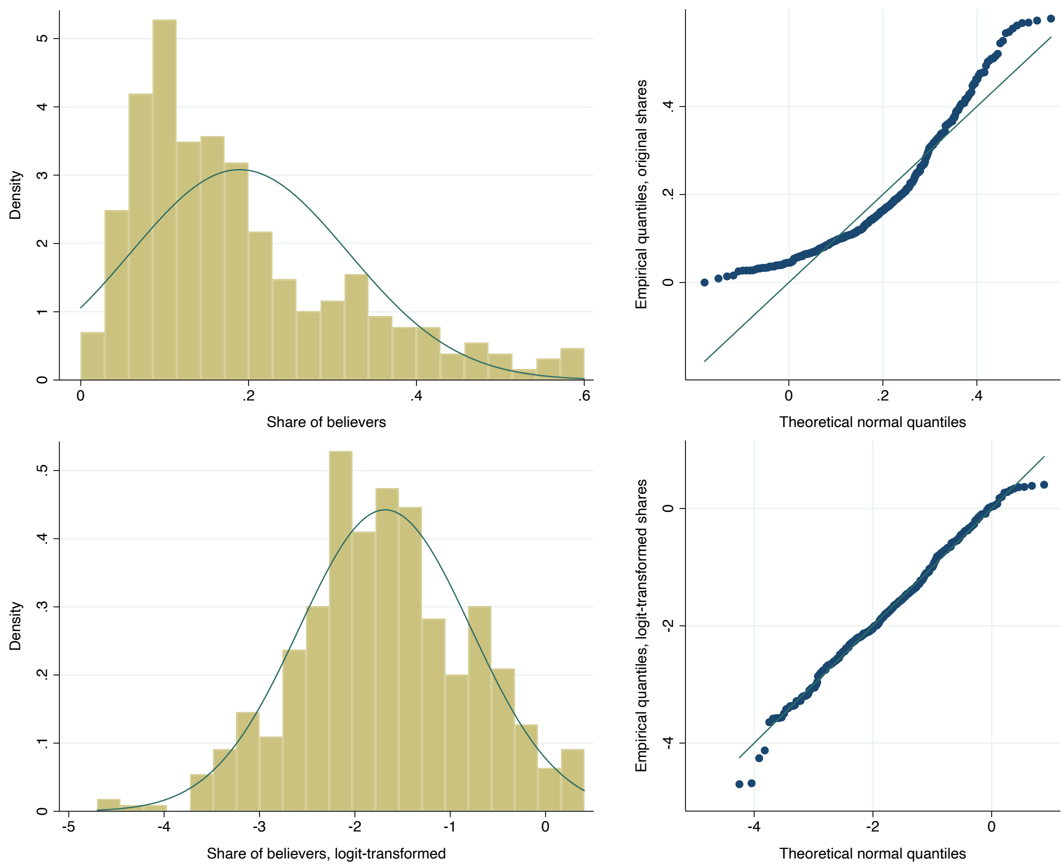
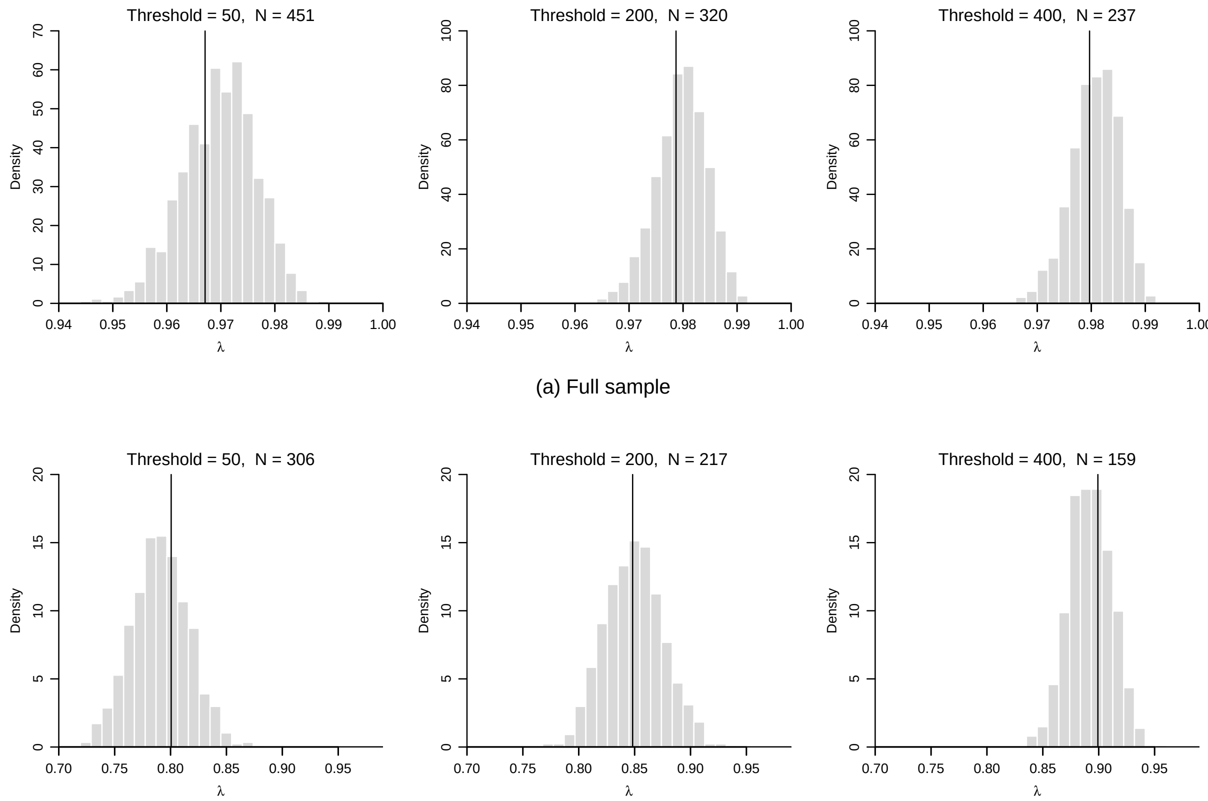



Figure A.1: Original and logit-transformed shares of believers across ethnolinguistic groups.

*Notes.* Histograms overlaid with an appropriately scaled normal density (with the same mean and standard deviation as the data) shown on the left. Q-Q plots shown on the right. Sample size is 451, based on the threshold of at least 50 observations per ethnolinguistic group.




(a) Full sample

(b) Atlantic−Congo

Figure A.2: Distributions of Pagel's $\lambda$ across alternative language trees.

*Notes.* Each panel reports the distribution of Pagel's $\lambda$ values estimated across all 902 language trees in the available sample. The solid vertical line marks the MCC tree estimate. "Threshold" refers to the minimum number of individuals per ethnolinguistic group and $N$ is the total number of groups.