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Independent histories underlie global musical, linguistic, and genetic diversity

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Abstract:

Music is a universal, yet diverse cultural trait shaped by cultural and biological evolution. The degree to which global musical diversity traces the historical movements of people and their languages has been controversial, with recent studies comparing musical, genetic, and linguistic diversity in different regions producing conflicting results. Here, we use a global musical dataset of 5,242 songs and 719 societies to identify six major axes of musical diversity to probe this conflict at a global scale. These dimensions show that musical traits contain geographically constrained patterns of between-society diversity, comparable to patterns in language diversity. Having identified our musical traits that contain historical signal, we pair musical profiles to genetic and linguistic relationships, creating a set of 121 paired societies (containing 981 songs, 1,296 genetic individual profiles, and 121 languages). We show that musical traditions contain similar, albeit weaker, patterns of spatial decay to linguistic diversity and genetic diffusion, but that the structure of musical similarity is different to linguistic or genetic histories. Musical relationships do capture some geographic, genetic, and linguistic relationships at the regional scale, but these relationships are not globally consistent. Overall, our results suggest that global musical traditions are surprisingly distinct from non-musical aspects of human history.

Main Text:

Do people and their cultures move together or independently? Darwin proposed “curious parallels” (Atkinson & Gray, 2005) between genetic and cultural evolution, such that “a perfect pedigree of mankind... would afford the best classification of the various languages now spoken throughout the world” (Darwin, 1871). Darwin’s proposal stimulated studies of cultural evolution that attempted to trace ancient population movement by combining linguistic, archaeological, and/or genetic narratives (Atkinson, 2011; Bouckaert et al., 2018; Cavalli-Sforza et al., 1988; J. Diamond & Bellwood, 2003; Gray et al., 2009; Henn et al., 2012; Robbeets et al., 2021). While some have argued that the phylogenetic patterns in language are a good proxy for the movement of human populations (Gray et al., 2009; Grollemund et al., 2015; Koile et al., 2022) and their cultural trajectories (Bouckaert et al., 2012), opposition to this assumption has also been persistent (Boas, 1940; Donohue & Denham, 2010; Kroeber, 1939; Terrell, 1988). Quantitative data comparing global genetic and linguistic diversity shows that the genetic delineations between populations mostly corresponds to language family groupings, but also that in around 20% of cases populations are genetically closer to linguistically unrelated groups (Barbieri et al., 2022). The mismatch of demographic trajectories and linguistic classifications suggests that there are complex models of cultural transmission occurring through human history. To understand the complexities, we must build consider the multi-perspectivity of human history.

Language is only one universal aspect of human culture. Music is also culturally universal but presents considerable diversity within and between societies (Brown & Jordania, 2013; Jacoby & McDermott, 2017; Lomax, 1968; McDermott et al., 2016; Mehr et al., 2019; Rzeszutek et al., 2012; Savage et al., 2015). As a ubiquitous cultural trait, what can music tell us about human history? Based on existing literature, there are two existing narratives for the role of music in human history: music moves with people and maintains information on ancient connections between societies which are approximated through a process of genetic diffusion (Brown et al., 2014; Grauer, 2022; Leroi & Swire, 2006; Savage, 2018). (Lomax, 1968) argued that “the geography of song styles traces the main paths of human migration” and that “musical style changes less than any other aspect of human culture – such as religion, language, etc....folk music can become a historical touchstone like the radioactive substances studied by geologists” (unpublished letter cited in (Szwed, 2011)). Many are skeptical of these claims, citing examples of rapid musical change independent of demographic turnover (Feld, 1984; Nettle, 2006; Stock, 2006). The second possibility is that musical traits are inherited through cultural lineages alongside the process of language evolution, as seen in other central cultural traits like religion (Gray & Watts, 2017; Matsumae et al., 2021). Direct quantitative comparison of musical, genetic, and linguistic diversity has been restricted to regional studies producing mixed results, with evidence of significant correlations between musical and genetic diversity in Taiwan and Sub-Saharan Africa (Brown et al., 2014; Callaway, 2007) but not in Northeast Asia (Matsumae et al., 2021). A third untested possibility is that music has undergone a historical process of its own and creates connections in the landscape unrelated to genes or language, providing alternative insight to the relationships between societies.

It is likely that each narrative plays some role in developing a musical style, and that different musical characteristics could align with any (or none) of these possibilities. As is widely discussed in linguistics (Nichols, 2017), the stability of musical traits is likely variable: some may persist deep into human history (Aguirre-Fernández et al., 2020), some may be

inherited cultural traditions, some may create a new path of cultural diffusion, and others may be the result of innovation.

Unlike language, which is at least lexically stable within societies, the production and use of music within a society varies considerably. The variability of musical production within societies has pointed to many universal features of music and musicality, such as social bonding, or lullabies (Savage et al., 2021; Yurdu et al., 2022). Despite the universality of some musical features, there is no research that claims that music sounds the same everywhere. Music is a rich source of cultural heritage and tradition and (Harris et al., 2019), and these traditions have an untapped potential to compliment many of the existing models of human history (Savage & Brown, 2013). Patterns between societies in music style have been a long-term focus in ethnomusicology (Lomax, 1968), but these depend on the assumption that there are reliable differences in musical style. Recent regional work has shown that although within-society variance is high, we can also attribute large amounts of variance to between society differences (Daikoku et al., 2020; Mehr et al., 2019).

Global analysis on the axes of musical diversity, the extent of between-group variance, and comparisons of musical diversity against genetic, and linguistic relationships were not previously possible because detailed public data on cross-cultural musical diversity were not available. A database of several thousand expert-coded songs, the Global Jukebox, was built and analyzed in the 1960s before global genetic comparisons became available (Lomax, 1968; Lomax & Berkowitz, 1972). We have now digitized and published this data for almost 6,000 songs from almost 1,000 societies coded with 37 standardized “Cantometric” features of musical style (Wood et al., 2022) (table S1 and Section S1 for details). Recent research has implemented automated and computational techniques for quantifying music (Panteli et al., 2017), although these approaches promise fast and wide comparisons, they are yet to capture the dimensions of musical experts use to differentiate music (Daikoku et al., 2022). The digital release of the Global Jukebox coincided with the release of a global database linking genetic and linguistic diversity (GeLaTo; Barbieri et al. (2022)). Combining these two datasets with a global language super tree (Bouckaert et al., 2022), we can quantitatively address many of the questions surrounding music and its role in understanding human history. First, we quantify the major axes of musical diversity in a global sample, identifying six primary factors, as well as calculating an aggregate measure of general musical similarity. These dimensions present various independent axes of musical variation from which we can assess the variability in stability. Second, we quantify the relative importance the relative importance of between- and within-society diversity. Finally, we correlate our musical diversity with measures of genetic, linguistic, and geographic similarity to test the hypothesis of how music moves through human history.

Six dimensions of Cantometric musical diversity

We begin by identifying the principal axes of musical variation around the globe. Historical linguistics sometimes claim certain domains of language, such as basic vocabulary (Swadesh, 1952), are better suited for reconstructing the past, but these dimensions are debated and have not been identified in musicology (Grauer, 2022; Lomax, 1968; Savage & Brown, 2013; Stock, 2006). To test candidate musical dimensions using a global sample, we reduce the Cantometrics dataset to societies with two or more songs and summarize diversity into six latent variables of musical performance, which broadly represent the types of features in the dataset. This results in a dataset totaling 5,242 Cantometric coded songs from 719 ethnolinguistic groups (Figure 1 and Figure S1; median of 6 songs per society; See Supplementary section S1 for details of data pre-processing; see Supplementary Section S2 for sensitivity analysis of societies with ≥ 10 songs).

The six latent dimensions identified via factor analysis are: 1) Articulation (lyric repetition and enunciation); 2) Organization (number of and relationships between different vocal and instrumental parts); 3) Tension (vocal width, nasality, raspiness); 4) Ornamentation (the amount of decorative singing within a song), 5) Rhythm (meter and tempo); and 6) Dynamics (volume, register, and intensity; see supplementary section S2 for more detail on variable construction and examples for all variables). We also create an aggregate musical dimension of all independent Cantometric variables, similar to the ‘modal profiles’ used in early Cantometrics studies (Lomax, 1980). To explore the relationship of musical diversity to linguistic, genetic, and geographic distances, we matched societies from the Global Jukebox to languages and genetic populations (see Supplementary Methods). We match 121 societies across our musical, genetic, and linguistic datasets, represented by 981 songs, the genomic profiles of 1,296 individuals, and 121 languages across 38 language families (Figure 1).



Figure 1: Map of 719 Cantometrics societies (represented by 5,242 songs). These songs are used to determine Latent variables, sized by the number of songs per society. 121 societies (represented by 1,296 songs) matched to both genetic and linguistic data are indicated in red (societies without matching genetic and linguistic data are in grey).

Music varies between societies

For music to tell us about human history, we must be confident that musical diversity can be differentiated between societies and that closer societies are more similar. Figure 2a shows that although musical diversity presents as a continuous phenomenon, there is also underlying structure. Figure 2b shows a distinction between songs from within two language families, Atlantic-Congo and Sino-Tibetan, imposed over the topography of the entire sample. Each of these families exist across the range of possibilities in these dimensions, but importantly differ in their preferences. Sino-Tibetan music tends to have more ornamentation, whereas Atlantic-Congo societies tend to perform with regular rhythm. Highlighting two societies within these

language families (Red squares: Ubangi; Blue squares: Burmese) shows the diversity of music within societies. As with language families, the variance of music within societies is high, but the tendencies for particular musical traits reflect the influence of a broader cultural style.

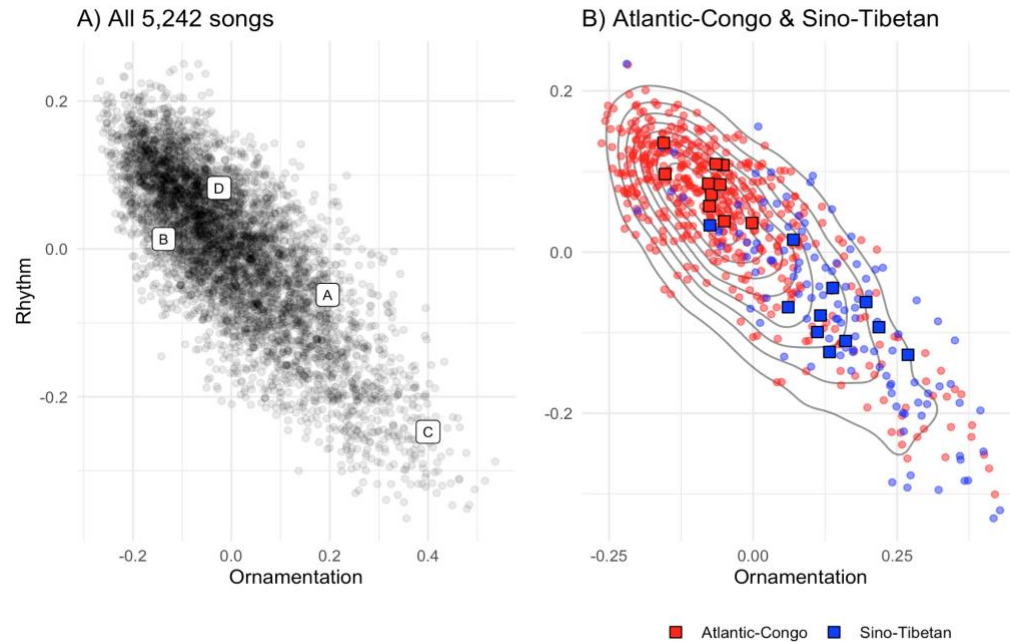


Figure 2: A) Scatter plots between Ornamentation and Rhythm latent variables for 5,242 songs and B) showing the distribution within language families. A). Labels within the graph refer to exemplar songs described in S2.2: A) Song with Xylophone - Burmese B) Djokobo - Mbendjele C) Caravan Song - Tibet D) Alima Song - Mbuti. B) Topographical gridlines show the density of the scatter plots in Figure 2a, overlaid with points from the Atlantic-Congo language family (red) and Sino-Tibetan language family (blue). Squares show songs from the Atlantic-Congo society Ubangi (red), and the Sino-Tibetan society Burmese (blue). The dispersal of squares gives an indication of within society diversity.

To formally test whether societies can be differentiated musically, we use an AMOVA (analysis of molecular variance) test on a set of 636 societies with linked languages families, totaling 5,131 songs. AMOVA parses the variance of a trait to show the relative importance of within-society and between-society diversity (Table S8; Table S9 for ≥ 10 songs per society; Table S10 shows the minimal difference in results). In genetics, within-population variance accounts for 93% - 95% of variance and between-populations constitute around 3% to 5% of the variance (Rosenberg et al., 2002). Amongst our musical variables, within-society diversity explains between 54% - 72% of total variation. Between-societies / within-macrogroup diversity (either Language family or Macroarea) contains between 29% - 43%. Between-society within-group variance is higher in the dimensions that might reflect cultural preferences in music: Articulation, Organization, Ornamentation, and Tension; compared to dimensions that align more with the context in which the music is produced: Dynamics and Rhythm. Comparing musical and genetic fixation statistics (measures of similarity between populations; (Handley & Mathew, 2020)) showed that the differences in music were between 10% and 40% higher than genetic differences between populations, although between-society musical diversity was also more variable (Figure

S6, Table S12). In general, while musical diversity within-societies is large, when compared to genetic populations there are substantial differences between-societies. However, we caution that the relative between- vs. within-society variation is calculated slightly differently for music and genetics (see Supplementary Material), and the greater diversity within music may partially reflect the diversity of different musical genres coexisting with a given society's repertoire.

Music is more similar between geographically closer societies

Societies have identifiable musical differences, but do these differences reflect historical movements of people and their languages? If they do, geographically neighboring societies should be the most musically similar, since similarities should diffuse with the contact or movement of people (Ross et al., 2013). However, if musical diversity is rapidly innovative we would not expect a geographically constrained relationship (Stock, 2006). We find evidence that geographically closer societies are also more musically similar, using a correlation test for spatial autocorrelation (Figure 3). Within the aggregate measure of musical similarity, spatial autocorrelation persists up to 4,500km on average, slightly less than the level of autocorrelation seen between languages and genetic populations which persist to around 5,000km and 5,500km, respectively. Within the musical dimensions, Articulation, Ornamentation, Organization, and Rhythm all show autocorrelation to between 3,000km and 3,500km. Tension shows a slightly more restricted range of 2,500km and Dynamics shows almost no autocorrelation (Figure S7). The strength of musical autocorrelation is considerably lower than we observe in the decay of genetic similarity between populations but is comparable to the decay of similarity within the histories based on language genealogies.

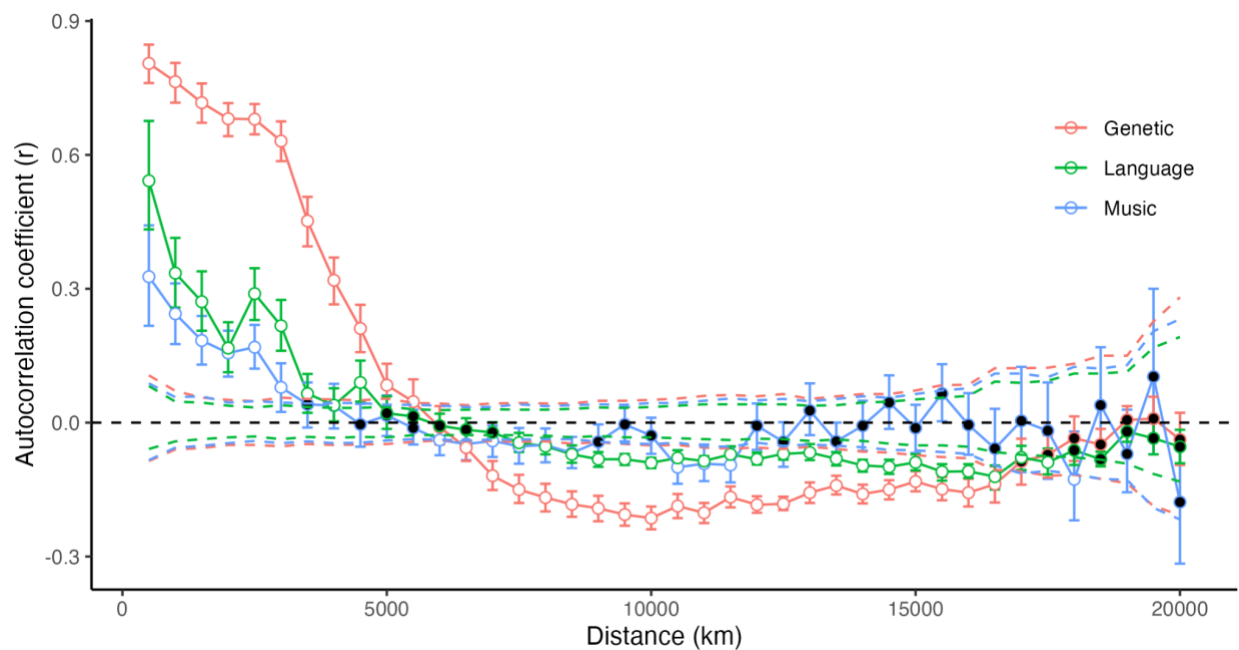


Fig. 3: Spatial Autocorrelation correlogram showing the autocorrelation coefficients (r) as a function of distance for population-level pairwise measures of Genetic F_{ST} distances, phylogenetic distance from the EDGE tree, and Musical Ph_{IST} distances. White circles indicate significant autocorrelation, black circles indicate non-significant autocorrelation. See Figure S7 for the same graph for the individual musical metrics.

Musical similarity contains independent structure compared to language and genetics

The AMOVA and spatial autocorrelation results show that musical diversity can differentiate societies and contains patterns of similarity consistent with human movement. To dissect whether the patterns align more closely with linguistic, of genetic diversity (if either) we use two correlation permutation methods (partial redundancy analysis (RDA) (Matsumae et al., 2021) and partial mantel tests (Mantel, 1967)) to test the correlation between population-level measures of musical style (Ph_{IST}), genetic similarity (F_{ST}), and linguistic similarity (Figure 4). These methods provide the correlation between two distance processes, while conditioning on a third. There is reason to interpret Mantel tests with caution (Harmon & Glor, 2010), but by comparing results from two methods, we should have a clear idea of which effects are robust. We additionally explore how each of the linguistic, genetic, and spatial processes relates to one another, when conditioning on the third process. Partial RDA and partial mantel results are shown in table S13 (≥ 10 song sample in table S14).

Across the entire sample music shows mostly weak relationships to language, genes, and geography. Music shows the closest relationship to linguistic similarity, closely followed by geographic distance. However, the size of the spatial relationship is partially mediated by language. Genetics presents the weakest relationship to musical diversity. Exploring the six musical dimensions shows that the aggregated musical similarity linguistic correlations are driven by Articulation, Ornamentation, Rhythm, and Tension. Dynamics shows no significant relationship language, genes, or geography on the global scale. The general message is that although the data presents a significant relationship between music and either genes, language, or geography, the weakness of the relationships suggest they are not reliably global processes. The correlations we observe may be driven by local variation.

Correlations within the three regions with largest sample, Africa ($n = 20$ societies), Europe ($n = 25$), and Southeast Asia ($n = 12$), show us how variable the evolution of music may be, with the caveat of smaller samples (Figure 4). Within Africa, musical similarity shows the strongest correlation to a pattern of spatial diffusion. As in the global patterns, African music is also tied with linguistic distances, although rather than the spatial relationship mediating language, the linguistic relationship is mediated by spatial relationships. African patterns of Articulation, Organization, Tension, and Dynamics present a strong spatial effect, but Ornamentation shows a strong relationship to language. Across Europe, all correlations are weak, but most notably, linguistic distance shows a negligible relationship to any musical process. European music also shows much stronger, albeit still weak, correlations to genetic similarity. In Southeast Asia, geographic diffusion appears to be the prominent driver of musical diversity, containing some of the strongest correlations observed.

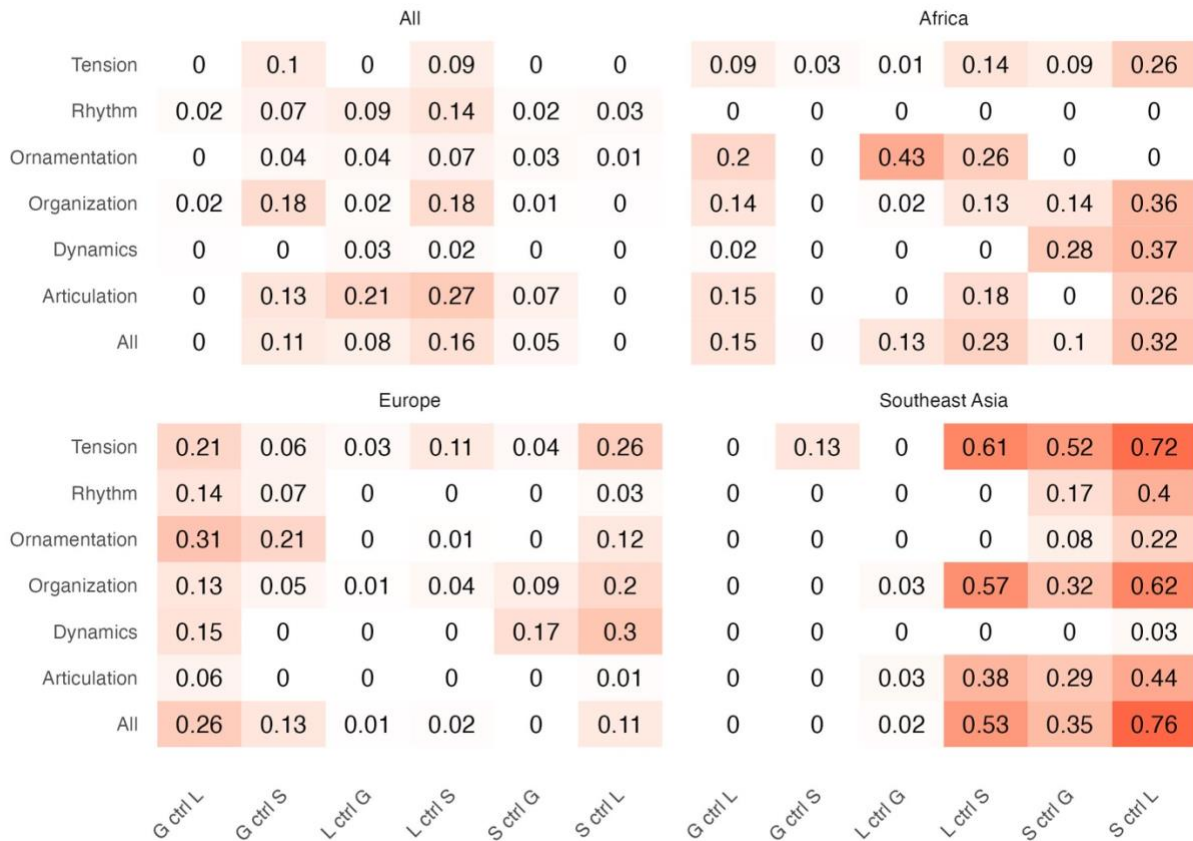


Figure 4: Heat map of the Adjusted R^2 from partial RDA tests for each aspect of musical diversity. RDA tests show the amount of variation explained by (G)enetic, (L)inguistic, or (S)patial distances, while controlling (ctrl) for a second process. From top-left, clockwise, Global distances, within Africa, Within Europe, and within Southeast Asia.

Discussion: Music has a story to tell

The history of human culture is a complex multi-narrative. Sometimes, the parallels between the movement of people and culture tell a coherent story, but sometimes they will tell different tales (Barbieri et al., 2022; Bortolini et al., 2017; Tehrani & d'Huy, 2017). This paper shows that it is also the case that different cultural traits trace different patterns of human history. Musical diversity fits the conditions for a cultural trait to tell us about between-societal relationships but does not strongly correlate with the diffusion of language or genes on a global scale. The independence between these processes suggests that music can tell us something new. Although music has been previously seen as touchstones to ancient relationships (Grauer, 2022), these results do not preclude the possibility that musical traits, much like particular language cognates (Dahl, 2013), cannot tell us about specific migrations or connections. Nor does it rule-out the possibility of localized relationships between different diffusional processes. But it does emphasize the potential decoupling of linguistic, genetic, and musical histories.

To understand the paths of musical deep histories, more research on the conservation of musical traits is needed. We have presented some aspects of music derived from existing data that show variable patterns of autocorrelation and regional relationships to genetic diffusion, geographic diffusion, and linguistic similarity. However, musical diversity is highly multidimensional, and the best mode of comparability is yet undecided. There have been new

coding schemes (Savage et al., 2012), and debates on the importance of musical expertise (Daikoku et al., 2022), but the field is yet to reach agreement. In language, robust discussion on the rates of change, and patterns of evolution have whittled the field to traits that exhibit extreme conservatism. Musicology must resolve these discussions.

Some prominent musicological theorists predicted a strong correlation between musical and genetic similarities (Grauer, 2022). We surprisingly find weak relationships between musical and genetic similarities in the global sample. There are regional correlations between musical traits and genetic similarity in Europe, and weaker relationships in Africa, but there is no generalizable support for musical similarity mapping the major diffusion of humans. The separation between genetic and musical similarity in is consistent with analyses focused on Northeast Asia (Matsumae et al., 2021), but are contrary to a previous analyses focused on Taiwan (Brown et al., 2014) and sub-Saharan Africa (Callaway, 2007). The pattern of these results points to regional variation of a music-gene connection, prompting us to ask what differences drive this variability? The general conclusion we present is that music has its own story to tell about human history, sometimes that may align with genetic diffusion, and in other times it can tell us something new.

The global comparison of musical diversity to linguistic, and genetic diversity represents a substantial increase in size and geographic scope over previous regional analyses, our data remain limited in important ways. In particular, the sample of 121 societies with matching genetic and linguistic data is only a small and non-random subset of the full musical sample of 719 societies (cf. Fig. 1), due to the limited genetic data available from indigenous populations in the Americas, Africa, and Oceania. Even the full sample of Cantometrically coded musical data and linguistic and geographic data used to generate the linguistic phylogeny only represent simplified reductions of the full complexity of cross-cultural musical and linguistic diversity (cf. (Savage, 2018; Wood, 2018; Wood et al., 2022) for critical discussion of the Cantometrics sample and methodology). Nevertheless, the decoupling of the three processes in our analysis highlights the possibilities for music to tell us more about the relationships between societies. This may help to overcome potential limitations with relying on linguistic phylogenies alone as a proxy for cultural history (Lukas et al., 2021), with calls to expand both the geographic scope and the breadth of evidence used for building holistic models of human cultural history (Aguirre-Fernández et al., 2021; Barbieri et al., 2022; Tambets et al., 2018). Considering the evidence for between group difference in music, we could potentially integrate the models of linguistic and musical diversity to enhance our knowledge on the ‘shape and fabric’ of cultural evolution (Gray et al., 2010).

Ultimately, we show that cross-cultural diversity in music contains information on the relationships between societies. The relationships music contains has parallels with, yet is fundamentally different from, linguistic and genetic diversity. The mechanisms that maintain musical similarity and drive musical change will require future study. However, with further understanding, it is feasible to build musical models of history that parallel the knowledge learned from language (Gray et al., 2007). Cultural evolution is complex, and it is likely that music and other cultural traits have evolved through a variety of inter-woven pathways. We hope these results encourage others that adding music to the study of cultural evolution can enrich our understanding of human history.

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Methods

Data

The Global Jukebox contains Cantometric codings for 5,778 songs from 992 societies on 37 different variables (Wood et al., 2022). The complete dataset used here contains 5,242 songs from the 719 societies represented by at least 2 songs. For these analyses we use only the 24 variables without built-in redundancies (see supplementary materials for details). Songs can display multiple characteristics within a Cantometric Line throughout the performance, meaning some songs can have multiple codes for any particular variable. For analytical reasons, we require one value per song, per variable which we select at random. This affects 3% of the dataset. All Cantometrics Lines are standardized to a 0 - 1 scale for comparability. We reverse the codes of a number of existing Cantometric variables so that all variables align high values with a more frequent occurrence of what the variable measures. These are listed in table S2. Codes are reversed by subtracting the standardized scores from 1. See supplementary material for more information on data pre-processing.

Primary Analyses

Latent variable modelling: Latent variable modelling is performed using R v4.1 (R Core Team, 2021) and the package lavaan v0.6-9 (Rosseel, 2012). This model meets all standard latent variable model statistics: RMSEA = 0.06, SRMR = 0.06, and CFI = 0.93. In addition to the six latent variables, the model estimated the correlation between latent variables, and incorporated seven correlations between Cantometric variables which were not explained by the latent variables. A written description of the latent variable model is given in table S3. The results provided are a completely standardized solution.

AMOVA: AMOVA analysis is performed using R v4.1 and ade4 v1.7-18 (Dray & Dufour, 2007). Information on Language family and the geographic Region categorisation are taken from Cantometrics metadata. Euclidean distances are calculated between songs.

Musical Ph_{IST} & Genetic F_{ST} : Musical Ph_{IST} matrices are created using the pairPhiST function within the haplotypes R Package (Aktas, 2020). See the recipe Ph_{IST} in the MakeFile for details. Genetic distances between populations are calculated with the standard Weir and Cockerham F_{ST} formula (Weir & Cockerham, 1984) implemented in the software PLINK v. 1.9 (Chang et al., 2015), using the following script (https://github.com/epifaniarango/Fst_forLargeDatasets). The genetic data comes from published sources which used the Human Origins SNP Chip, a panel which includes ~550,000 SNPs selected to be variable in populations from all continents (Patterson et al., 2012). F_{ST} values are calculated from a sample of 121 populations, with a minimum of 5 individuals per population, a mean of 9, and a maximum of 75, and a total of 1,492 individuals.

Partial RDA and Partial Mantel: Musical Ph_{IST} distance matrices were created using the function pairPhist in the haplotypes package (Aktas, 2020). Partial RDA was performed

following analyses and code performed in (Matsumae et al., 2021). All distance matrices are first transformed to key dimensions using Principal coordinate analyses. We extract all dimensions that explain more than 3% variance. Because musical distance is built from a set of latent dimensions, each component of a dimension explains a small amount of variance. Partial Mantel tests were performed using `mantel.partial` in the `vegan` package (Oksanen et al., 2013). Results in table S13.

Sensitivity Analyses

Latent variable modelling: We compare our latent variables to principal component analyses of Cantometric variables, finding that all variables significantly correlate with at least one component, suggesting these components align with high variance dimensions of the dataset (Fig S4). See the supplementary material for more details.

AMOVA: AMOVA analysis is additionally performed on societies with ≥ 10 songs, and language families and Macroareas with ≥ 10 societies, to ensure the results are not biased by societies with low numbers of songs, or groupings with few societies. The results show negligible differences between the two samples (Table S10).

Partial RDA and Partial Mantel tests: Partial mantel and RDA tests are performed with societies represented by ≥ 10 songs in table S14.

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Author contributions:

PES, SP, and ALCW conceived the project;

SP conducted the analyses with methodology recommended by PES, CB, QDA, ALCW, and DS;

CB provided the genetic data;

SP, CB, DS, and HD curated, matched, and cleaned the data;

HD conducted code review;

SP and PES wrote the initial draft;

CB, DS, ALCW, and QDA contributed to the final draft.

Competing interests: The authors have declared that no competing interests exist.

Data and materials availability: All data and analysis code are publicly available at <https://osf.io/4wu75/>. Some results take significant computing time, and pre-computed results are kept in the same repository. Genetic data is available in the form of F_{ST} population distances and genetic population identifiers, with their respective genetic publication sources. The data is elaborated and expanded from the GeLaTo dataset (Genes and Languages Together - Barbieri et al. (Submitted)). See Wood et al. (2021) for detailed description of the full Cantometric dataset (<https://github.com/theglobaljukebox/cantometrics>), including streaming audio recordings and detailed explanation of the Cantometric coding scheme with audio examples (<http://theglobaljukebox.org>). Please cite (Wood et al., 2022) if using Cantometrics, or other Global Jukebox data. The datasets are archived with ZENODO, and the DOI provided by ZENODO should be used when citing releases of Global Jukebox datasets, which are available within the GitHub organization. For transparency, we registered a preliminary pre-registration of secondary data analysis, also available within the OSF archive. In the process of carrying out the analysis our methods have changed substantially (e.g., expanding the latent variable analysis from 3 to 6 variables after realizing that 3 did not satisfactorily capture the structure of musical variation).

Supplementary Materials

S1 Musical Data sources

S2 Latent variable modeling

S3 AMOVA & PhiST Analysis

S4 Genetic Data description

S5 Partial RDA & Partial Mantel tests

S6 Autocorrelation Structure

S9 Musical Distance vs Genetic, Linguistic, and Spatial Distance

Figs. S1 to S22

Table S1 to S22