

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

## Evolution and Human Behavior

journal homepage: [www.elsevier.com/locate/ens](http://www.elsevier.com/locate/ens)

## Phylogenetic reconstruction of the cultural evolution of electronic music via dynamic community detection (1975–1999)

Mason Youngblood<sup>a,b,\*</sup>, Karim Baraghith<sup>c</sup>, Patrick E. Savage<sup>d</sup><sup>a</sup> Dept. of Psychology, The Graduate Center, City University of New York, New York, USA<sup>b</sup> Dept. of Biology, Queens College, City University of New York, Flushing, USA<sup>c</sup> Dept. of Philosophy, DCLPS, Heinrich-Heine University, Düsseldorf, Germany<sup>d</sup> Faculty of Environment and Information Studies, Keio University, Fujisawa, Japan

## ARTICLE INFO

## Keywords:

Cultural evolution  
Electronic music  
Phylogenetics  
Community detection  
Horizontal transmission

## ABSTRACT

Phylogenetic trees or networks representing cultural evolution are typically built using methods from biology that use similarities and differences in cultural traits to infer the historical relationships between the populations that produced them. While these methods have yielded important insights, researchers continue to debate the extent to which cultural phylogenies are tree-like or reticulated due to high levels of horizontal transmission. In this study, we propose a novel method for phylogenetic reconstruction using dynamic community detection that focuses not on the cultural traits themselves (e.g., musical features), but the people creating them (musicians). We used data from 1,498,483 collaborative relationships between electronic music artists to construct a cultural phylogeny based on observed population structure. The results suggest that, although vertical transmission appears to be dominant, the potential for horizontal transmission (indexed by between-population linkage) is relatively high and populations never become fully isolated from one another. In addition, we found evidence that electronic music diversity has increased between 1975 and 1999. The method used in this study is available as a new R package called *DynCommPhylo*. Future studies should apply this method to other cultural systems such as academic publishing and film, as well as biological systems where high resolution reproductive data is available, and develop formal inferential models to assess how levels of reticulation in evolution vary across domains.

## 1. Introduction

Historically, researchers have relied on phylogenetic comparative methods from biology to create phylogenetic trees or networks of cultural evolution known as “cultural phylogenies”. These methods use differences and similarities in the cultural products of different populations (analogous to differences and similarities in DNA) to reconstruct the historical relationships between them. Traditional phylogenetic methods, which assume the tree-like structure typical of genetic evolution, have yielded critical insights, particularly in linguistics (Bouckaert et al., 2012; Levinson & Gray, 2012; Pagel, Atkinson, & Meade, 2007). However, researchers have debated whether cultural phylogenies are fundamentally tree-like, or whether high levels of horizontal transmission lead to a more reticulated structure (Borgerhoff Mulder, Nunn, & Towner, 2006; Boyd, Borgerhoff-Mulder, Durham, & Richerson, 1997; Cabrera, 2017; Gray, Bryant, & Greenhill, 2010;

Rivero, 2016). For example, biologist Stephen Jay Gould wrote that:

“Biological evolution is a bad analogue for cultural change [...] Biological evolution is a system of constant divergence without subsequent joining of branches. Lineages, once distinct, are separate forever. In human history, transmission across lineages is, perhaps, the major source of cultural change.” – Gould (1991).

Certainly, this is an oversimplification. Horizontal transmission also frequently occurs in biology and sometimes provides problems for the practice of classification (Doolittle, 2009). Horizontal transmission is for instance the primary mechanism for the spread of antibiotic resistance in bacteria (Gyles & Boerlin, 2014), but it also occurs in vertebrates, invertebrates, and plants (Bock, 2010; Crisp, Boschetti, Perry, Tunnacliffe, & Micklem, 2015). Nevertheless, Gould had a fair point. Although cultural traits evolve through a process of variation, selection and

\* Corresponding author.

E-mail address: [masonyoungblood@gmail.com](mailto:masonyoungblood@gmail.com) (M. Youngblood).<https://doi.org/10.1016/j.evolhumbehav.2021.06.002>

Received 5 March 2021; Received in revised form 10 June 2021; Accepted 13 June 2021

Available online 18 July 2021

1090-5138/© 2021 The Authors.

Published by Elsevier Inc.

This is an open access article under the CC BY-NC-ND license

<http://creativecommons.org/licenses/by-nc-nd/4.0/>.

reproduction that results in observable fissions of cultural lineages, branches of the “tree of culture” can reunify later on and frequently do so, for instance in the case of shared practices or customs.

That being said, there is substantial variation in reticulation across cultural domains (Cabrera, 2017; Gray et al., 2010), and depending on the conditions (e.g. co-inheritance of traits) horizontal transmission may or may not interfere with traditional phylogenetic reconstruction (Currie, Greenhill, & MacE, 2010; Nunn, Arnold, Matthews, & Mulder, 2010; Nunn, Mulder, & Langley, 2006). In language evolution, for example, horizontal transmission of basic vocabulary (e.g., numbers, kinship terminology) is relatively low and phylogenetic relationships can be reliably reconstructed (Greenhill, Currie, & Gray, 2009). In other domains, such as material culture, rates of horizontal transmission can be higher and more variable (Cochrane & Lipo, 2010; Jordan & Shennan, 2003; Tehrani & Collard, 2002), leading to phylogenies that clearly contradict the historical record (Tëmkin & Eldredge, 2007). For contemporary culture in the digital age (Acerbi, 2020), where rapid within-generational changes are the norm (Youngblood, 2019b, a), the effects of horizontal transmission on phylogenetic signal are likely to be even more extreme. More recent advancements in network-based phylogenetics allow researchers to estimate reticulation (Bouckaert et al., 2019; Gray et al., 2010; Heggarty, Maguire, & McMahon, 2010; Howe & Windram, 2011; Mesoudi, 2017; Rivero, 2016), but these methods are typically unrooted (Morrison, 2014a,b; Tehrani, 2013) [i.e. cannot be used to infer chronology (Dunn, 2004)] and thus remain complementary to traditional phylogenetic reconstruction (Tehrani & D’Huy, 2017).

Additionally, outside of linguistics it can be extremely challenging to characterize complex cultural traits in a manner suitable for phylogenetic analysis (Howe & Windram, 2011; Tëmkin, 2016). In practice, this means that cultural phylogenies are often limited to very specific domains with variation that can be more easily characterized. For example, researchers have begun applying cultural evolutionary methods to the domain of music (Savage, 2019), but application of phylogenetic methods has been restricted to traditional rhythmic patterns (Díaz-Báñez, Farigu, Francisco, Rappaport, & Toussaint, 2004; Toussaint, 2003), individual instruments (Tëmkin & Eldredge, 2007), the works of a single composer (Liebman, Ornoy, & Chor, 2012; Windram, Charlston, & Howe, 2014), specific variants of folk song melodies (Savage, Chiba, Currie, Suzuki, & Atkinson, 2020), or folk music within a single region (Brown et al., 2014; Le Bomin, Lecointre, & Heyer, 2016; Matsumae et al., 2021). All of these studies also focus primarily on attributes of the music itself (e.g., rhythmic patterns, melodic sequences, instrument construction, singing style), rather than relationships among the musicians making the music.

Given these limitations, it would be valuable to be able to construct large-scale phylogenies for complex cultural traits while explicitly accounting for and measuring horizontal transmission (Nunn et al., 2006). If phylogenies represent changes in population structure over time (Duda & Zrzavý, 2016; Tehrani, Collard, & Shennan, 2010; Velasco, 2013), then one way forward might be to assess population structure from the bottom-up. This is, of course, a complicated proposition. Population structure in biology is typically determined by genetic variation driven by the combined effects of evolutionary processes such as recombination, mutation, genetic drift, demographic history, and natural selection. Unfortunately, population concepts are not often discussed in the cultural evolutionary literature.

According to philosopher of biology Roberta Millstein's definition of a (biological) population, the “boundaries of a population are those groupings where the rates of interactions are much higher within than without” (Millstein, 2010). She calls this definition the “causal interactionist population concept”, or CIPC for short. If agents are represented as nodes in a network graph, where links represent interactions relevant for reproduction (e.g. mating, transferring information), then populations are groups of agents that interact significantly more with one another than with other agents. In general, the rates of interactions between agents are lower between populations than within them, and

this feature is precisely what gives them their (sometimes fuzzy) boundaries. According to this interpretation, populations represent a specific kind of “nearly decomposable system” (Simon, 1962) in that they are emergent properties of the behavior of semi-independent agents. Naturally, agents in these kinds of nearly decomposable systems will be hierarchically organized on different levels, for example into communities, populations, and metapopulations.

It has recently been suggested to use this “inner interactive connectivity”, i.e. cohesion in cultural population structure, as the population defining criterion in cultural evolution (Baraghith, 2020). Specifically, Baraghith (2020) formalized the CIPC by using graph theory to calculate a cohesion index (CI), or the ratio of a population candidate's internal to external connections, that can be maximized to identify populations in a larger network of agents. The CI is a straightforward and effective indicator for populations in static networks, but identifying evolving populations requires a community detection method designed for dynamic networks. The TILES algorithm, designed by Rossetti, Pappalardo, Pedreschi, and Giannotti (2017), is a good candidate for dynamic community detection in cultural evolution. TILES is an online algorithm in that it works with an “interaction stream” of nodes and links. In other words, individuals enter and exit communities as they form and break relationships with other individuals. A node is considered to be a “core” community member if it forms a triangle with other community members, and a “peripheral” member if it is one link away from a core node. Community composition is recomputed throughout this process, each time that a new link enters or exits the network. Snapshots of the community composition are then collected at a regular time interval. Tests with simulated networks indicate that TILES outperforms other community detection algorithms in both processing time and accuracy, and is able to identify events that are critical for evolutionary research (e.g. splitting, death) (Rossetti et al., 2017). Most importantly, the TILES algorithm closely resembles the formalization of the CIPC (Baraghith, 2020) in that it is based on the relative density of links within and between communities and allows for overlap on the periphery.

In the following, we propose a new method for phylogenetic reconstruction based on the CIPC that uses the TILES dynamic community detection algorithm to identify distinct populations and track how they change over time.<sup>1</sup> We will treat different groups under investigation as populations or metapopulations, rather than as species. Deciding whether a member belongs to a specific community in this framework is not a question of whether they share as many relevant hereditary traits as possible (like “genes” in biological evolution) with the other members of the grouping. Instead, what counts is the relative number of social interactions within (and outside) the community.

More specifically, we are using genres of electronic music as a test case. Although musicologists recognize that genres are generated by evolving communities of artists (Klement & Strambach, 2019; Lena, 2012), previous attempts to quantitatively map genres have depended on listener habits (Lambiotte & Ausloos, 2005), instrument similarity (Percino, Klimek, & Thurner, 2014), or sub-genre tags on streaming platforms (Mauch, Maccallum, Levy, Leroi, & Mauch, 2015). By using artist co-release data (who collaborates with who) we can explicitly track how populations of artists, and the genres that they correspond to, evolve over time. This approach is similar to qualitative attempts at reconstructing music phylogenies that rely on historical accounts of how artist communities grow, diverge, and influence each other over time (Crauwels, 2016; Ishkur, 2000). We chose to study electronic music because, like heavy metal (Koch, Silvestro, & Foster, 2020), it is known for its rapid differentiation into competing genres and subgenres (van Venrooij, 2015), particularly during the 1990s (McLeod, 2001). In addition, collaboration links between electronic music producers are already known to be important for cultural transmission (Youngblood,

<sup>1</sup> For clarification, we use the terms population and lineage interchangeably since populations in this framework exist in both space and time.

2019b, a) and community structure (Janosov, Musciotto, Battiston, & Iñiguez, 2020).

The aim of this study is to assess the degree to which the cultural phylogeny of electronic music is tree-like. As the tree-likeness of cultural phylogenies exists on a continuum (Gray et al., 2010; O'Brien, Collard, Buchanan, & Boulanger, 2013) and there is not enough reliable comparative data to generate neutral predictions about typical levels of horizontal transmission, it seems unwise to attempt to do hypothesis-testing about whether or not a given phylogeny is fundamentally tree-like or reticulated. Instead, we aim to simply characterize tree-likeness by estimating the ratio of vertical to horizontal transmission. Here, we use the proportion of links in the network that are between populations as a proxy measure for horizontal transmission. Since collaborative links between artists are meaningful for cultural transmission (Youngblood, 2019b), the level of collaboration between two populations likely reflects the potential for cultural transmission between them. This simple metric is consistent with the common definition of horizontal transmission as the level of cultural transmission between extant populations (Borgerhoff Mulder et al., 2006; Currie et al., 2010; Greenhill et al., 2009), and reflects the conceptualization of horizontal transmission in biological phylogenetics. The original definition of horizontal transmission proposed by Cavalli-Sforza and Feldman (1981), which was simply cultural transmission occurring within the same generation, is insufficient here because it does not take population structure into account.

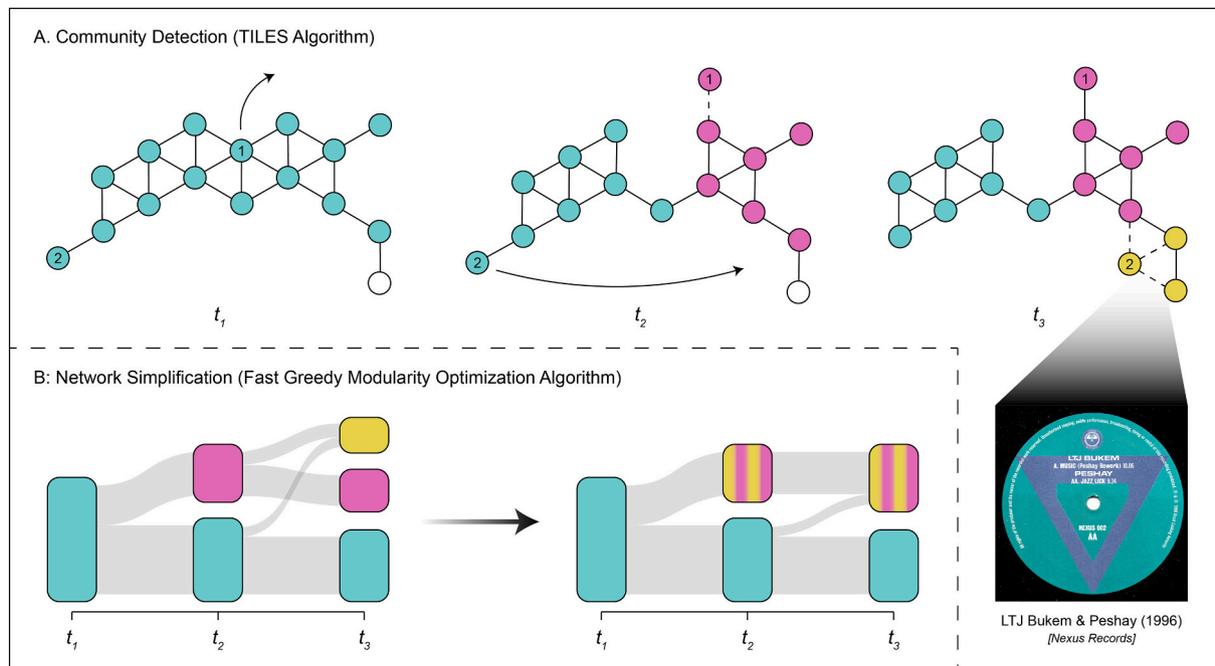
## 2. Methods

### 2.1. Data collection

All data used in the current study was collected from Discogs in April 2020. Discogs is a large, user-generated database of music releases that has better coverage of electronic music than other sources (Bogdanov & Serra, 2017; van Venrooij, 2015). We chose to use the releases data rather than the masters data because it has better coverage of EPs, singles, remixes, and other smaller releases. First, we extracted all collaborative releases with the “Electronic” genre tag. Then, we retrieved the release IDs, release years, style tags, and artists from these releases, including any featured artists, remixers, and producers from the tracklists. Due to computational limitations, we only included releases from between 1970 and 1999. Collaborations were converted into an unweighted dynamic edgelist for input into TILES. More details about data collection and computational limitations can be found in the appendix.

### 2.2. Community detection

Community detection was conducted using the Python implementation of TILES (Rossetti et al., 2017) (see Fig. 1). Each link persisted for 365 days and community composition was recorded at the beginning of each year. Links from collaborative releases were assigned random dates within the year they were released, so that changes in community



**Fig. 1.** A simplified visual summary of community detection using the TILES algorithm (A: top), and network simplification using the fast greedy modularity optimization algorithm (B: bottom). In A, arrows depict the movement of nodes (artists), dotted lines depict newly formed links (collaborations), and different colors represent different communities. Each link in the network corresponds to a collaborative release like the one shown in the bottom right (<https://bit.ly/3jvofD8>). Both core and peripheral artists are included, and artists in multiple communities are assigned to the largest one. Between  $t_1$  and  $t_2$ , artist 1 breaks all but one of its previous ties. Since artist 1 is no longer in a triangle with those other artists, the network splits into two communities (green and pink). Between  $t_2$  and  $t_3$ , artist 2 breaks its tie with the green community and establishes a collaboration with a peripheral member of the pink community and an unassigned artist. Since these three artists form a new triangle they are classified as a new community (yellow). In the left side of B, each node represents a community from A in the corresponding time point, and the links between communities represent the number of individuals moving between them. The right side of B is the same visualization after network simplification, where the pink and yellow communities have been compressed into a single population. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

membership were continuous. We chose to set link persistence to 365 days so that the resolution of the phylogeny matched the resolution of the collaboration data. Preliminary analyses indicated that lower values fragment the overall network structure, whereas higher values bias the results towards vertical transmission.

The output of TILES is a set of community memberships for each year, where each individual may be part of multiple overlapping communities. In order to visualize the results, we required a single community membership for each individual. We assigned each individual in multiple communities to the community with highest network density, or the proportion of actual to possible connections. Ties were broken by group size. Both core and peripheral community members were included in the visualization and analysis.

### 2.3. Network simplification

The dynamic community composition for all of the electronic releases, in which each node is a community of artists and each directed link represents artists moving between communities from year to year, was too large to visualize in its original form. To simplify the network we conducted a cluster analysis using the fast greedy modularity optimization algorithm (Clauset, Newman, & Moore, 2004) and merged nodes assigned to the same cluster within each year using the *igraph* package in R (Csardi & Nepusz, 2006) (see Fig. 1). Links were combined to represent the total number of artists moving between each set of merged nodes. The simplified network can be thought of as a hierarchical network with two layers. Each node represents a population of communities (identified by TILES) which are further separable into individual artists.

The fast greedy algorithm is a hierarchical agglomeration clustering method that optimizes the modularity, or the observed minus expected proportion of within-cluster links, of the entire network. In other words, the algorithm clusters groups of communities that interact significantly more with one another than with other communities into populations, as consistent with the CIPC (Baraghith, 2020; Millstein, 2010). We chose to use the fast greedy algorithm because it yielded the highest modularity relative to other clustering methods (see Table S1), as well as a manageable number of populations for interpretation. In addition, it results in accurate estimates of the proportion of links between clusters in simulated networks of various population sizes (Yang, Algesheimer, & Tessone, 2016), which is directly relevant for our measurements of horizontal transmission.<sup>2</sup>

### 2.4. Horizontal transmission/population linkage

To estimate horizontal transmission between two populations, we divided the total number of weighted links between populations by the sum of the number of internal weighted links from each population. In other words, we calculated the percentage of links in the sub-network that flow between the two populations.

In addition, we calculated the cohesion index (CI), or the ratio of internal to external links, for each individual population (Baraghith, 2020). Although this application of the CI differs from its original formulation, as populations in the dynamic network have a temporal dimension, it is still an intuitive metric for the degree to which a population is distinct from other populations in the phylogeny. Since the weighted links are summed during both community detection and network simplification, the CI can be calculated at any level of the hierarchical network.

<sup>2</sup> Despite the name “fast greedy algorithm”, this algorithm does not sacrifice quality for speed.

### 2.5. Visualization algorithm

The phylogeny was visualized with a sankey plot using the *sankeyD3* package in R (Breitwieser, Gandrud, Allaire, Russell, & Bostock, 2017). This method expands on recent work by Mall, Langone, and Suykens (2015) and others (Liechti & Bonhoeffer, 2020; Rosvall & Bergstrom, 2010; Wu et al., 2016). As you go from left to right in the visualization, each node is a population of communities identified by TILES in the corresponding year on the x-axis. The links depict movement between populations over time, where thickness corresponds to population size. Only the largest connected component of the network was plotted to maximize the clarity of the visualization. The layout of the nodes in the sankey plot is algorithmically generated by (1) minimizing the overlap between links and (2) maximizing the horizontal alignment of nodes. In other words, the visualization algorithm maximizes both the clustering of nodes and the continuity of links. The distances between and the positions of populations do not convey information like they do in a standard phylogeny, so the specific y-axis location of each node is not meaningful.

### 2.6. Topic modelling

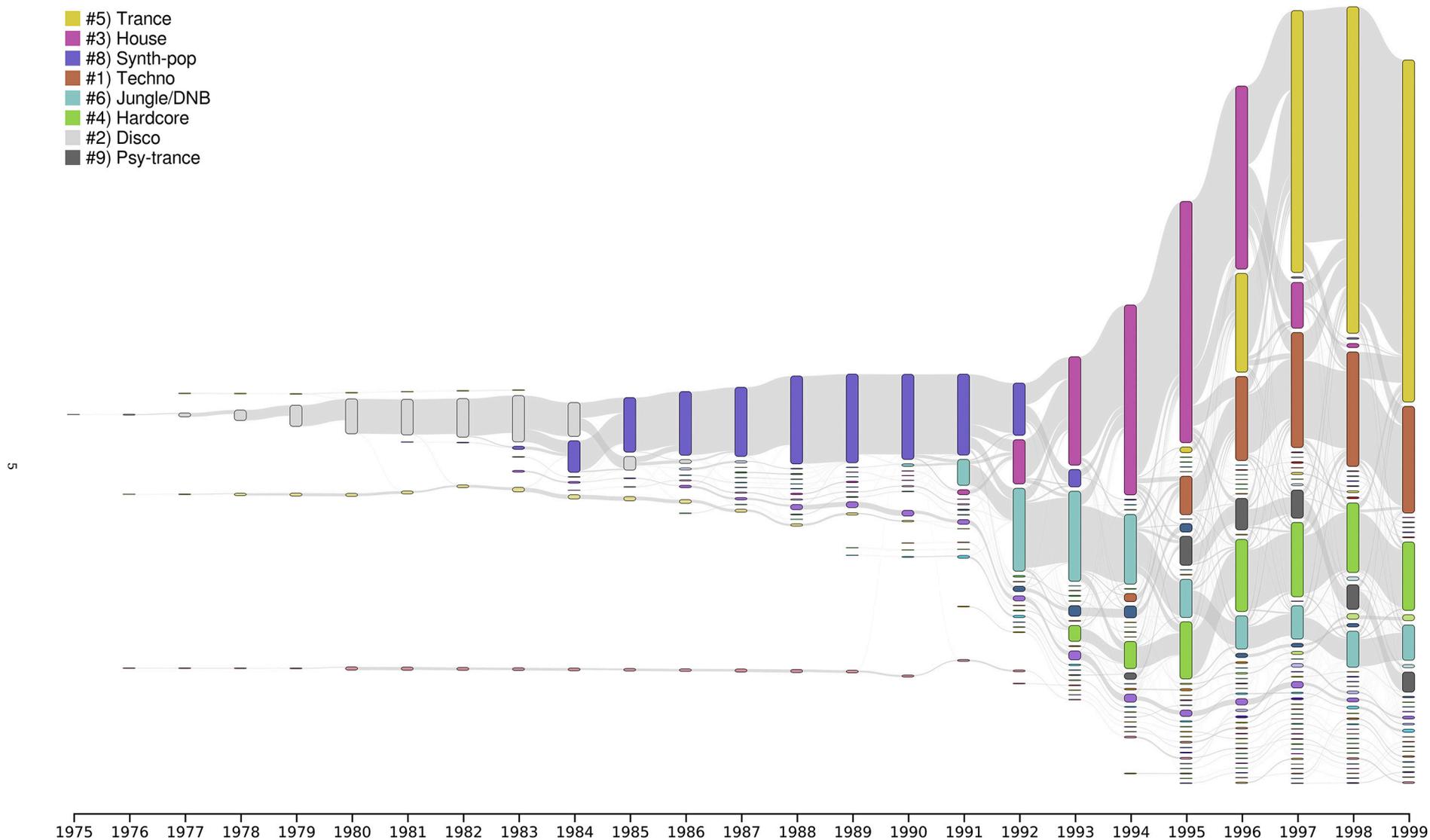
To determine whether or not populations of artists correspond to distinct subgenres, we compiled the style tags for all releases from each population and conducted Latent Dirichlet Allocation (LDA) topic modelling. LDA models are Bayesian mixture models that take large corpora of words from different sources and identify clusters of words, or “topics” (Grün & Hornik, 2011). Each source is assigned a distribution of topics, one of which is identified as the most distinctive to that source. In this case, we looked for clusters of style tags that were distinctive to each population. Style tags from Discogs have been successfully used to quantitatively identify genres in the past (Mauch et al., 2015), which is unsurprising given that their purpose is subjectively denoting genres. Releases by artists from multiple populations (42.5%) were excluded from the topic modelling so that the samples were independent from one another. We used all style tags for each group rather than unique style tags to account for frequency of use. The LDA model was fitted using variational expectation maximization using the R package *topicmodels* (Grün & Hornik, 2011).  $k$ , or the target number of topics, was set to the number of populations.

## 3. Results

We analyzed 1,498,483 collaborative relationships between 93,831 artists from 53,581 different electronic music releases between 1970 and 1999. TILES identified 8354 communities, of which we visualized the largest connected component. This component contained 90.2% of the communities, appearing between 1975 and 1999. Network simplification reduced the dynamic community composition to 72 populations with a modularity score of 0.65. The geographic distribution of releases from these populations can be seen in Fig. S1.

The resulting phylogeny can be seen in Fig. 2. Each node is a set of communities identified by TILES, which are further separable into individual artists. Nodes with the same color belong to the same population. Each link corresponds to the number of artists moving between nodes. In the interactive version of Fig. 2 ([https://masonyoungblood.github.io/electronic\\_music\\_phylogeny.html](https://masonyoungblood.github.io/electronic_music_phylogeny.html)) you can zoom, navigate, and hover over nodes for the three most distinctive style tags and 10 most distinctive artists from each population (identified by weighted log-odds, calculated using uninformative Dirichlet priors), and hover over links for the number of individuals moving between nodes. Details about the eight largest populations in the phylogeny can be seen in Table 1.

Population #5 (yellow) includes a diverse array of four-on-the-floor dance music but leans towards trance. Most of the top artists are from Germany. Population #3 (pink) also includes a diverse array of dance music but leans towards house. The top artists are from America,



**Fig. 2.** A phylogeny based on the dynamic community composition of electronic music over time. Each node is a set of communities, and each link corresponds to the number of artists moving between nodes. Nodes with the same color belong to the same population, and the height of each node corresponds to the number of artists. The visualization algorithm maximizes both the clustering of nodes and the continuity of links. The population names in the legend are simplified versions of the more detailed classifications in the results, and the overall population size over time can be seen in Fig. S2. Interactive version: [https://masonyoungblood.github.io/electronic\\_music\\_phylogeny.html](https://masonyoungblood.github.io/electronic_music_phylogeny.html)

**Table 1**

The size, cohesion index, top styles and top artists (calculated by weighted log-odds) from the eight largest populations in the phylogeny.

	N	CI	Top styles	Top artists
5	15,413	1.73	Trance, House, UK Garage	Sash!, Vengaboys, 666, Paul van Dyk, Brooklyn Bounce, The Mackenzie, ATB, Fiocco, Da Hool, Nalin & Kane
3	10,891	1.45	House, Euro House, Italo-dance	Cappella, Jon Of The Pleased Wimmin, Reel 2 Real, Sasha, 2 Unlimited, Corona, DJ Duke, DJ BoBo, Jeremy Healy, Dave Seaman
8	8228	4.61	Synth-pop, Italo-Disco, Disco	Madonna, Depeche Mode, Pet Shop Boys, Black Box, Janet Jackson, Technotronic, Paula Abdul, Whitney Houston, New Order, Sandra
1	8152	1.05	Techno, Hard House, Experimental	Mike Flores, DJ Spooky, AM/FM Alexander, George Centeno, Bill Laswell, Mad Professor, Pookie Bear, Mark Broom, Nemesis, Angel Alanis
6	5622	1.57	Jungle, Drum n Bass, Hardcore	Grooverider, DJ SS, DJ Hype, Micky Finn, DJ Ratty, LTJ Bukem, Ellis Dee, Randall, DJ Phantasy, Kenny Ken
4	5243	1.98	Hardcore, Happy Hardcore, Noise	Force & Styles, Hixxy, Scott Brown, Bass Generator, Billy 'Daniel' Bunter, Buzz Fuzz, Eruption, Sy & Unknown, DNA, DJ Fade
2	3885	4.87	Disco, Synth-pop, New Wave	Commodores, Donna Summer, Giorgio Moroder, Patrick Cowley, Sylvester, Boney M., Kraftwerk, Gino Soccio, Yazoo, The Human League
9	2283	1.05	Goa Trance, Psy-Trance, Progressive Trance	Astral Projection, Prana, Chakra, Quirk, MFG, S.U.N. Project, GMS, Pleiadians, X-Dream, ManMadeMan

England, and all over Europe. “Euro House”, the second top style in this population, is associated with the radio-friendly popular dance music that rose to prominence in Europe in the mid 1990s. Population #8 (purple) includes artists like Madonna, Pet Shop Boys, and Technotronic that were incorporating electro, hip-hop, and techno into pop and rock music in the late 1980s and early 1990s. Population #1 (orange) includes a diverse array of artists from American and Europe making techno, hard house, and experimental music. Population #6 (blue) is the branch of the “hardcore continuum” of high-BPM rave genres that includes jungle and drum n bass. Most of the top artists are from London and the surrounding suburbs. Population #4 (green), on the other hand, is the heavier branch of the “hardcore continuum” that includes happy hardcore, gabber, and noise. Most of the top artists are from rural England and Scotland. Population #2 (light gray) includes both disco and synth-pop throughout the 1980s, including Giorgio Moroder and Donna Summers who transformed dance music with their 1977 hit “I Feel Love”. Population #9 (dark gray) corresponds to Goa trance and psy-

trance. Goa trance first emerged in India in the early 1990s and became known as psy-trance once it reached Europe and the rest of the world. Most of the top artists are from Europe and the Middle East. The most distinctive artists from each population do not necessarily represent the most innovative or influential artists from the subgenres that they correspond to. For example, the originators of Detroit techno music (e.g. Juan Atkins, Derrick May, and Kevin Saunderson (Sicko, 2010)) do not appear in the most distinctive artists from Population #1 (orange), and the originators of Chicago and New York house music (e.g. Frankie Knuckles and Larry Levan (Reynolds, 2012)) do not appear in the most distinctive artists from Population #3 (pink). The rise and fall of each of these lineages, as well as the interactions between them, are intuitive and broadly consistent with the historical record (Collins, Schedel, & Wilson, 2013; Reynolds, 2012; Sicko, 2010).

The percentage of links between the eight largest populations in the phylogeny can be seen in Table 2. 20.9% of links in the phylogeny are between rather than within populations (mean of 25.7% with different network simplification methods, as per Table S1), indicating that while the potential for horizontal transmission is relatively high the phylogeny still has a fundamentally branching structure. Interestingly, both the number of populations and the percentage of between-population links has increased over time (Fig. 3). The large spike in the percentage of between-population links between 1984 and 1986 is likely due to the large movement of artists from Population #2 (light gray) to Population #8 (purple), which appears to be caused by an influx of new artists collaborating with existing artists and disrupting the original population structure.

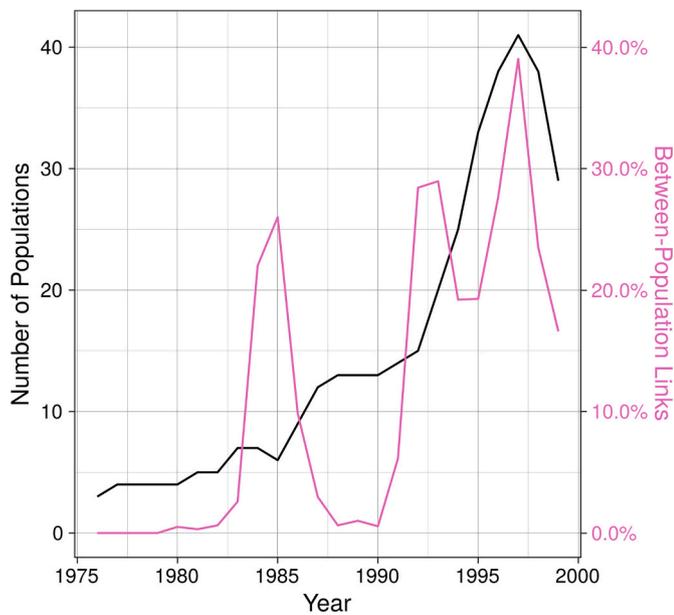
The LDA topic model identified 48 unique topics across 69 of the populations in the simplified network. Three populations (#53, #57, #62) were excluded from the topic model because they did not have any unique releases. The  $\alpha$  value of the fitted model, which gets smaller as more topics correspond one-to-one with groups, was 0.019. 64.6% of topics corresponded to a single population, 27.1% corresponded to two populations, and 8.3% corresponded to three populations. This indicates that populations of artists have distinctive style tags associated with their releases, and likely represent distinct subgenres of electronic music. The top 10 terms from each topic assigned to the eight largest populations in the phylogeny can be seen in Fig. S3.

The style tag diversity from each year, calculated with all releases in the phylogeny using the Simpson and Shannon diversity indices, can be seen in Fig. 4. We used the effective number of styles, or the number of equally-abundant styles required to get the same diversity index (Jost, 2006), because it scales linearly and has been used in previous work on musical diversity (Mauch et al., 2015). Between 1975 and 1999 the diversity of styles tags in the phylogeny has increased by more than order of magnitude.

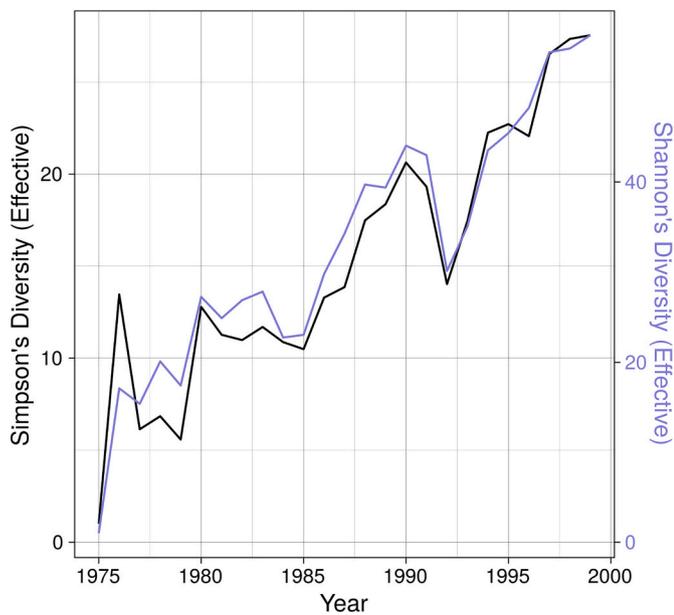
**Table 2**

The percentage of links between the eight largest populations in the phylogeny. Each value represents the percentage of links in the sub-network that flow between the two populations. In other words, we divided the total number of weighted links between populations by the sum of the number of internal weighted links from each population.

	5	3	8	1	6	4	2	9
5	—	12.3%	0.0%	12.9%	2.4%	4.0%	0.0%	3.9%
3		—	4.3%	7.0%	7.4%	2.7%	0.0%	3.0%
8			—	0.0%	2.7%	0.1%	5.3%	0.0%
1				—	5.2%	5.1%	0.0%	3.6%
6					—	6.4%	0.0%	1.8%
4						—	0.0%	2.3%
2							—	0.0%
9								—



**Fig. 3.** The number of populations identified in each year (left y-axis), as well as the percentage of between-population links between each year and the previous year (right y-axis). The percentage of between-population links can be treated as a global proxy measure of horizontal transmission.



**Fig. 4.** The effective number of styles from each year calculated using Simpson's (left y-axis) and Shannon's (right y-axis) diversity indices.

#### 4. Discussion

By applying dynamic community detection methods to an exhaustive dataset of electronic music releases spanning three decades, we have constructed a cultural phylogeny built explicitly from population structure. Most importantly, we found that although vertical transmission appears to be dominant, as the majority of links in the phylogeny are within lineages (79.1%), the potential for horizontal transmission is relatively high and populations never become fully isolated from another. Additionally, the percentage of links between populations increased between 1975 and 1999. This is consistent with

anecdotal accounts (Lindop, 2011) and another recent quantitative study that found that hybridization between genres increased over the same period, using genre tags from music databases (Gagen, 2019). Taken together these results indicate that although communication technologies like the internet have increased rates of horizontal transmission between human populations (Carrignon, Bentley, & Ruck, 2019), allowing music producers to collaborate and influence one another despite significant geographical distance (Youngblood, 2019b), the cultural evolution of music is still relatively tree-like.

We also observed a large increase in style tag diversity. In combination with population diversification, this indicates that electronic music diversity has increased between 1975 and 1999. This result contradicts two recent studies on the cultural evolution of popular music, which concluded that musical diversity has either remained relatively constant (Mauch et al., 2015) or declined (Serrà, Corral, Boguñá, Haro, & Arcos, 2012) in recent decades. Although it is possible that diversification patterns in electronic music are different than in contemporary music as a whole, both studies have some important limitations that reduce their generalizability. Mauch et al. (2015) only used data from the Billboard Top 100. Estimates of diversity based on the Billboard charts alone will inevitably underestimate the diversity in music being produced at all levels of an ever-expanding industry. Although Serrà et al. (2012) used a more extensive dataset their conclusions are based solely on pitch transitions, timbre, and loudness, measures that only capture a fraction of musical variation and are less relevant for recent musical innovations (e.g. experimental, noise, drum-based, and lyric-based music). That being said, the quantitative audio analysis methods used by both Mauch et al. (2015) and Serrà et al. (2012) better capture patterns of musical diversity than style tags. Future studies should combine quantitative audio analysis with our process-based phylogenetic approach to better understand the diversification of contemporary music.

The fact that the structure of the phylogeny is relatively tree-like may be surprising to some, given the prevalence of horizontal transmission in contemporary culture (Carrignon et al., 2019). We suspect that our observed level of within-population links is due to a combination of factors. Geography, for example, plays an important role in structuring cultural variation (Bouckaert et al., 2012; Currie, Meade, Guillon, & Mace, 2013; Gray, Drummond, & Greenhill, 2009; Kauhanen, Gopal, Galla, & Bermúdez-Otero, 2021; Schillinger & Lycett, 2019), and the top artists from certain populations in the phylogeny tend to come from particular countries. Although the widespread adoption of the internet has reduced the influence of geography on musical collaboration (Youngblood, 2019b), most of our data is from the 1980s and 1990s when electronic music subcultures were often associated with particular locations like Detroit or London (Collins et al., 2013; Reynolds, 2012; Sicko, 2010). Transmission isolating mechanisms (TRIMS), or cultural norms that reduce levels of transmission between lineages, may be present as well (Durham, 1992). TRIMS are comparable to intrinsic reproduction barriers that exist between members of different biological species. Individuals in “underground” electronic music communities often define themselves in opposition to mainstream music culture, and are deeply invested in the shared identity of their community (Lindop, 2011; Thornton, 1995). The common underlying concern, that too much mainstream recognition could reduce the longevity and undermine the integrity of music communities, is actually supported by previous research on electronic music in the UK (van Venrooij, 2015). Artists who receive mainstream recognition are sometimes subject to criticism (Hesmondhalgh, 1998; Noys, 1995; Thornton, 1995), and may even adopt aliases to reinforce their commitment to the “scene” (Formilan & Stark, 2020). Artists also appear to intentionally adopt styles that sound distinctive relative to more popular artists (Klimek, Kreuzbauer, & Thurner, 2019), which could be further reinforced by conformity bias within groups (Youngblood, 2019a). Communal experiences in clubs and raves, sometimes supplemented with drug use, also enhance social bonding (Hutson, 2000; Savage et al., 2020; St John, 2006) and

reinforce community boundaries (Kavanaugh & Anderson, 2008). Some scholars have even posited that obscure subgenre names and other forms of jargon function in “maintaining clear boundaries that define in-group/out-group relations” (McLeod, 2001). We hypothesize that these cultural norms may act as TRIMS by enhancing the longevity and cohesion of music communities, and thus reducing the likelihood that they are integrated into larger and more popular genres (Lena, 2012).

Importantly, many populations evolve independently and only later connect to the larger phylogeny. In some cases this is likely due to the fact that external connections to other genres are not shown, but in other cases it could represent independent evolution via shared technology. For example, the emergence of electronic music in India in the 1970s, most notably in Bollywood (#15 in Fig. 2), was driven by the introduction of novel synthesizer technologies rather than the influence of American and European artists (Pandey, 2019; Purgas & Morgan, 2020). Additionally, the level of reticulation that we observed for electronic music has likely been enhanced by communication technologies and a globalized music industry, and is not necessarily reflective of traditional music. Diversity in Gabonese folk music, for example, appears to show signatures of vertical transmission (Le Bomin et al., 2016), and phylogenetic studies indicate that folk music variation can be relatively conserved within genetic lineages (Brown et al., 2014; Pamjav, Juhász, Zalán, Németh, & Damdin, 2012). Unfortunately, our method can only be used in cases where detailed collaboration data is available, which is unlikely to be the case for any form of traditional music.

Several limitations of this study need to be highlighted. Firstly, the phylogeny was exclusively constructed from collaboration links, which do not account for all cultural transmission. For example, contemporary artists routinely draw inspiration from recorded music, live events, new technologies, etc. These alternate modes of cultural transmission are more likely to be horizontal, especially towards the end of our study period when internet-use became more widespread. Thus, the phylogeny really only captures the “core” of these cultural lineages (Boyd et al., 1997), and may under-represent reticulation across all transmission modes. Secondly, the data was limited to releases tagged as “electronic” on Discogs, so external connections to other genres (e.g. rock and pop music) are not shown. Thirdly, we did not compare the results of our dynamic community detection approach with generative models, as is often done in contemporary phylogenetics to test assumptions and check robustness. Finally, our analysis focuses on the evolution of interactions among artists, and does not analyze the evolution of the sound of the musical works themselves (Savage, Chiba, et al., 2020; Serrà et al., 2012). Future studies should investigate the ways in which musical sounds and the artists making them may or may not coevolve.

Our framework also has the potential to improve music recommendations on streaming platforms like Spotify. Currently, Spotify's recommendation algorithms are primarily based on listener habits (Johnston, 2019). In other words, related artists are identified based on what their fans are also listening to. Spotify's algorithms have been observed to reduce the diversity of listeners' music consumption (Anderson, Maystre, Anderson, Mehrotra, & Lalmas, 2020), and have the potential to exacerbate existing inequalities in the music industry based on popularity (Abdollahpouri & Mansoury, 2020; Abdollahpouri, Mansoury, Burke, & Mobasher, 2020), gender (Werner, 2020), and other factors (O'Dair & Fry, 2020). These issues may be further compounded by a recently announced policy allowing artists to “pay” (via reduced royalties) for an algorithmic boost (Hern, 2020). Supplementing recommendation algorithms with data on collaborative population structure would allow for the identification of artists from the same community independently of listeners' biases.

Future research should apply this method to high resolution data from other cultural domains (e.g. co-citation patterns in academic fields (Youngblood & Lahti, 2018), institutional membership in the arts (Fraiberger, Sinatra, Resch, Riedl, & Barabási, 2018), or the composition of Hollywood film crews (Tinits & Sobchuk, 2020)) to determine whether the observed level of reticulation in this study is typical of other

contemporary cultural systems. Additionally, this method is theoretically generalizable to biological evolution as well. For example, researchers that study the evolution of insects in the lab could use motion tracking (Crall, Gravish, Mountcastle, & Combes, 2015) to estimate population structure from mating events, and then measure how genetic changes map onto lineages over time. In some long-term study systems, such as Darwin's finches, researchers have collected enough detailed mating data to reconstruct population structure in the wild. Applying this method where interbreeding between closely related species has led to hybrid speciation and clear genetic changes (Lamichhaney et al., 2018) could provide new insight into the process of reproductive isolation. Finally, previous studies have used cases where the historical relationships between cultural lineages are known (e.g. transmission chains (Schillinger, Mesoudi, & Lycett, 2016; Spencer, Davidson, Barbrook, & Howe, 2004) and simulations (Currie et al., 2010; Greenhill et al., 2009)) to assess the efficacy of traditional phylogenetic methods under particular conditions. By using an agent-based model of cultural transmission that outputs both population structure and trait features and allows for movement between lineages (Premo & Hublin, 2009), future studies could provide ground truth estimates of horizontal transmission from traditional phylogenetic methods against those from dynamic community detection.

#### Data & code availability statement

The method used in this study is available as a new R package called *DynCommPhylo* on Github (<https://github.com/masonyoungblood/DynCommPhylo>). The “example” subfolder of the R package includes our processed data and analysis script. The interactive version of Fig. 2 is also available on Github ([https://masonyoungblood.github.io/electronic\\_music\\_phylogeny.html](https://masonyoungblood.github.io/electronic_music_phylogeny.html)). The raw data used in this study came from the April 2020 XML archive of releases on Discogs (<http://bit.ly/DiscogsApril2020>).

#### Declaration of Competing Interest

None.

#### Acknowledgments

First and foremost, we thank the artists whose work inspired this project and made our analysis possible. We also thank the many Discogs users who contributed so much time and effort to cataloguing the history of electronic music. This research was supported, in part, by Grant-in-Aid 19KK0064 from the Japan Society for the Promotion of Science, National Science Foundation Grants CNS-0958379, CNS-0855217, ACI-1126113 and the City University of New York High Performance Computing Center at the College of Staten Island.

#### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.evolhumbehav.2021.06.002>.

#### References

- Abdollahpouri, H., & Mansoury, M. (2020). *Multi-sided exposures bias in recommendation*. arXiv. [arXiv:2006.15772](https://arxiv.org/abs/2006.15772).
- Abdollahpouri, H., Mansoury, M., Burke, R., & Mobasher, B. (2020). *Addressing the multistakeholder impact of popularity bias in recommendation through calibration*. arXiv. [arXiv:2007.12230](https://arxiv.org/abs/2007.12230).
- Acerbi, A. (2020). *Cultural evolution in the digital age*. Oxford University Press.
- Anderson, A., Maystre, L., Anderson, I., Mehrotra, R., & Lalmas, M. (2020). Algorithmic effects on the diversity of consumption on Spotify. In , 2020. *Proceedings of the World Wide Web conference, WWW* (pp. 2155–2165). <https://doi.org/10.1145/3366423.3380281>.
- Baraghith, K. (2020). Investigating populations in generalized Darwinism. *Biology and Philosophy*, 35, 1–27. <https://doi.org/10.1007/s10539-020-9735-6>.

- Bock, R. (2010). The give-and-take of dna: Horizontal gene transfer in plants. *Trends in Plant Science*, 15, 11–22. <https://doi.org/10.1016/j.tplants.2009.10.001>.
- Bogdanov, D., & Serra, X. (2017). Quantifying music trends and facts using editorial metadata from the Discogs database. In *18th international society for music information retrieval conference, Suzhou, China* (pp. 89–95).
- Borgerhoff Mulder, M., Nunn, C. L., & Towner, M. C. (2006). Cultural macroevolution and the transmission of traits. *Evolutionary Anthropology*, 15, 52–64. <https://doi.org/10.1002/evan.20088>.
- Bouckaert, R., Lemey, P., Dunn, M., Greenhill, S. J., Alekseyenko, A. V., Drummond, A. J., ... Atkinson, Q. D. (2012). Mapping the origins and expansion of the Indo-European language family. *Science*, 337, 957–961. <https://doi.org/10.1126/science.1219669>.
- Bouckaert, R., Vaughan, T. G., Barido-Sottani, J., Duchêne, S., Fourment, M., Gavryushkina, A., ... Drummond, A. J. (2019). BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*, 15, 1–28. <https://doi.org/10.1371/journal.pcbi.1006650>.
- Boyd, R., Bogerhoff-Mulder, M., Durham, W. H., & Richerson, P. J. (1997). Are cultural phylogenies possible? In P. Weingart, S. D. Mitchell, P. J. Richerson, & S. Maasen (Eds.), *Human by nature* (pp. 355–386). Mahwah, NJ: Lawrence Erlbaum.
- Breitwieser, F., Gandrud, C., Allaire, J., Russell, K., & Bostock, M. (2017). sankeyD3: D3 JavaScript Sankey Graphs from R. <https://github.com/fbreitwieser/sankeyD3> (r package version 0.3.2).
- Brown, S., Savage, P. E., Ko, A. M. S., Stoneking, M., Ko, Y. C., Loo, J. H., & Trejaut, J. A. (2014). Correlations in the population structure of music, genes and language. *Proceedings of the Royal Society B: Biological Sciences*, 281. <https://doi.org/10.1098/rspb.2013.2072>.
- Cabrera, F. (2017). Cladistic parsimony, historical linguistics and cultural phylogenetics. *Mind and Language*, 32, 65–100. <https://doi.org/10.1111/mila.12133>.
- Carrignon, S., Bentley, R. A., & Ruck, D. (2019). Modelling rapid online cultural transmission: Evaluating neutral models on Twitter data with approximate Bayesian computation. *Palgrave Communications*, 5. <https://doi.org/10.1057/s41599-019-0295-9>.
- Cavalli-Sforza, L. L., & Feldman, M. W. (1981). *Cultural transmission and evolution: A quantitative approach*. Princeton, NJ: Princeton University Press.
- Clauset, A., Newman, M. E. J., & Moore, C. (2004). Finding community structure in very large networks. *Physical Review E*, 70. <https://doi.org/10.1103/physreve.70.066111>.
- Cochrane, E. E., & Lipo, C. P. (2010). Phylogenetic analyses of Lapita decoration do not support branching evolution or regional population structure during colonization of remote Oceania. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365, 3889–3902. <https://doi.org/10.1098/rstb.2010.0091>.
- Collins, N., Schedel, M., & Wilson, S. (2013). Electronic music. In *Cambridge introductions to music*. Cambridge University Press. <https://doi.org/10.1017/CBO9780511820540>.
- Crall, J. D., Gravish, N., Mountcastle, A. M., & Combes, S. A. (2015). Beetag: A low-cost, image-based tracking system for the study of animal behavior and locomotion. *PLoS One*, 10, 1–13. <https://doi.org/10.1371/journal.pone.0136487>.
- Crauwels, K. (2016). <https://musicmap.info/>.
- Crisp, A., Boschetti, C., Perry, M., Tunnacliffe, A., & Micklem, G. (2015). Expression of multiple horizontally acquired genes is a hallmark of both vertebrate and invertebrate genomes. *Genome Biol.*, 16. <https://doi.org/10.1186/s13059-015-0607-3>.
- Csardi, G., & Nepusz, T. (2006). The igraph software package for complex network research. In *InterJournal complex systems* (p. 1695). <http://igraph.org>.
- Currie, T. E., Greenhill, S. J., & MacE, R. (2010). Is horizontal transmission really a problem for phylogenetic comparative methods? A simulation study using continuous cultural traits. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365, 3903–3912. <https://doi.org/10.1098/rstb.2010.0014>.
- Currie, T. E., Meade, A., Guillon, M., & Mace, R. (2013). Cultural phylogeography of the bantu languages of sub-saharan africa. *Proceedings of the Royal Society B*, 280, 20130695. <https://doi.org/10.1098/rspb.2013.0695>.
- Díaz-Báñez, J. M., Farigu, G., Francisco, G., Rappaport, D., & Toussaint, G. T. (2004). El Compás Flamenco: A phylogenetic analysis. In *Proceedings of BRIDGES: Mathematical connections in art, music and science* (pp. 61–70).
- Doolittle, W. F. (2009). The practice of classification and the theory of evolution, and what the demise of Charles Darwin's tree of life hypothesis means for both of them. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 364, 2221–2228. <https://doi.org/10.1098/rstb.2009.0032>.
- Duda, P., & Zrzavý, J. (2016). Human population history revealed by a supertree approach. *Scientific Reports*, 6, 29890. <https://doi.org/10.1038/srep29890>.
- Dunn, M. (2004). Language phylogenies. In , 7. *The Routledge handbook of historical linguistics* (pp. 190–211). <https://doi.org/10.4324/9781315794013.ch7>.
- Durham, W. (1992). Applications of evolutionary culture theory. *Annual Review of Anthropology*, 21, 331–355. <https://doi.org/10.1146/annurev.anthro.21.1.331>.
- Formilan, G., & Stark, D. (2020). Underground testing: Name-altering practices as probes in electronic music. *British Journal of Sociology*, 1–18. <https://doi.org/10.1111/1468-4446.12726>.
- Fraiberger, S. P., Sinatra, R., Resch, M., Riedl, C., & Barabási, A. L. (2018). Quantifying reputation and success in art. *Science*, 362, 825–829. <https://doi.org/10.1126/science.aau7224>.
- Gagen, J. (2019). *Hybrids and fragments: Music, genre, culture and technology*. Ph.D. thesis. Goldsmiths: University of London. <https://doi.org/10.25602/GOLD.00028228>.
- Gould, S. J. (1991). *Bully for brontosaurus*. New York: W. W. Norton.
- Gray, R. D., Bryant, D., & Greenhill, S. J. (2010). On the shape and fabric of human history. *Philosophical Transactions of the Royal Society B*, 365, 3923–3933. <https://doi.org/10.1098/rstb.2010.0162>.
- Gray, R. D., Drummond, A. J., & Greenhill, S. J. (2009). Language phylogenies reveal expansion pulses and pauses in Pacific settlement. *Science*, 323, 479–483. <https://doi.org/10.1126/science.1166858>.
- Greenhill, S. J., Currie, T. E., & Gray, R. D. (2009). Does horizontal transmission invalidate cultural phylogenies? *Proceedings of the Royal Society B: Biological Sciences*, 276, 2299–2306. <https://doi.org/10.1098/rspb.2008.1944>.
- Grün, B., & Hornik, K. (2011). topicmodels: An R package for fitting topic models. *Journal of Statistical Software*, 40, 1–30. <https://doi.org/10.18637/jss.v040.i13>.
- Gyles, C., & Boerlin, P. (2014). Horizontally transferred genetic elements and their role in pathogenesis of bacterial disease. *Veterinary Pathology*, 51, 328–340. <https://doi.org/10.1177/0300985813511131>.
- Heggarty, P., Maguire, W., & McMahon, A. (2010). Splits or waves? Trees or webs? How divergence measures and network analysis can unravel language histories. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365, 3829–3843. <https://doi.org/10.1098/rstb.2010.0099>.
- Hern, A. (2020). Spotify to let artists promote music for cut in royalty rates. <https://www.theguardian.com/technology/2020/nov/03/spotify-artists-promote-music-exchange-cut-royalty-rates-payola-algorithm>.
- Hesmondhalgh, D. (1998). The British dance music industry: A case study of independent cultural production. *The British Journal of Sociology*, 49, 234–251.
- Howe, C. J., & Windram, H. F. (2011). “Phylomemetics” evolutionary analysis beyond the gene. *PLoS Biology*, 9, Article e1001069. <https://doi.org/10.1371/journal.pbio.1001069>.
- Hutson, S. R. (2000). The rave: Spiritual healing in modern western subcultures. *Anthropological Quarterly*, 73, 35–49.
- Ishkur. (2000). <https://music.ishkur.com/>.
- Janosov, M., Musciotto, F., Battiston, F., & Iñiguez, G. (2020). Elites, communities and the limited benefits of mentorship in electronic music. *Scientific Reports*, 10, 3136. <https://doi.org/10.1038/s41598-020-60055-w>.
- Johnston, M. (2019). How “fans also like” works. <https://artists.spotify.com/blog/how-fans-also-like-works>.
- Jordan, P., & Shennan, S. (2003). Cultural transmission, language, and basketry traditions amongst the California Indians. *Journal of Anthropological Archaeology*, 22, 42–74. [https://doi.org/10.1016/S0278-4165\(03\)00004-7](https://doi.org/10.1016/S0278-4165(03)00004-7).
- Jost, L. (2006). Entropy and diversity. *Oikos*, 113, 363–375.
- Kauhanen, H., Gopal, D., Galla, T., & Bermúdez-Otero, R. (2021). Geospatial distributions reflect temperatures of linguistic features. *Science Advances*, 7. <https://doi.org/10.1126/sciadv.abe6540>.
- Kavanaugh, P. R., & Anderson, T. L. (2008). Solidarity and drug use in the electronic dance music scene. *Sociological Quarterly*, 49, 181–208. <https://doi.org/10.1111/j.1533-8525.2007.00111.x>.
- Klement, B., & Strambach, S. (2019). How do new music genres emerge? Diversification processes in symbolic knowledge bases. *Regional Studies*, 53, 1447–1458. <https://doi.org/10.1080/00343404.2019.1580817>.
- Klimek, P., Kreuzbauer, R., & Thurner, S. (2019). Fashion and art cycles are driven by counter-dominance signals of elite competition: Quantitative evidence from music styles. *Journal of the Royal Society Interface*, 16. <https://doi.org/10.1098/rsif.2018.0731>.
- Koch, B., Silvestro, D., & Foster, J. (2020). *The evolutionary dynamics of cultural change (as told through the birth and brutal, blackened death of metal music)*. SocArXiv. <https://doi.org/10.31235/osf.io/659bt>.
- Lambiotte, R., & Ausloos, M. (2005). Uncovering collective listening habits and music genres in bipartite networks. *Physical Review E - Statistical, Nonlinear, and Soft Matter Physics*, 72, 1–11. <https://doi.org/10.1103/PhysRevE.72.066107>.
- Lamichhaney, S., Han, F., Webster, M. T., Andersson, L., Grant, B. R., & Grant, P. R. (2018). Rapid hybrid speciation in Darwin's finches. *Science*, 359, 224–228. <https://doi.org/10.1126/science.aao4593>.
- Le Bomin, S., Lecointre, G., & Heyer, E. (2016). The evolution of musical diversity: The key role of vertical transmission. *PLoS One*, 11, 1–17. <https://doi.org/10.1371/journal.pone.0151570>.
- Lena, J. C. (2012). *Banding together: How communities create genres in popular music*. Princeton, NJ: Princeton University Press.
- Levinson, S. C., & Gray, R. D. (2012). Tools from evolutionary biology shed new light on the diversification of languages. *Trends in Cognitive Sciences*, 16, 167–173. <https://doi.org/10.1016/j.tics.2012.01.007>.
- Liebman, E., Ornoy, E., & Chor, B. (2012). A phylogenetic approach to music performance analysis. *Journal of New Music Research*, 41, 195–222. <https://doi.org/10.1080/09298215.2012.668194>.
- Liechti, J. L., & Bonhoeffer, S. A time resolved clustering method revealing longterm structures and their short-term internal dynamics. (2020). [arXiv:1912.04261](https://arxiv.org/abs/1912.04261).
- Lindop, R. (2011). Re-evaluating musical genre in UK psytrance. In G. St John (Ed.), *Taylor & Francis: Vol. 6. The local scenes and global culture of psytrance* (pp. 114–130). <https://doi.org/10.4324/9780203847879-14>.
- Mall, R., Langone, R., & Suijken, J. A. K. (2015). Netgram: Visualizing communities in evolving networks. *PLoS One*, 10, Article e0137502. <https://doi.org/10.1371/journal.pone.0137502>.
- Matsumae, H., Ranacher, P., Savage, P. E., Blasi, D. E., Currie, T. E., Koganebuchi, K., ... Bickel, B. (2021). In press. Exploring correlations in genetic and cultural variation across language families in Northeast Asia. *Science Advances*. <https://doi.org/10.1126/sciadv.abd9223>.

- Mauch, M., Maccallum, R. M., Levy, M., Leroi, A. M., & Mauch, M. (2015). The evolution of popular music: USA 1960–2010. *Royal Society Open Science*, 2. <https://doi.org/10.1098/rsos.150081>.
- McLeod, K. (2001). Genres, subgenres, sub-subgenres and more: Music and social differentiation within electronic/dance music communities. *Journal of Popular Music Studies*, 13, 59–75.
- Mesoudi, A. (2017). Pursuing Darwin's curious parallel: Prospects for a science of cultural evolution. *Proceedings of the National Academy of Sciences of the United States of America*, 114, 7853–7860. <https://doi.org/10.1073/pnas.1620741114>.
- Millstein, R. (2010). The concepts of population and metapopulation in evolutionary biology and ecology. In *Evolution since Darwin: The first 150 years* (pp. 61–68). Sunderland: Sinauer.
- Morrison, D. A. (2014a). Is the tree of life the best metaphor, model, or heuristic for phylogenetics? *Systematic Biology*, 63, 628–638. <https://doi.org/10.1093/sysbio/syu026>.
- Morrison, D. A. (2014b). Phylogenetic networks: A new form of multivariate data summary for data mining and exploratory data analysis. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, 4, 296–312. <https://doi.org/10.1002/widm.1130>.
- Noys, B. (1995). Into the 'Jungle'. *Popular Music*, 14, 321–332.
- Nunn, C. L., Arnold, C., Matthews, L., & Mulder, M. B. (2010). Simulating trait evolution for cross-cultural comparison. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365, 3807–3819. <https://doi.org/10.1098/rstb.2010.0009>.
- Nunn, C. L., Mulder, M. B., & Langley, S. (2006). Comparative methods for studying cultural trait evolution: A simulation study. *Cross-Cultural Research*, 40, 177–209. <https://doi.org/10.1177/1069397105283401>.
- O'Brien, M. J., Collard, M., Buchanan, B., & Boulanger, M. T. (2013). Trees, thickets, or something in between? Recent theoretical and empirical work in cultural phylogeny. *Israel Journal of Ecology and Evolution*, 59, 45–61. <https://doi.org/10.1080/15659801.2013.825431>.
- O'Dair, M., & Fry, A. (2020). Beyond the black box in music streaming: The impact of recommendation systems upon artists. *Popular Communication*, 18, 65–77. <https://doi.org/10.1080/15405702.2019.1627548>.
- Pagel, M., Atkinson, Q. D., & Meade, A. (2007). Frequency of word-use predicts rates of lexical evolution throughout Indo-European history. *Nature*, 449, 717–720. <https://doi.org/10.1038/nature06176>.
- Pamjav, H., Juhász, Z., Zalán, A., Németh, E., & Damdin, B. (2012). A comparative phylogenetic study of genetics and folk music. *Molecular Genetics and Genomics*, 287, 337–349. <https://doi.org/10.1007/s00438-012-0683-y>.
- Pandey, B. (2019). *Bollywood synth pioneer bappi lahiri's 303 experiments*. Red Bull. <http://www.redbull.com/in-en/tb-303-synthesizer-bollywood-bappi-lahiri>.
- Percino, G., Klimek, P., & Thurner, S. (2014). Instrumental complexity of music genres and why simplicity sells. *PLoS One*, 9, 1–16. <https://doi.org/10.1371/journal.pone.0115255>.
- Premo, L. S., & Hublin, J. J. (2009). Culture, population structure, and low genetic diversity in Pleistocene hominins. *Proceedings of the National Academy of Sciences of the United States of America*, 106, 33–37. <https://doi.org/10.1073/pnas.0809194105>.
- Purgas, P., & Morgan, F. (2020). *Electronic India 1969–73 revisited*. The Wire. <https://www.thewire.co.uk/in-writing/interviews/electronic-india-moog-interview-pa-ul-purgas>.
- Reynolds, S. (2012). *Energy flash: A journey through rave music and dance culture*. New York, NY: Soft Skull Press.
- Rivero, D. G. (2016). Darwinian archaeology and cultural phylogenetics. In L. Mendoza Straffon (Ed.), *Cultural phylogenetics: Concepts and applications in archaeology* (pp. 43–72). Springer. [https://doi.org/10.1007/978-3-319-25928-4\\_3](https://doi.org/10.1007/978-3-319-25928-4_3).
- Rossetti, G., Pappalardo, L., Pedreschi, D., & Giannotti, F. (2017). Tiles: An online algorithm for community discovery in dynamic social networks. *Machine Learning*, 106, 1213–1241. <https://doi.org/10.1007/s10994-016-5582-8>.
- Rosvall, M., & Bergstrom, C. T. (2010). Mapping change in large networks. *PLoS One*, 5, 1–7. <https://doi.org/10.1371/journal.pone.0008694>.
- Savage, P. E. (2019). *Cultural evolution of music*. 5. Palgrave Communications. <https://doi.org/10.1057/s41599-019-0221-1f5z3>.
- Savage, P. E., Chiba, G., Currie, T. E., Suzuki, H., & Atkinson, Q. D. (2020). *Sequence alignment of folk song melodies reveals cross-cultural mechanisms of musical evolution*. PsyArXiv preprint. <https://doi.org/10.31234/osf.io/5rj6y>.
- Savage, P. E., Loui, P., Tarr, B., Schachner, A., Glowacki, L., Mithen, S., & Fitch, T. (2020). Music as a coevolved system for social bonding. *Behavioral and Brain Sciences*. <https://doi.org/10.1017/S0140525X20000333>.
- Schillinger, K., & Lycett, S. (2019). The flow of culture: Assessing the role of rivers in the inter-community transmission of material traditions in the upper Amazon. *Journal of Archaeological Method and Theory*, 26, 135–154. <https://doi.org/10.1007/s10816-018-9369-z>.
- Schillinger, K., Mesoudi, A., & Lycett, S. J. (2016). Copying error, evolution, and phylogenetic signal in artifactual traditions: An experimental approach using "model artifacts". *Journal of Archaeological Science*, 70, 23–34. <https://doi.org/10.1016/j.jas.2016.04.013>.
- Serrà, J., Corral, Á., Boguñá, M., Haro, M., & Arcos, J. L. (2012). Measuring the evolution of contemporary western popular music. *Scientific Reports*, 2. <https://doi.org/10.1038/srep00521>.
- Sicko, D. (2010). *Techno rebels: The renegades of electronic funk* (2nd ed.). Detroit, Michigan: Wayne State University Press.
- Simon, H. A. (1962). The architecture of complexity. *Proceedings of the American Philosophical Society*, 106, 467–482.
- Spencer, M., Davidson, E. A., Barbrook, A. C., & Howe, C. J. (2004). Phylogenetics of artificial manuscripts. *Journal of Theoretical Biology*, 227, 503–511. <https://doi.org/10.1016/j.jtbi.2003.11.022>.
- St John, G. (2006). Electronic dance music culture and religion: An overview. *Culture and Religion*, 7, 1–25. <https://doi.org/10.1080/01438300600625259>.
- Tehrani, J., & Collard, M. (2002). Investigating cultural evolution through biological phylogenetic analyses of Turkmen textiles. *Journal of Anthropological Archaeology*, 21, 443–463. [https://doi.org/10.1016/S0278-4165\(02\)00002-8](https://doi.org/10.1016/S0278-4165(02)00002-8).
- Tehrani, J. J. (2013). The phylogeny of little red riding hood. *PLoS One*, 8. <https://doi.org/10.1371/journal.pone.0078871>.
- Tehrani, J. J., Collard, M., & Shennan, S. J. (2010). The cophylogeny of populations and cultures: Reconstructing the evolution of Iranian tribal craft traditions using trees and jungles. *Philosophical Transactions of the Royal Society B*, 365, 3865–3874. <https://doi.org/10.1098/rstb.2010.0020>.
- Tehrani, J. J., & D'Huy, J. (2017). Phylogenetics meets folklore: Bioinformatics approaches to the study of international folktales. In *Math meets myths: Quantitative approaches to ancient narratives* (pp. 91–114). [https://doi.org/10.1007/978-3-319-39445-9\\_6](https://doi.org/10.1007/978-3-319-39445-9_6).
- Tëmkin, I. (2016). Homology and phylogenetic inference in biological and material cultural evolution. In F. Panebianco, & E. Serrelli (Eds.), *Understanding cultural traits: A multidisciplinary perspective on cultural diversity* (pp. 287–313). <https://doi.org/10.1007/978-3-319-24349-8>.
- Tëmkin, I., & Eldredge, N. (2007). Phylogenetics and material cultural evolution. *Current Anthropology*, 48, 146–153. <https://doi.org/10.1086/510463>.
- Thornton, S. (1995). *Club cultures: Music, media and subcultural capital*. Cambridge: Polity Press.
- Tinits, P., & Sobchuk, O. (2020). Open-ended cumulative cultural evolution of Hollywood film crews. *Evolutionary Human Sciences*, 2, Article e26. <https://doi.org/10.1017/ehs.2020.21>.
- Toussaint, G. (2003). Classification and phylogenetic analysis of African ternary rhythm timelines. In *Proceedings of BRIDGES: Mathematical connections in art, music and science* (pp. 1–18).
- Velasco, J. D. (2013). Phylogeny as population history. *Philosophy and Theory in Biology*, 5, Article e402. <https://doi.org/10.3998/ptb.6959004.0005.002>.
- van Venrooij, A. (2015). A community ecology of genres: Explaining the emergence of new genres in the UK field of electronic/dance music, 1985–1999. *Poetics*, 52, 104–123. <https://doi.org/10.1016/j.poetic.2015.06.005>.
- Werner, A. (2020). Organizing music, organizing gender: Algorithmic culture and Spotify recommendations. *Popular Communication*, 18, 78–90. <https://doi.org/10.1080/15405702.2020.1715980>.
- Windram, H. F., Charlston, T., & Howe, C. J. (2014). A phylogenetic analysis of Orlando Gibbons's prelude in G. *Early Music*, 42, 515–528. <https://doi.org/10.1093/em/cau100>.
- Wu, Y., Pitipornvivat, N., Zhao, J., Yang, S., Huang, G., & Qu, H. (2016). egoslider: Visual analysis of egocentric network evolution. *IEEE Transactions on Visualization and Computer Graphics*, 22, 260–269.
- Yang, Z., Algesheimer, R., & Tessone, C. J. (2016). A comparative analysis of community detection algorithms on artificial networks. *Scientific Reports*, 6, 30750. <https://doi.org/10.1038/srep30750>.
- Youngblood, M. (2019a). Conformity bias in the cultural transmission of music sampling traditions. *Royal Society Open Science*, 6, 191149. <https://doi.org/10.1098/rsos.191149>.
- Youngblood, M. (2019b). Cultural transmission modes of music sampling traditions remain stable despite delocalization in the digital age. *PLoS One*, 14, 1–12. <https://doi.org/10.1371/journal.pone.0211860>.
- Youngblood, M., & Lahti, D. (2018). A bibliometric analysis of the interdisciplinary field of cultural evolution. *Palgrave Communications*, 4. <https://doi.org/10.1057/s41599-018-0175-8>.