

Measuring the cultural evolution of music: With case studies of British-American and Japanese folk, art, and popular music

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Darwin's theory of evolution provided striking explanatory power that has come to unify biology and has been successfully extended to various social sciences. In this dissertation, I demonstrate how cultural evolutionary theory may also hold promise for explaining diverse musical phenomena, using a series of quantitative case studies from a variety of cultures and genres to demonstrate general laws governing musical change.

Chapter one describes previous research and debates regarding music and cultural evolution. Drawing on major advances in the scientific understanding of cultural evolution over the past three decades, I clarify persistent misconceptions about the roles of genes and progress in definitions of evolution, showing that neither is required or assumed. I go on to review older and recent literature relevant to musical evolution at a variety of levels, from Lomax's macroevolutionary interpretation of global patterns of song-style to microevolutionary mechanisms by which minute melodic variations give rise to large tune families. To highlight the complex dynamics of musical evolution in action, I provide an autoethnographic case study of my own performance of folk songs in Japan. After addressing criticisms of the roles of individual agency and reductionism in studying musical evolution, I highlight ways in which cultural evolutionary theory can contribute to applied ethnomusicology in the domains of education, copyright, and sustainability.

Chapter two introduces a new method for quantifying aspects of musical evolution. This method builds off of the tune family concept, but adds quantitative rigour by adapting tools from molecular genetics. In particular, I highlight analogies between protein evolution and melodic evolution. The former can be modeled as sequences constructed from an "alphabet" of 20 amino acids, while the latter can be modeled as

sequences constructed from an "alphabet" of 12 notes, corresponding to the equal-tempered chromatic scale. This makes it possible to adapt sequence alignment methods from molecular genetics to quantify the evolution of any music - Western or non-Western - that can be approximated by standard staff notation, and to make automated comparisons on scales far beyond the capabilities of unassisted humans. I use examples of melodic evolution (*Scarborough Fair*) and protein evolution (avian influenza) to demonstrate analogies in the process of coding and analyzing their evolution.

Chapter three tests hypotheses about general trends in musical evolution against a large sample of 4,125 British-American "Child ballads" notated between 1575-1972. Using the sequence alignment methods developed in Chapter two, I automatically identified and analysed 172 pairs of highly related (>85% identity) melodic variants encompassing a total of 15,786 notes. Mutation rates varied greatly (over 100-fold) in ways that followed general predictions of cultural evolutionary theory: 1) written notation evolves more slowly than oral transmission, 2) functional notes are more resistant to change than ornamental notes, and 3) substitutions are more likely to occur between small melodic distances than large ones. In addition, insertions and deletions greatly outnumbered substitutions, but there was no clear trend toward complexity (i.e., insertion) or simplification (i.e., deletion). I hypothesize that these trends are governed primarily by universal cognitive constraints, and thus are likely to characterize musical evolution cross-culturally.

Chapter four extends the method developed in Chapter two to explore the generality of the trends identified in Chapter three using a diverse set of case studies in which the history of musical evolution has already been qualitatively documented: 1) the divergence of the Scottish 17th c. *Lady Cassiles Lilt* into nearly unrecognizable 20th c. American descendants, 2) the merging of work songs from distant prefectures into the Japanese folk song *Esashi Oiwake*, 3) the simultaneous performance of vestigial, inaudible 1,000-year-old Chinese melodies and their radically changed descendants in the Japanese *gagaku* piece *Seigaiha*, and 4) the legal cases finding George Harrison's *My Sweet Lord* (1970) and Robin Thicke and Pharrell Williams' *Blurred Lines* (2013)

liable for plagiarism. Although the precise mechanisms differ and absolute rates of evolution vary almost 400-fold within and between these case studies, the general trends supported my predictions from Chapter three regarding: 1) the relative ease of mutations to nearby pitches, 2) the relative predominance of insertions/deletions over substitutions, 3) the relative stability of functional notes (e.g., stressed vs. unstressed), and 4) the relative stability of written over oral traditions. Both increases and decreases in complexity were observed, with no clear trend favouring one or the other.

This dissertation demonstrates that musical evolution can be rigorously measured by adapting theoretical and methodological tools from cultural evolution and molecular genetics, and applies this to show that musical evolution follows some general rules analogous to ones governing genes and non-musical domains of culture. Although cultural evolutionary theory and methods alone will not solve all the problems facing musicologists interested in the phenomenon of musical change, they do offer a new unified set of tools that help answer at least some longstanding questions of broad general concern.

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0. Preface

0-1. Background to this dissertation

The goal of this dissertation is to develop and test new quantitative methods to determine whether there are any general laws governing the cultural evolution of music. The topic of music and evolution has been a central theme of my research since I began at graduate school. My first thesis was entitled "Musical evolution and human migration" (Savage 2011), and the term "evolution" figures prominently in most of my published research.

In some cases, my research has focused more on the biological evolution of the capacity for making music, rather than the cultural evolution of music itself. Biological evolution has been the focus of my work on musical universals (Savage, Brown, et al. 2015; Savage in press) and on cross-species comparisons between human and bird songs (Savage, Tierney, and Patel 2017).

The majority of my previous research, however, focused on the cultural evolution of music - in other words, on trying to understand how and why the similarities and differences among different musics arose. Most of this work was inspired by Alan Lomax's Cantometrics Project (Lomax 1968; Savage in prep.), and tried to emulate its focus on large-scale cross-cultural comparison of song style that could be performed on audio recordings. A major goal of this work was to compare cross-cultural patterns of musical diversity with patterns of linguistic and genetic diversity to see if musical evolution could add to our understanding of human evolutionary history more generally (Savage 2011, 2014; Savage et al. 2012; Savage and Brown 2013, 2014a, 2014b; Savage and Atkinson 2015; Savage, Matsumae, et al. 2015; Brown, Savage, et al. 2014; Rzeszutek, Savage, and Brown 2012; Ellis et al. 2016; Leroi et al. 2015; Takezawa et al. 2014).

There were several major limitations of the Cantometric approach, however. One limitation was the difficulty in distinguishing between stylistic similarities that were due to descent from a common ancestor and those that were due to chance or developed independently ("convergent evolution"). More fundamentally, evolution is defined as "the process by which the frequencies of variants in a population change *over time*" (Danchin et al. 2011: 483, emphasis added). Thus, a complete understanding of musical evolution requires an ability to identify musical variants that are historically related and document the accumulation of differences over time. This is very difficult when attempting cross-cultural stylistic comparison using the shallow historical record provided since the advent of audio recording late in the 19th century.

Instead, for this dissertation, I have chosen to take a different approach to the cultural evolution of music, one inspired by the "tune family" research developed by Cecil Sharp (1907, 1932), Bertrand Bronson (1959-72, 1969, 1976), Samuel Bayard (1950, 1954), and others (Bartók 1931; Wiora 1953; 町田と竹内 1965). Instead of focusing on cross-cultural comparison of audio recordings, this approach focuses on comparison of melodic variants descended from a common ancestral melody or melodies, with the goal of understanding whether there are any general laws that govern the process of musical evolution. I will attempt to show that this approach holds promise for a cross-cultural understanding of the phenomenon of musical change.

0-2. Chapter structure and publication plans

My work on this dissertation has led to me publishing several articles, with several more that I intend to eventually submit for publication. In addition to helpful feedback from my PhD committee, I have also discussed the ideas here and published some of this work in collaboration with Steven Brown, Quentin Atkinson, and Thomas Currie. However, all content (including both written and statistical analysis) in this dissertation is entirely my own.

Chapter 1 explains general theoretical ideas about the cultural evolution of music. The theoretical framework builds off and expands on one that I published with Steven Brown (Savage and Brown 2013). I then go on to show how this theory can synthesize a variety of musicological research ranging from early comparative musicology, Cantometrics, tune family research, and applied musicology. I use an autoethnographic case study from my own experience performing Japanese folk song to address criticisms involving agency and reductionism. I submitted a revised (single-authored) version of this chapter to *Ethnomusicology*.

I wanted to develop a method for studying musical evolution that would be useful to study general patterns of musical evolution across many different types of music from many different cultures. I published such a technique in collaboration with Quentin Atkinson, focusing on the problem of identifying tune families (Savage and Atkinson 2015). I have explained and expanded the logic of this approach in Chapter 2, focusing not on tune family identification but on the main topic of this dissertation: measuring musical evolution.

The most comprehensive source of highly related melodic variants spanning large amounts of time and space is Bronson's (1959-72) compilation of 4,125 melodic variants of the British-American "Child ballads". One of the goals of this dissertation was to perform an in-depth analysis of musical evolution in Bronson's collection of Child ballads, which appears in Chapter 3. I plan to submit a revised version of this chapter to *Nature*, co-authored with Thomas Currie and Quentin Atkinson.

Finally, in Chapter 4, I try to test the efficacy of the method developed in Chapter 2 and the generality of the predictions from Chapter 3 on a diverse set of case studies including British-American and Japanese folk songs, Japanese *gagaku* and 20th century popular music. Overall, I find that although each case has its own unique historical factors that determine the precise mechanisms and rates of evolution, the methods and principles I outline in this dissertation help to explain a number of general trends in

musical evolution.

All supplementary data, including coded and aligned sequences and metadata for all 4,125 Child ballad melodic variants analyzed in Chapter 3 and the code I used for automatic analysis (R V3.2.3; R Core Team 2015), are available at the following link:

https://www.dropbox.com/s/9kj2q21bx5zzfnj/Savage_PhD_SI_Data.zip?dl=0

1. Cultural evolution of music

The concept of evolution played a central role during the formation of academic musicology in the late 19th century (Adler 1885/1981; Rehding 2000). During the 20th century, theoretical and political implications of evolution were heavily debated, leading evolution to go out of favour in musicology and cultural anthropology (Carneiro 2003). In the 21st century, refined concepts of biological evolution were reintroduced to musicology through the work of psychologists such as Steven Brown (Wallin, Merker, and Brown 2000; Savage and Brown 2013) and Aniruddh Patel (2008) to the extent that the biological evolution of the capacity to make and experience music ("evolution of musicality") has returned as an important topic of contemporary musicological research (Huron 2006; Lawson 2012; Tomlinson 2013; Honing et al. 2015). Yet the concept of cultural evolution of music itself ("musical evolution") remains largely taboo among musicologists, despite an explosion of recent research on cultural evolution in related fields such as linguistics. This taboo has been especially prominent in ethnomusicology, but is also observable in historical musicology and other subfields of musicology¹.

One major exception to this taboo was the two-volume special edition of *The World of Music* devoted to critical analysis of Victor Grauer's essay entitled "Echoes of Our Forgotten Ancestors" (Stock 2006b; Grauer 2006; Grauer later expanded this into book form in Grauer 2011). Grauer proposed that the evolution and global dispersal of human song-style parallels the evolution and dispersal of anatomically modern humans out of Africa, and that contemporary African hunter-gatherers retain the ancestral

¹ For reasons of space and expertise, I will focus here primarily on the ethnomusicological literature, but the concept of cultural evolution of music should also be applicable to other sub-fields, not least the evolution of contemporary Western classical music from medieval Gregorian chant over the course of the second millennium AD.

singing style shared by all humans tens of thousands of years ago. The two evolutionary biologists contributing to this publication found the concept of musical evolution self-evident enough that they simply opened their contribution by stating: "Songs, like genes and languages, evolve" (Leroi and Swire 2006: 43). However, the musicologists displayed much confusion and concern over the concept of cultural evolution.

My goal in this chapter is to clarify some of these issues in terms of the definitions, assumptions, and implications involved in studying the cultural evolution of music to show how cultural evolutionary theory can benefit musicology in a variety of ways.

1-1. Does music "evolve"?

One of the most basic misconceptions about evolution is the idea that it only applies to genes. Rahaim's response to Grauer implies this, arguing that musical evolution is merely a "metaphor" that is "certainly not the same kind of process that evolutionary biologists now talk about" (Rahaim 2006: 29, 32). Kartomi (2001: 306) states this more explicitly when she rejects the application of evolutionary theory in classifying musical instruments because "the concepts of evolution and lineage are not applicable to anything but animate beings, which are able to inherit genes from their forebears"².

While it is true that the discovery of genes and the precise molecular mechanisms by which they change revolutionized evolutionary biology, Darwin formulated his theory of evolution without the concept of genes. In fact, Darwin's ideas were strongly influenced by pre-existing ideas developed by linguists such as Sir William Jones (Darwin 1859/2009; van Wyhe 2005; Atkinson and Gray 2005), and Darwin (1871:

² Kartomi has since changed her views, writing "I now think that music has evolved in a measurable way, as long as 'evolved' is not defined as 'improved'" (personal communication, June 10th 2016 email).

89-90) noted that language and species evolution were "curiously parallel...the survival or preservation of certain favoured words in the struggle for existence is natural selection". Scholars of cultural evolution have tabulated a number of such curious parallels, to which I have added musical examples (Table 1.1).

Instead of genes, Darwin's theory of evolution by natural selection contained three key requirements: 1) there must be *variation* among individuals; 2) variation must be *inherited* via intergenerational transmission; 3) certain variants must be more likely to be inherited than others due to competitive *selection* (Darwin 1859/2009; Lewontin 1970). These principles apply equally to biological and cultural evolution (Mesoudi 2011). Indeed, the official definition of folk music adopted by the International Folk Music Council (the ancestor of today's International Council for Traditional Music³) explicitly invoked evolution and these three key mechanisms (albeit using "continuity" instead of "inheritance"):

*Folk music is the product of a musical tradition that has been **evolved** through the process of oral transmission. The factors that shape the tradition are: (i) **continuity** which links the present with the past; (ii) **variation** which springs from the creative impulse of the individual or the group; and (iii) **selection** by the community, which determines the form or forms in which the music survives.* (International Folk Music Council 1955: 23, emphasis added)

³ Lineages of organizations, composers, performers, etc. are a potentially productive area of studying musical evolution, but I will not discuss them in detail here due to limitations of space and expertise.

Table 1.1. A simplified comparison of biological, linguistic, and musical evolution⁴

Biological evolution	Linguistic evolution	Musical evolution
Discrete heritable units (e.g., amino acids, genes)	Discrete heritable units (e.g., phonemes, words)	Discrete heritable units (e.g., notes, phrases)
DNA copying	Teaching, learning and imitation	Teaching, learning and imitation
Mutation	Mistakes, sound changes	Mistakes, embellishment, composition
Homology	Lexical cognates, language families	Melodic cognates, tune families
Natural selection	Social selection and trends	Selection by audience, performers, judges, consumers, etc.
Hybridization (e.g., horse with zebra)	Creoles (e.g., Surinamese)	Syncretic music (e.g., Afro-Caribbean)
Fossils	Ancient texts	Ancient notation, audio/video recordings
Extinction	Language death	Repertoire loss

⁴ Biological evolution and linguistic evolution columns are adapted from Atkinson and Gray (2005: 514) and Pagel (2016: 2).

Evolution did often come to be defined in purely genetic terms during the 20th century, but recent advances in our understanding of cultural evolution, epigenetics, and ecology have led to a new inclusive definition of evolution as:

'the process by which the frequencies of variants in a population change over time', where the word 'variants' replaces the word 'genes' in order to include any inherited information....In particular, this...should include cultural inheritance. (Danchin et al. 2011: 483-484)

The theoretical and empirical work of cultural evolutionary scholars has been crucial in demonstrating that evolution occurs "Not By Genes Alone" (Richerson and Boyd 2005; Dawkins 1976; Cavalli-Sforza and Feldman 1981; Boyd and Richerson 1985; Mesoudi, Whiten, and Laland 2006; Mesoudi 2011; Howe and Windram 2011; Whiten et al. 2012; Fuentes and Wiessner 2016). Scholars have recently applied cutting-edge tools from evolutionary biology to help understand complex cultural evolutionary processes in a variety of domains including languages, fairy tales, canoes, textiles, religion, kinship, and political complexity (Gray, Drummond, and Greenhill 2009; Bouckaert et al. 2012; Graça da Silva and Tehrani 2016; Rogers and Ehrlich 2008; Tehrani, Collard, and Shennan 2010; Watts et al. 2016; Opie et al. 2014; Currie et al. 2010). The field has now blossomed to the extent that researchers recently created a dedicated academic society: the Cultural Evolution Society (Brewer et al. 2017).

The evolution of basic vocabulary has proven to be particularly amenable to evolutionary analysis. For example, applying phylogenetic methods from evolutionary biology to standardized lists of 200 of the most universal and most slowly changing words (e.g., numbers, body parts, kinship terminology) from hundreds of existing and ancient languages has allowed researchers to reconstruct the timing, geography, and specific mechanisms of change by which the descendants of proto-languages such as Proto-Indo-European or Proto-Austronesian evolved to become languages such as English, Hindi, Indonesian and Maori that are spoken today (Atkinson and Gray 2005;

Levinson and Gray 2012). These evolutionary relationships can be represented (with some caveats) as phylogenetic trees or networks, which can in turn be useful for exploring more complicated evolutionary questions, such as regarding the existence of cross-cultural universals (including universal aspects of music (including universal aspects of music [Savage, Brown, et al. 2015] and language [Dunn et al. 2011]) or gene-culture coevolution (e.g., the coevolution of lactose tolerance and dairy farming [Mace and Holden 2005]).

Steven Brown and I have previously outlined some of this cultural evolutionary theory as part of one of five major themes in a "new comparative musicology" (Savage and Brown 2013, 2014b), including the relationships between cultural evolution and our other four themes (classification, human history, universals, and biological evolution). Here I want to focus more specifically on cultural evolution and its relevance to disparate existing research in musicology (ignoring for now the fascinating and productive areas of biological evolution and gene-culture evolution of musicality [Honing et al. 2015]).

1-2. Progressive evolution and early comparative musicology

The other major misconception about evolution is that it assumes directional progress. Thus, Nettl's response to Grauer invokes the "the dictionary definition of the word - 'a series of related changes in a certain direction'" (Nettl 2006: 62), while Mundy's response more explicitly criticizes that "the conception of progress inherent in evolution creates its own hierarchies" (Mundy 2006: 22). However, there is nothing about progress or direction contained in Danchin et al.'s scholarly definition quoted above: evolution simply refers to changes in the frequencies of heritable variants. These changes can be in the direction of simple to complex - and it is possible that there may be a general trend towards complexity (McShea and Brandon 2010; Currie and Mace 2011) - but the reverse is also possible, as are non-directional changes with little or no functional consequences (Nei, Suzuki, and Nozawa 2010).

Part of the problem is that the evolution *has* been associated with notions of progress, most notoriously through the unfortunately named Social Darwinism of the 19th and 20th century. This movement sought to justify the oppression of the weak by the powerful as survival of the fittest (Hofstadter 1955; Laland and Brown 2011). It is no accident that Zallinger's famous March of Progress drawing showed a gradual lightening of the skin from dark-skinned, ape-like ancestors to light-skinned humans: evolution was used to justify scientific racism by eugenicists (Gould 1989). Although both the lightening of skin and the linear progression from ape to man are inaccurate (Gould 1989), this image unfortunately remains extremely enduring and is commonly adapted to represent all kinds of evolution, including musical evolution (Fig. 1.1).

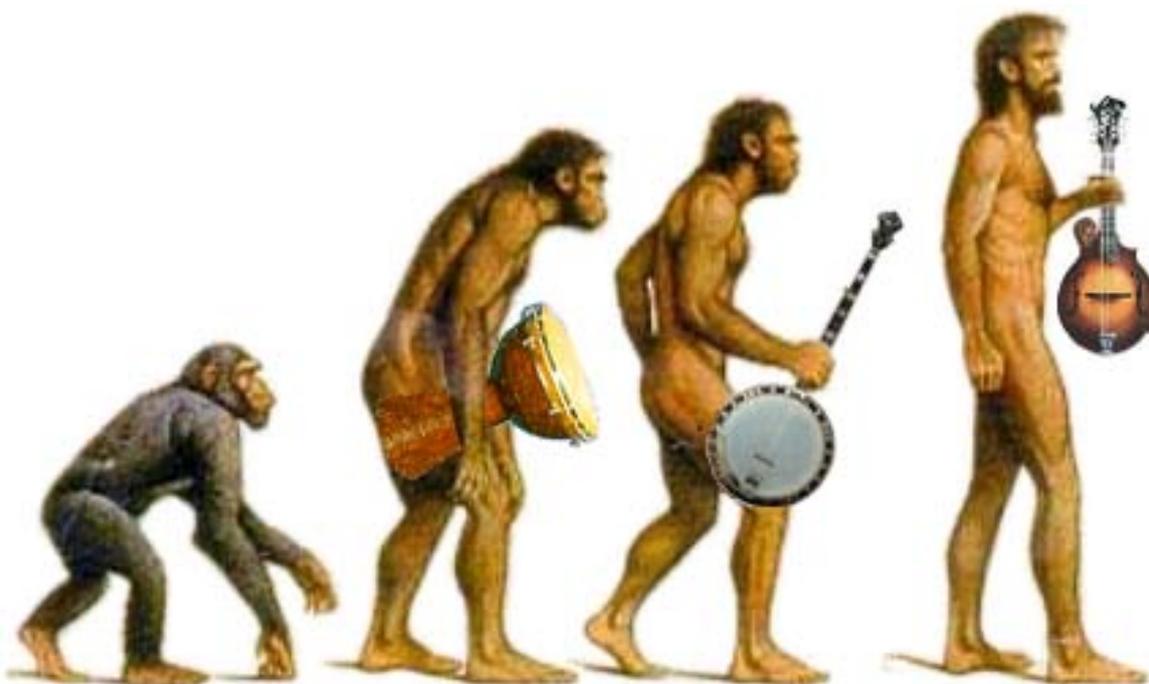


Figure 1.1. An example of an inaccurate but widespread representation of evolution as a linear march of progress⁵

⁵ Source: <http://www.mandolincafe.com/archives/spoof.html> (retrieved March 22, 2016)

In fact, Social Darwinism was not very reflective of Darwin's ideas, but rather the ideas of Herbert Spencer (1875), who coined the term "survival of the fittest". While Darwin's own feelings about the way his ideas were adopted are debated, today's scholars of cultural evolution unequivocally reject such political misappropriation of evolutionary theory (Laland and Brown 2011; Mesoudi 2011; Richerson and Boyd 2005). Instead, they focus not on the notion of progress but on the notion of phylogenesis (phylo=family, genesis=origin), as represented visually by the trees that constituted the only diagram in Darwin's (1859/2009) *Origin of Species* (Fig 1.2).

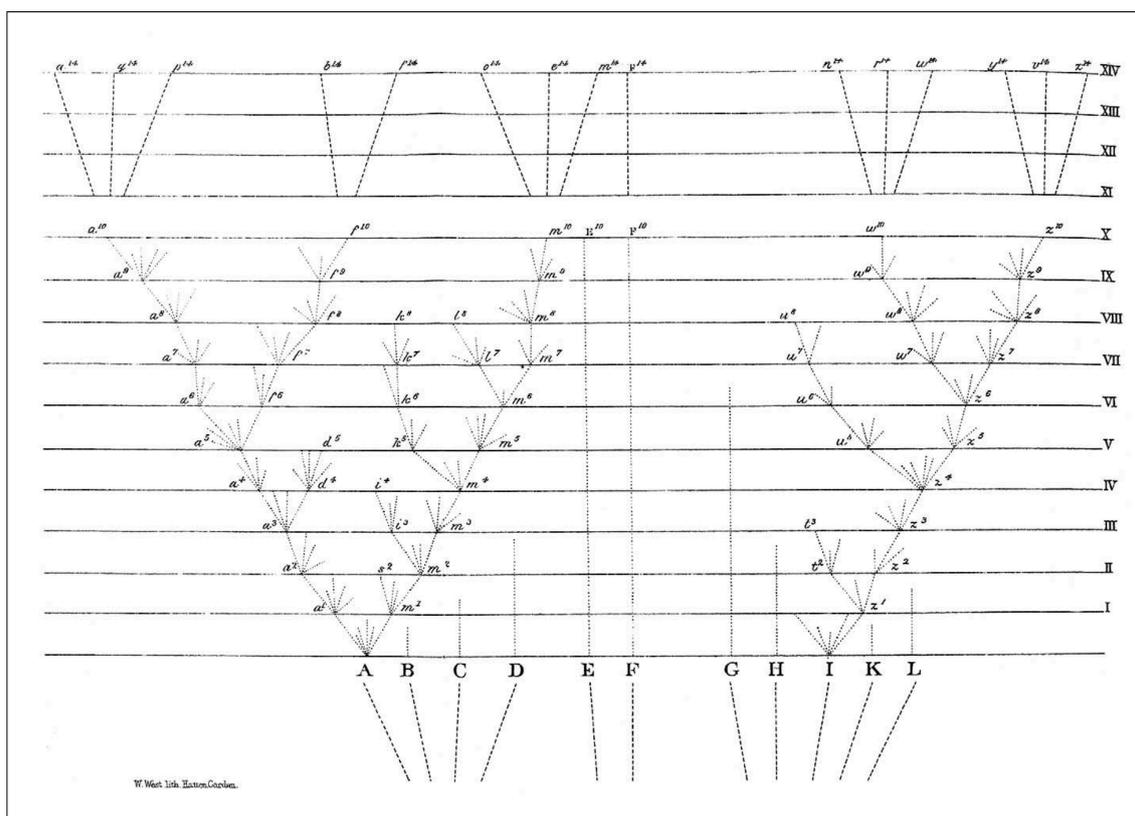


Figure 1.2. The sole figure from Darwin's (1859/2009: 91) *The Origin of Species* used phylogenetic trees to represent evolution as a process of branching diversification, not linear progress⁶

⁶ Capital letters represent ancestors, lower case letters represent their descendants at later time periods, which are in turn represented by roman numerals.

The roots of the phylogenetic trees represent common ancestors, with branches representing diversification into different lineages or species. Some lineages become extinct (due to natural selection or other mechanisms including random drift), while others continue to the present. Similar logic applies to the origin of contemporary biological species like chimpanzees and humans from their common ancestor (the relative ape-like-ness of which is debated; Sayers, Raghanti, and Lovejoy 2012) or the origin of contemporary languages like Spanish and Italian from their common ancestor of Latin (Campbell 2013). The tree metaphor is intentionally simplified: the degree to which both biological and cultural evolution can be modeled as a neatly branching tree with a single root versus interlocking networks with many overlapping roots continues to be debated (W. F. Doolittle 1999; Gray, Bryant, and Greenhill 2010; Le Bomin, Lecointre, and Heyer 2016; Tëmkin and Eldredge 2007; Collard, Shennan, and Tehrani 2006).

Unfortunately, early comparative musicologists relied on Spencer's notion of progressive evolution rather than Darwin's of phylogenetic diversification (Rehding 2000; Toner 2007)⁷. Two assumptions were fundamental to much of the work of the founding figures of comparative musicology:

1. *Cultures evolved from simple to complex, and as they do so they move from primitive to civilized.*
 2. *Music evolves from simple to complex within societies as they progress.*
- (Stone 2008: 25)

For example, in *The Origins of Music*, Carl Stumpf wrote of "the most primitive songs, e.g. those of the Vedda of Ceylon.... One may label them as mere preliminary stages or even as the origins of music." (Stumpf 1911/2012: 49). As late as 1943, Curt Sachs wrote of "the plain truth that the singsong of Pygmies and Pygmoids stands infinitely

⁷ Of the musicologists responding to Grauer's essay, only Rahaim (2006: 29) carefully distinguished between these two, using the terms "progressive" and "situated" evolution, respectively.

closer to the beginnings of music than Beethoven's symphonies and Schubert's lieder...the only working hypothesis admissible is that the earliest music must be found among the most primitive peoples" (Sachs 1943: 20-21).

Ideas of progressive evolution went into disrepute in the second half of the twentieth century, particularly after the full extent of the eugenics horrors perpetrated in their name became known after World War II (Carneiro 2003). But while fields like biology worked to improve the theoretical and empirical foundations of evolution through a better understanding of its molecular mechanisms, musicology (along with much of cultural anthropology) simply threw out the baby with the bathwater.

1-3. Macroevolution and Cantometrics

One striking exception to the general tendency to avoid theories of musical evolution in the second half of the twentieth century was Alan Lomax's Cantometrics Project (Lomax 1968, 1980, 1989; Lomax and Berkowitz 1972). Although mostly (in)famous for its highly contested claims for a causal relationship between song style and social structure (cf. Erickson 1976), an often-overlooked aspect was Lomax's evolutionary interpretation of the global distribution of song style itself.

Through standardized classification and statistical analysis of 36 stylistic features from ~1,800 traditional songs from 148 cultural groups (Lomax 1980)⁸, Lomax classified the world's musical diversity into 10 regional styles and organized them into a crude phylogenetic tree:

This tree of performance style appears to have two roots: (1) in Siberia and (2) among African Gatherers. The Siberian root has two branches: one into the Circum-Pacific and Nuclear America, thence into Oceania through

⁸ Discrepancies in published numbers and further details are explained in a forthcoming article (Savage in prep).

Melanesia and into East Africa, the second branch to Central Asia and thence into Europe and Asian High Culture...the main facts of style evolution may be accounted for by the elaboration of two contrastive traditions.... As their cultural base became more complex, these two root traditions became more specialized: the Siberian producing the virtuosic solo, highly articulated, elaborated, and alienated style of Eurasian high culture, the Early Agriculture tradition developing more and more cohesive and complexly integrated choruses and orchestras. West Europe and Oceania, flowering late on the borders of these two ancient specializations, show kinship to both. (Lomax 1980: 39-40)

Although this tree retains some aspects of progressivism (e.g., contemporary African gatherers occupying the "roots" while other traditions "became more complex", West Europe "flowering late"), it also shows more sophisticated concepts such as the possibility of multiple ancestors (polygenesis) and of borrowing/merging between lineages (horizontal transmission). With some modifications, it can be converted into a phylogenetic model as a working hypothesis for future testing/refinement (Fig. 1.3).

Cantometrics provided the major point of departure both for Grauer's essay (Grauer was heavily involved in the Cantometrics Project as both the co-inventor of the Cantometric classification scheme and primary coder of the Cantometric data) and for a series of recent scientific studies exploring parallels in musical and genetic evolution. Some of these studies have directly compared patterns of musical and genetic diversity among populations of certain regions (e.g., Sub-Saharan Africa [Callaway 2007], Eurasia [Pamjav et al. 2012], Taiwan [Brown et al. 2014], Northeast Asia [Savage, Matsumae, et al. 2015]), while others have analyzed musical change using theories and methods from evolutionary biology (e.g., tracing the rise and fall of Western popular [Bentley et al. 2007; Serrà et al. 2012; Mauch et al. 2015] and classical [Zivic, Shifres, and Cecchi 2013] music styles). Although the details differ greatly, these studies share a common thread in arguing that musical evolution follows patterns and processes that are similar, but not identical, to genetic evolution.

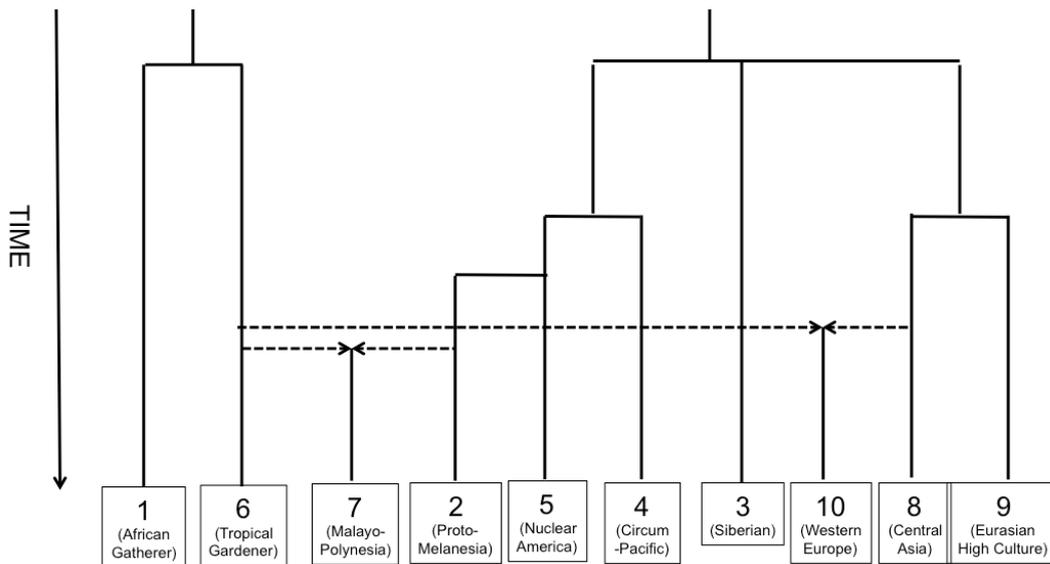


Figure 1.3. A simplified phylogenetic model of global macroevolution of 10 song-style regions⁹

Like Cantometrics, most of these studies are more interested in the macroevolutionary relationships between cultures/genres than in microevolutionary relationships among songs within cultures/genres¹⁰. This makes them more amenable to broad

⁹ Adapted from Fig. 2 of Lomax (1980: 39), which is based on an analysis of ~1,800 songs from 148 cultural groups using 36 Cantometric features. Lomax originally placed cultures at different stages along the time axis, but here all cultures are represented at the present time and the distance along the phylogenetic branches instead represents approximate time since diverging from a shared ancestral musical style. Dashed arrows represent horizontal transmission (borrowing/fusion) between lineages. Lomax's song-style region names varied - here I chose the most geographically descriptive names from Lomax's 1980 and 1989 publications (e.g., "Eurasian High Culture" instead of "Old High Culture"). Although not shown here, finer-scale relationships within and among groups can also be modeled using evolutionary methods (cf. Fig. 3 of Lomax 1980: 41; Rzeszutek, Savage, and Brown 2012).

¹⁰ Macroevolution generally refers to changes among populations (e.g., species,

cross-cultural comparison with domains such as population genetics and linguistics, as focusing on ethnolinguistically defined populations has proved useful in other fields of cultural and biological evolution. However, some musicologists have expressed doubts that exploring relationships involving such deep macroevolutionary time-spans is either possible or interesting, preferring to focus on the kinds of small microevolutionary changes that can be documented over historical time and are often more meaningful to performers (e.g., Stock 2006a).

1.4 Microevolution and tune family research

Given the preference of many musicologists for studying microevolution, one area of research strikingly absent from the discussion of musical evolution surrounding Grauer's essay was the extensive research on microevolution of tune families (groups of melodies sharing descent from a common ancestor or ancestors; Bayard 1950; Cowdery 1984). Tune family research was particularly influenced by Cecil Sharp's realization in the early twentieth century that many traditional ballads that had become moribund or extinct in England were flourishing in modified forms far away in the US Appalachian mountains (Sharp 1932). Sharp's folk song collecting led him to formulate a theory of musical evolution incorporating three principles: 1) Continuity, 2) Variation, and 3) Selection (Sharp 1907). These three principles were later developed by his disciple, Maud Karpeles, and enshrined in the IFMC's definition of folk music quoted above (Karpeles was part of the IFMC commission that drafted the definition).

The general mechanisms proposed by Sharp for British-American tune family evolution were explored more thoroughly by scholars such as Bertrand Bronson (1959-72, 1969, 1976), Samuel Bayard (1950, 1954), Charles Seeger (C. Seeger 1966), and James Cowdery (1984). In some cases, the melodic parallels were made explicit by aligning notes thought to share descent from a common ancestor and by verbally

cultural groups), while microevolution generally refers to changes within populations.

reconstructing the historical process of evolutionary changes. For example, Bayard used a series of melodic alignments to illustrate the "process, often conceived but seldom actually observed... of a tune's having material added onto its end and also losing material from its beginning", giving "evolution of one air out of another by variation, deletion, and addition" (Bayard 1954: 25). Charles Boilès (1973) even proposed a formal method for reconstructing ancestral proto-melodies, based on the linguistic comparative method for reconstructing proto-languages.

During my own studies in Japan, I learned that scholars of Japanese music had developed similar approaches based on alignment of related melodies to understand musical evolution, although without explicit reference to tune family research. For example, Kashō Machida and Tsutomu Takeuchi (1965) traced the evolution of the famous folk songs *Esashi Oiwake* and *Sado Okesa* from their simpler, unaccompanied beginnings in the work songs of distant prefectures, and Atsumi Kaneshiro (1990) developed a quantitative method that he used to test proposed relationships within *Esashi Oiwake's* tune family. Meanwhile, Laurence Picken and colleagues traced the evolution of modern Japanese *gagaku* melodies for flute and reed-pipe back over a thousand years to the simpler and faster ancient melodies of China's Tang court (Picken, Wolpert, and Nickson 1981-2000; Marett 1985; Hughes 2010).

Tune family scholarship has not been limited to British-American and Japanese music - those just happen to be the two traditions I am most familiar with. Elsewhere, scholars such as Béla Bartók (1931) and Walter Wiora (1953) studied tune family evolution in European folk songs, Joep Bor (1975) and Wim van der Meer (1975) made detailed arguments for treating North Indian ragas as evolving "melodic species" (Bor 1975: 17). I suspect that similar approaches may well have been developed independently for lesser-known traditional musical cultures around the world.

Recently, scientists have attempted to apply microevolutionary methods to a variety of Western and non-Western genres in the form of sequence alignment techniques adapted from molecular biology (Mongeau and Sankoff 1990; van Kranenburg et al.

2009; Toussaint 2013; Windram, Charlston, and Howe 2014; Savage and Atkinson 2015). Such techniques make it possible to automate things like quantifying melodic similarities and identifying boundaries between tune families, making analysis possible on vast scales that would be impossible to perform manually (Savage and Atkinson 2015). For example, in Chapter 3 it took my computer only one week to calculate similarities among all ~8.5 million possible pairs from Bronson's compilation of 4,125 Child ballad melodic variants: a scale that would have been logistically impossible to perform manually.

In addition, some scientists have explored musical microevolution in the laboratory, using techniques originally designed to explore controlled evolution of organisms and languages. Thus, one group mimicked sexual reproduction by having short audio loops recombine and mutate, then used an online survey to allow listeners to mimic the process of natural selection on the resulting music, finding that aesthetically pleasing music evolved from nearly random noise over the course of several thousand generations solely under the influence of listener selection (MacCallum et al. 2012). Using a different experimental paradigm similar to the children's game Telephone, other groups found that melodies and rhythms became simpler and more structured in the course of transmission, paralleling findings from experimental language evolution (Ravignani, Delgado, and Kirby 2016). Like biological evolution and language evolution, our knowledge of musical evolution can be enhanced by combining ecologically valid studies of musical evolution in the wild (i.e., in its cultural context) with controlled laboratory experiments.

So far, the microevolution of tune families has been investigated largely independently in a variety of cultures and genres, without much attempt at comparing them to explore general patterns of musical evolution. One reason for this is that a broader cross-cultural comparison would require standardized methods for analyzing and measuring musical evolution in different contexts. In Chapters 2-4, I propose such a method and apply it to several of the cases studies discussed above. Figure 1.4 shows

an example of this method using a well-known and unequivocal example of melodic microevolution: Simon & Garfunkel's version of Scarborough Fair.

By demonstrating consistent cross-cultural and cross-genre trends in the rates and mechanisms of melodic evolution, this dissertation shows that musical evolution, like biological evolution, follows some general rules. For example, notes with stronger structural function are more resistant to change (e.g., rhythmically accented notes more stable than ornamental notes), and mutations are more likely to melodically neighboring notes (e.g., 2nds) than distant ones (e.g., 7ths; cf. Fig. 1.4). This suggests that a general theory of evolution may prove a helpful unifying theory in musicology, as it has in biology.

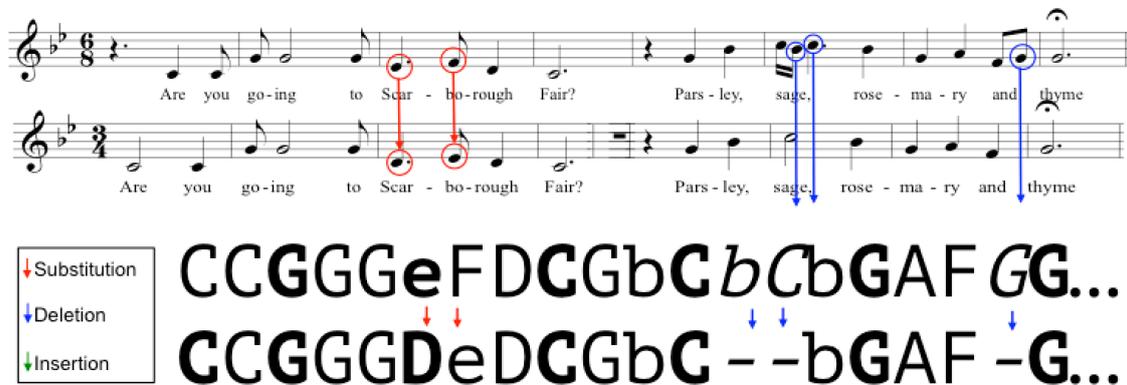


Figure 1.4. An example of analyzing tune family microevolution through melodic sequence alignment¹¹

¹¹ The opening two phrases of Simon and Garfunkel's (1966) phenomenally successful version of "Scarborough Fair" (bottom melody) and its ancestor, Martin Carthy's (1965) version (top melody) are shown, transposed to the common tonic of C (cf. Kloss 2012 for a detailed discussion of the historical evolution of this ballad). See Chapter 2 for how this evolution can be quantified (percent melodic identity = 81%; mutation rate = 0.25 per site per year) and Chapters 3 and 4 for discussion of the mechanisms of note substitutions (red arrows) and deletions (blue arrows) shown here.

1.5 Musical evolution in action: An autoethnographic case study

The abstract nature of the discussion above may give the impression that I view musical evolution as a dehumanized, predictably law-like process, but that is not at all the case. Instead, the general trends in musical structure I have described above emerge only probabilistically over a large number of cases out of the dynamic, largely unpredictable actions of many individual musicians. The melodic changes in Scarborough Fair (Fig. 1.4) are consistent with the general mechanisms I describe in my dissertation, but the deeper questions about exactly why Simon & Garfunkel made these changes and whether or not they were conscious remain for future research. For example, the first substitution from Eb to D is accompanied by a harmonic change (the guitar accompaniment moves to bVII rather than staying on i). Was this melodic substitution made intentionally to accommodate this harmonic change, or did an unintentional melodic change drive the harmonic change? Paul Simon has yet to respond to my query, and perhaps even he may no longer remember.

As an example of the dynamic nature of musical evolution, I want to briefly describe a performance I gave on July 5th, 2012, at the Pink Cow bar's "Japanese Lounge Night" event in Shibuya, Tokyo (Fig. 1.5). Being my own performance, I have the luxury of having insight into my own creative thought process.

As with much of the world's traditional music, folk song and other traditional genres are struggling to maintain relevance in modern Japan (Tokita and Hughes 2008). Loss of traditional rural performance contexts and competition from Western and other globalized popular musics mean that the pool of people who still know how to sing traditional folk songs is ageing and dwindling (Hughes 2008). For example, in folk song competitions I've performed in between 2012 to 2016, performers over the age of 60 usually constituted more than 80% of the total entrants.

While fears of a "cultural grey-out" (Lomax 1968: 4) of traditional music in Japan and elsewhere have a long history, they have yet to be realized. Even as tradition-bearers



Figure 1.5. A snapshot of musical evolution in action¹²

pass away, new generations of performers are born and adapt the traditional styles to modern performance contexts and tastes. Japanese Lounge Night was one such event where younger performers of traditional Japanese music aimed to appeal to new audiences. The general theme of this event was to promote traditional Japanese music to a young, cross-cultural audience who normally have little exposure to it. This was done by cultivating a relaxed atmosphere where people can eat, drink, chat, and engage with the performers rather than sit in silence as is common in concert contexts.

Of course, another goal was to make money for the bar and the performers. This balance between audience accessibility and economic realities was attempted by having no cover charge but an informal rule that audience were expected to order

¹² David Hughes (left) and myself (center) sing a hip-hop remix of the Japanese traditional folk song *Nanbu Tawara Tsumi Uta* with a combination of live accompaniment by Toshinobu Shishido on the *shamisen* (right) and an electronic backing track from Timbaland's *The Way I Are*. Source:

<https://youtu.be/PkkcpS3QvFY>

meals and drinks. The main organizers were paid an unspecified amount, while their students and friends (including myself) performed for no payment other than a free drink, and were still expected to order meals. Unfortunately, this system did not prove financially viable in the long term, and after several years of lively but unprofitable events, Japanese Lounge Night briefly changed its venue and funding model before eventually collapsing - an (unfortunate, from my perspective) example of the complex dynamics of cultural selection in action.

The July 5th event was organized by the owner of the venue, Traci Consoli, and by the *shamisen* musicians Toshinobu Shishido and Kumiya Fujimoto, who also performed along with their students and friends. My own set included myself and David Hughes singing, Shishido on *shamisen*, Miyama McQueen-Tokita on *koto*, and my wife Sawa Matsueda Savage dancing with me in one song. We performed six songs: one British-American folk song (*Scarborough Fair*), three mainland Japanese folk songs (*Esashi Oiwake*, *Yosare Tairyo Bushi*, and *Nanbu Tawara Tsumi Uta*), one Okinawan folk song (*Nakuni*), and one popular *enka* song (*Umiyuki*). Only two of these - *Yosare Tairyo Bushi* and *Nakuni* - would be considered arguably "traditional" performances, and even these were sung by foreigners (David Hughes and me). The other four songs represented various types of cross-cultural or intra-cultural fusions: Miyama improvised *koto* accompaniments to two songs that traditionally don't include *koto* (*Esashi Oiwake* and *Scarborough Fair*), I re-mixed *Nanbu Tawara Tsumi Uta* by sampling Timbaland's *The Way I Are*, and Sawa and I performed *Umiyuki* complete with its original hip-hop dance (the original fusion of hip-hop choreography alongside traditional Japanese *enka* lyrics and vocal style symbolically reflected the mixed African-American and Japanese ancestry of its singer, Jero).

I spent quite a deal of creative energy and time planning these fusions, rehearsing the singing and dancing, etc. However, in doing so, I took very few liberties with the original melodies of each piece (which I learned primarily through a combination of formal lessons and by copying commercial and archival recordings). In most traditions

I've performed in, changing the core notes of a pre-existing melody is usually considered strange/wrong unless done through fairly drastic arrangements (although I've found that such changes are relatively more accepted/encouraged in more improvisational traditions such as jazz). Although I considered the possibility of melodic alterations such as modifying the scale to fit with the distinctive *in* (*miyakobushi*) Japanese scale to which the *koto* is usually tuned, I felt like such a change would destroy the Dorian modality that makes Scarborough Fair so beautiful to me. I did make some intentional changes to the overall formal structure of pieces for logistical reasons (e.g., cutting a verse of Scarborough Fair to allow Miyama a solo). In listening back over my performances, I did notice a few small unintentional errors of lyrics (e.g., I accidentally sang "thread" instead of "seam"), rhythmic timing, melodic intonation, etc. However, for the most part, my performances preserved the core melodic sequences of the type that are analyzed in this dissertation.

This informal autoethnographic case study suggests that different domains of music (melody, lyrics, instrumentation, etc.) may have different rates and mechanisms of evolutionary change, and that these differences may be related to the relative sense of agency experienced by musicians. For example, the melodies and lyrics I sang changed only through small, unconscious mistakes, while I made drastic, conscious changes to the instrumental accompaniment. Indeed, as I show in Chapters 3-4, even within the domain of melody, rhythmically accented notes are more resistant to change than unaccented ones, and this suggests that performers have more agency in experimenting with melodies in places that have less structural function.

Although the discussion of melodic evolution in the preceding sections may have seemed abstract and dehumanized, my intention in this section was to show the dynamic and complex ways in which melodies coevolve with aesthetic, economic, political, and other extra-melodic factors that are of growing interest to musicologists. Part of my reasoning for focusing on melodic evolution in this dissertation was the intuition that melody is particularly resistant to change and amenable to evolutionary

analysis. However, understanding other domains of musical evolution beyond melody will be crucial in forming a broader theory of the cultural evolution music, including the roles of individual agency and cultural context¹³.

1.6 Musical evolution and applied musicology: Education, copyright, sustainability

I believe the cultural evolutionary approach to music can be of practical benefit to musicology. All musicology is in some sense applied through our research, teaching, and outreach, but some is more explicitly applied for the benefit of those outside of academia (Titon 1992; Pettan and Titon 2015). In this dissertation I argue that cultural evolutionary theory can provide a useful unifying theoretical framework to apply to research on understanding and reconstructing musical change at multiple levels (both macro and micro) across cultures, genres, and time periods. I now briefly discuss three other ways it can be more directly applied: education, copyright, and sustainability (especially of intangible cultural heritage).

1.6.1 Education

The world's musical diversity is woefully underrepresented at all levels of education. Often the job of correcting this falls to ethnomusicologists teaching survey courses on "World Music". As Rahaim notes, "as teachers, we often find ourselves in situations that require us to say something in short-hand about [musical] origins, and have few models at hand apart from evolution" (Rahaim 2006: 32). Evolutionary models like

¹³ Language evolution provides another good analogy. Much work in language evolution focuses on the evolution of basic vocabulary due to its resistance to change and amenability to evolutionary analysis (Pagel 2009). However, broader theories of language evolution incorporate many complex cognitive and social factors, including race, gender and class (Labov 1994-2010).

Lomax's world phylogenetic tree of regional song style (Fig. 1.3) provide a simple and convenient starting point for teaching about similarities and differences in the world's music, and are flexible enough to adapt to diverse contexts such as conservatory classrooms, instrument museums, or pop music recommendation websites. Such coarse models can be further improved and/or nuanced by following them with microevolutionary case studies of musical change in specific cultures. An evolutionary approach further provides the chance to teach about connections beyond music to other domains in order to understand the ways in which the global distribution of music may be related to the distributions of the people who make it and to other aspects of their culture such as language or social structure (Lomax 1968; Savage and Brown 2013; Brown et al. 2014; Grauer 2006).

1.6.2 Copyright

Since almost all music is influenced by the past in at least some way, whether such influence is within norms of creativity and tradition or amounts to plagiarism is connected to an understanding of processes of musical evolution. US copyright law resembles concepts of tune family evolution in that the core copyrightable essence of a song consists of its representation in musical notation, and that the degree of overall melodic correspondence at structurally significant places between two tunes is a primary criterion for deciding whether the level of similarity constitutes plagiarism (Cronin 2015; Fruehwald 1992; Müllensiefen & Pendzich 2009). Thus, one famous case concluded that the melody of George Harrison's *My Sweet Lord* (1970) was similar enough to the Chiffons' *He's So Fine* (1962) as to constitute subconscious plagiarism (Judge Owen 1976). In Chapter 4, I use new quantitative methods to confirm that the two tunes share 54% identical notes and that this is extremely unlikely to be due to chance ($p < .00001$).

However, the concept of individual ownership by composers in copyright law differs from concepts of folk song tune families, where traditional tunes are usually

considered to be general property of the community (Bronson 1969). They are also different from conceptions in many non-Western cultures in which the essence of song ownership may be considered to lie not in its notated melody but in the performance style, performance context, or other extra-melodic features (A. Seeger 1992).

The interpretation of copyright law can dramatically affect the livelihoods of musicians and communities around the world. Thus, a holistic understanding of general dynamics of musical evolution (including the many aspects beyond the melodic evolution that is the focus of this dissertation) and their specific manifestations in various musical cultures and genres may prove crucial to a more cross-culturally principled interpretation of concepts of creativity and ownership.

1.6.3 Sustainability

The issue of safeguarding and promoting the endangered musics of the world has been fundamental to ethnomusicology since Carl Stumpf and Erich von Hornbostel began compiling recordings for the Berliner Phonogramm-Archiv at the turn of the 20th century (Simon and Wegner 2000). Sustainability was again a central part of Lomax's (1977) "Appeal for Cultural Equity". But it has taken on renewed interest and urgency in the 21st century with UNESCO's "Convention on the Safeguarding of the Intangible Cultural Heritage" (UNESCO 2003; Howard 2012). The core purpose of the UNESCO convention is to provide resources to allow cultural traditions, including music and other performing arts, to continue to evolve by adapting to changing social contexts and avoiding cultural extinction.

UNESCO has also adopted similar policies for the conservation of biodiversity and linguistic diversity¹⁴. Catherine Grant (2014) has made a powerful case for adapting

¹⁴<http://www.unesco.org/new/en/culture/themes/endangered-languages/biodiversity-and-linguistic-diversity/>

UNESCO's Language Vitality and Endangerment framework into a Music Vitality and Endangerment Framework (MVEF) to apply to the challenge of music endangerment and sustainability, drawing on theoretical and methodological concepts of standardized comparative measurements that show some similarities with Lomax's Cantometrics. In his foreword, Anthony Seeger praises the MVEF as a "model for applied ethnomusicology", noting that:

The twelve factors in the MVEF...recognize that musical traditions depend on transmission, continuity, change, and interested audiences, but also that these take place in a context of emerging mass media, the involvement of outsiders, and the often unpredictable actions of local and national governments. The measures allow for the charismatic actions of an individual passionate actor and also for the results of media attention, national cultural policies, and tourism. (Grant 2014: ix)

Seeger's summary succinctly captures the three key evolutionary mechanisms of "continuity [inheritance], change [variation], and interested audiences [selection]" as well as their dynamic relationships with individual agency and cultural context.

I believe that musical sustainability initiatives such as Grant's could be further nuanced through a theoretical framework of musical evolution, just as biodiversity and linguistic diversity sustainability initiatives have been informed by a theoretical understanding of biological evolution and language evolution (Stockwell, Hendry, and Kinnison 2003; Hammarström 2016). For example, Grant's MVEF depends crucially on the key unit of "music genre", for which she gives an in-depth case study of Vietnamese *ca trù*. The ambiguity of differentiating such genre units from finer-grained sub-genres and/or coarser-grained super-genres is thus a major challenge for Grant's MVEF. Such differentiation has parallels in the distinction between species and varieties that motivated Darwin's *Origin of Species*, as well as the distinction between languages and dialects that is central to linguistics, and could likewise benefit from an evolutionary framework. An evolutionary framework might help Grant to clarify the multiple levels of relationships between *ca trù* performers as they compete

with one another, with rival *ca trù* groups, other closely related genres of Vietnamese traditional music, and with global popular music, just as an evolutionary framework for linguistics helps clarify the nested relationships among individual speakers, dialects, languages, and language families. *Ca trù* is on UNESCO's List of Intangible Cultural Heritage in Need of Urgent Safeguarding, and thus decisions by UNESCO about optimal resource allocation may benefit from an evolutionary framework in which the sustainability of *ca trù* is seen as interconnected with the sustainability of related sub-genres and super-genres.

1.7 Objections to musical evolution: Agency and reductionism

As I have shown, music literally evolves, and this evolution has been and continues to be of interest to musicologists and non-musicologists alike. In fact, many of the processes I discuss are immediately recognizable to many under the terminology of musical change, for which ethnomusicologists have long sought a rigorous theory. In Merriam's landmark book, he argued that ethnomusicology "needs a theory of change" (Merriam 1964: 307). Over a half century later, Nettl (2015: 292) summarizes that "there have been many attempts to generalize about change but no generally accepted theory". Why haven't musicologists interested in general theories of change adopted the framework of evolution (which is, simply put, a formal theory of change)?

I have presented versions of this argument at national ethnomusicology conferences in the USA¹⁵ and Japan¹⁶, receiving a variety of responses. Most objections to the use of evolutionary theory focused on three issues: implications of progress, individual

¹⁵ Savage, P.E. (2013). Cultural evolution of music. (*Talk presented at the 2013 meeting of the Society for Ethnomusicology, Indianapolis, IN, USA*)

¹⁶ Savage, P.E. (2014). 「音楽の文化的「進化」——「江差追分」の系統的分析——」 [Cultural evolution of music: A phylogenetic analysis of the Japanese folksong "Esashi Oiwake"] (Talk presented at the 2014 meeting of the 東洋音楽学会 [Society for Research in Asiatic Music], Shitennoji University, Osaka, Japan)

agency, and reductionism. Since I have already clarified misconceptions about progress at length above¹⁷, I will focus here on agency and reductionism.

1.7.1 Agency

Echoing arguments against cultural evolution by the evolutionary biologists Stephen Jay Gould and Richard Lewontin, Rahaim (2006: 36) argues: "Perhaps most importantly for ethnomusicologists, metaphors of both situated and progressive evolution turn attention away from the agency of individuals". But does the concept of musical evolution negate the agency of individuals to create their own music any more than the concept of biological evolution negates individual free will? In each case, our cultural/genetic inheritances are the product of long evolutionary processes shaped by historical factors, but cannot be simply reduced to or wholly explained by such factors.

Musicians are generally free to compose their own music or modify the existing repertoire in whatever ways they see fit (within the physical limits imposed by acoustics, neurobiology, etc.). But whether their creations will appeal to others and be passed on through the generations depends on a variety of factors beyond their control, including the sociopolitical context and the perceptual capacities of the audience. Thus, the role of the individual musicians in this process and their relationships with other actors (audiences, composers, accompanists, producers, judges, etc.) are in fact central

¹⁷ Unfortunately, the association of evolution with progress is particularly entrenched where I live in Japan, where the characters used to translate evolution (進化 [*shinka*]) literally mean "progressive change" (the English word *evolution* itself evolved from the Latin *evolutio*, meaning "unfolding"). In my opinion, ethnomusicologists avoiding the term "evolution" because of misconceptions about its meaning are contributing to this popular misconception. Instead I believe concerted effort by ethnomusicologists and others to correct this misconception for future generations is in order.

to understanding the cultural evolution of music, as I have attempted to show in my autoethnographic case study above.

This dissertation focuses on identifying general constraints that apply across many individuals, but this does not mean that other studies must or should do so. For example, one potentially productive area for exploring the role of individual agency in musical evolution might involve comparing different performers attempting to create their own signature versions of music originally composed and/or performed by others. This could easily apply to a variety of cultures and genres, including art (e.g., the same symphony performed by different orchestras), popular (e.g., cover songs), and folk (e.g., folk song variants; cf. the Scarborough Fair example in Fig. 1.4).

In fact, the presence of human agency and the intentional innovation that comes with it is one of the most exciting and interesting aspects about studying cultural evolution. In genetic evolution, natural selection provides the major explanatory mechanism due to the fact that genetic variation is arbitrary (i.e., genetic mutations are not directed towards particular evolutionary goals). However, in cultural evolution, both selection and variation can be directed consciously and unconsciously through a much broader range of mechanisms than typically found in genetic evolution. To accommodate this complexity, cultural evolutionary theorists have proposed dizzying array of mechanisms to expand the terminological framework of evolutionary biology to cultural evolution (e.g., transmission biases based on prestige, aesthetics, or conformity/anti-conformity; guided variation driven by cognition and/or emotion ; Cavalli-Sforza and Feldman 1981; Richerson and Boyd 2005; Mesoudi 2011; Fogarty, Creanza, and Feldman 2015). The relative strengths of these different types of evolutionary mechanisms and their implications for musical evolution in particular and cultural evolution in general are hotly debated (Claidière, Kirby, and Sperber 2012; Leroi et al. 2012). Thus, this is an area where musicologists and cultural evolutionary theorists could both learn much from one another.

1.7.2 Reductionism

A final critique I would like to mention is a broader but related one regarding reductionism and the neoliberalization of the humanities. This criticism was levelled at cultural evolution in general by Fracchia and Lewontin (1999: 507): "the demand for a theory of cultural evolution is really a demand that cultural anthropology be included in the grand twentieth-century movement to scientize all aspects of the study of society, to become validated as a part of 'social science'". It was also leveled directly at my own proposal with Steven Brown that included cultural evolution as one of five major themes in a new comparative musicology (Savage and Brown 2013). In a thorough and nuanced review entitled "On Not Losing Heart", David Clarke approved of our call for more cross-cultural comparison, but worried about our "strongly empiricist paradigm":

Lomax's particular mode of integration "between the humanistic and the scientific" [was] fuelled by a politics that had an emancipatory motive. In the metrics and technics of the new comparative musicology proposed by Savage and Brown, traces of any such informing polity melt into air....A political neutrality that is the correlate of an unalloyed empiricism is problematic....My own predilections here are perhaps more attuned to ethnomusicologists who are interested in the particularities of a culture and the actual experience of encounter in the field. By contrast, Savage, Brown, et al. advocate different epistemological values with a different ethos, based on the abstraction of music and people into data. To characterize that ethos as a recapitulation of Lomax, only without the heart, might be an unfair caricature. For the various statistical representations and correlations emerging from their research may well be sublimating a lot of passion, and Savage and Brown's own day-to-day dealings with musicians and musicking

*may be no less affective than anyone else's (it's just that they exclude this from their research)*¹⁸. (Clarke 2014: 6, 11-12)

While Clarke argues that our "political neutrality that is the correlate of an unalloyed empiricism is problematic", we had intentionally tried to maintain a relatively neutral political stance, in large part to avoid the problems of confirmation bias that were leveled at Lomax. With Cantometrics, Lomax sought to scientifically validate his strong political views about "cultural equity: the right of every culture to have equal time on the air and equal time in the classroom" (Pareles 2002). One of the concerns that doomed Cantometrics was that Lomax's analyses were viewed as being too strongly biased by his political views (Maranda 1970; Szwed 2010). Personally, I strongly share Lomax's views about the value of cultural equity, and I, too, see quantitative data as a helpful tool in arguing for the value of all of the world's music, particularly in today's political climate of evidence-based policy. However, I believe it

¹⁸ In point of fact, I do feel a lot of passion for the world's musicians and see one of my life's goals as being advocating for their value. My interest in folk song evolution was motivated not only by theoretical concerns about mechanisms of cultural microevolution, but on my own experiences learning and performing British-American and Japanese folk songs and my hopes that my (Japanese-New Zealand-American) daughter will be able to sing these songs that have been handed down to her over the course of hundreds of years from her ancestors on opposite sides of the world. I have won trophies in a number of Japanese folk song competitions, so questions about agency in performance and what types of musical (and extra-musical) variation are selected for or against are not merely academic but affect me personally. Do I think that all of these factors can be perfectly quantified? Absolutely not. But I do believe that theories of musical evolution informed by quantitative data could have a positive influence on musicology and beyond. As Clarke (2014: 12) later admits: "in fairness, the empirical and the metric have as much potential as any other paradigm to work to humanistic ends".

is legitimate to try to separate one's political beliefs from one's published work, and it may well be a more effective long-term strategy for the types of applications described in the previous section.

Certainly, neither a purely qualitative, ethnographic approach nor a purely quantitative, scientific approach will succeed in advancing our knowledge of how and why music evolves. But by combining the two approaches through cross-cultural comparative study, we can achieve a better understanding of the forces governing the world's musical diversity and their real-world implications (Savage and Brown 2013). For instance, my analysis of the *My Sweet Lord* plagiarism case in Chapter 4 gives a clear example where quantitative measurements of the degree of melodic similarity (54%) between two tunes and its qualitative interpretation in the context of copyright law has major practical implications in which millions of dollars are at stake.

1.8 Conclusion

Music evolves, through mechanisms that are both similar to and distinct from biological evolution. Cultural evolutionary theory has been developed to the point that it shows promise for providing explanatory power from the broad levels of macroevolution of global musical styles to the minute microevolutionary details of individual performers and performances. Musical evolution shows potential for applications beyond research to such disparate domains as education, copyright and sustainability.

However, I am aware that my review is inevitably incomplete and I have only been able to highlight a tiny fraction of the types of situations and methodologies through which the evolutionary framework can be fruitfully applied to music. To me, that incompleteness highlights the broad explanatory power of evolutionary theory, and broad explanatory theory is something that ethnomusicologists such as Timothy Rice (2010) have argued we are sorely in need of today.

Scientific interest in musical evolution is already growing rapidly, and will continue with or without the involvement of musicologists. Here again, we can learn from language evolution. Several high-profile articles on language evolution were published by teams of scientists without close collaboration with linguists (Gray and Atkinson 2003; Pagel, Atkinson, and Meade 2007; Atkinson 2011). This resulted in bitter disputes and accusations of "naïve arrogance" (Campbell 2013: 472) that have limited what could have been mutually beneficial collaboration (Marris 2008). I have chosen to try to avoid such pitfalls by being proactive and initiating a collaboration on musical evolution with one of the researchers at the center of these disputes to combine our knowledge and skills (Savage and Atkinson 2015). I will continue to strive toward productive interdisciplinary collaboration, and suggest that those who are worried about cultural evolutionary scientists (or even musicologists from different sub-fields such as myself) encroaching on their field may also find that they might actually benefit from interdisciplinary collaboration.

I do not intend by any means to imply that the predominantly quantitative approach I have presented here - strongly informed as it is by my collaborations with scientists studying cultural and biological evolution, as well as my own earlier training in psychology and biochemistry - is the only way to study musical evolution. One reason I have focused in this dissertation on a rigorously quantitative approach modeled on molecular genetics is that such quantitative approaches have shown success in rehabilitating cultural evolutionary theory after much criticism of earlier incarnations such as Dawkins' "memetics" (Dawkins 1976; Blackmore 1999; Jan 2007) as lacking in empirical rigour (Laland and Brown 2011; Mesoudi, Whiten, and Laland 2006). But I believe that one of the strengths of evolutionary theory is that it is flexible enough to be usefully adapted to a variety of scientific and humanistic methodologies, with plenty of room to coexist productively with non-evolutionary theories. As Ruth Stone (2008: 225) has noted, "there is no such thing as a *best* theory. Some theories are simply more suited for answering certain kinds of questions than others" (emphasis in

original). Even if the concept of cultural evolution cannot answer all our questions, I believe it helps to answer enough musical questions of abiding interest that it should be taboo no more.

Summary

Interest in the biological evolution of human capacities for making music is growing rapidly, but the terminology of "cultural evolution" remains practically taboo in ethnomusicology. Here I argue that this taboo should be lifted and that cultural evolution provides a powerful theoretical framework for (ethno)musicology. Drawing on major advances in the scientific understanding of cultural evolution over the past three decades, I clarify persistent misconceptions about the roles of genes and progress in definitions of evolution, showing that neither is required or assumed. I go on to review older and recent literature relevant to musical evolution at a variety of levels, from Lomax's macroevolutionary interpretation of global patterns of song-style to microevolutionary mechanisms by which minute melodic variations give rise to large tune families. To highlight the complex dynamics of musical evolution in action, I provide an autoethnographic case study of my own performance of folk songs in Japan. After addressing criticisms of the roles of individual agency and reductionism in studying musical evolution, I highlight ways in which cultural evolutionary theory can contribute to applied ethnomusicology in the domains of education, copyright, and sustainability. While cultural evolution will never explain all aspects of music in culture, it provides a powerful and much-needed theoretical framework for answering at least some questions of longstanding musicological interest.

The Scarborough Fair text can be traced back for several hundred years, but the evolution of the tune for it made famous by Simon and Garfunkel's has only been unambiguously traced back to an 1888 version entitled "Whittingham Fair" (Kloss 2012 describes the evolution of both tune and text in detail). Simon & Garfunkel recorded their version (Fig. 2.1, bottom) in 1966 after having learned it the previous year from Martin Carthy, who recorded his version (Fig. 2.1, top) that same year (1965).

Various different influenza strains have been documented for hundreds of years and

influenza A H7N9 virus isolates Anhui/1 and Hangzhou/1. The melody example shows the opening two phrases of "Scarborough Fair" (Child ballad No. 2) for Simon and Garfunkel's 1966 version (bottom melody) and its ancestor, Martin Carthy's 1965 version (top melody). Protein sequences can be converted from complex three-dimensional structures (**a**) into simplified aligned sequences (**c**) using an "alphabet" of 20-amino acids (**e**). Likewise, melodies can be converted from complex staff notation (**b**) into simplified aligned sequences (**d**) using a 12-note "alphabet" represented by notes on a keyboard octave (**f**). In each case, gaps in the alignment can be represented by a dash ("-"), although this is not required in this particular protein example. Adding temporal information in combination with contextual information then allows us to infer the rates and mechanisms of evolution. In this virus protein example (**g**), two amino acids have changed (T to P and Q to L) between 2012 and 2013, giving a percent identity of 80% and a mean mutation rate of .2 per site per year. In the musical example (**h**), additional contextual information is encoded by representing ornamental notes using italics and stressed notes using bold. This makes it possible to quantify the degree of evolutionary change represented by the three deletions (blue arrows) and two substitutions (red arrows). All three of the ornamental notes in the 1965 version are deleted, while both substitutions (e->D and F->e) involve small melodic distances of a 2nd. This musical example has a percent identity of 81% and a mean mutation rate of .25 per site per year (see text for further details).

have ancient origins. Of these, influenza A is the most widespread and infectious. Influenza A virus genomes consist of 8 sub-units. The haemmagglutinin (HA) sub-unit is the best studied because it experiences the strongest positive selection for antigenic drift as it rapidly evolves to evade recognition by the host immune system. These sub-units are often swapped among viruses, and such horizontal recombination is often the source of new infectious strains, including the 2013 H7N9 avian influenza epidemic. The HA sub-unit of the 2013 H7N9 virus (Fig. 2.1, bottom) has been traced to the H7 duck strain recorded in 2012 (Fig 2.1, top). The short section of HA shown in Fig. 2.1 includes the glutamine (Q) to leucine (L) amino acid substitution implicated in the jump from bird to human virulence (see Nelson and Holmes 2007; Liu et al. 2013 for further details).

I have chosen these short musical and biological sequence segments simply to illustrate the process of measuring evolution, not necessarily as being representative of evolution in general. Other examples from different musics/organisms (or even different sections within the same songs/viruses) may give different values.

2-1. Analogies between protein evolution and melodic evolution

Proteins and melodies share a number of analogies. Proteins are biological molecules that are composed of sequences of amino acids that form 3-dimensional structures (Fig. 2.1a) that function to catalyze biochemical reactions (Dayhoff, Schwartz, and Orcutt 1978). Meanwhile, melodies are composed of sequences of notes that form complex musical structures that function to carry song lyrics, accompany dance, etc. (Fig 2.1b). As such, methods for measuring protein evolution are a candidate for adapting to measure musical evolution.

2-2. Sequence coding

Music is much more than notes transcribed in a score, just as proteins are much more than sequences of amino acids. However, in order to understand musical evolution, we need a standardized method of comparing musical works across time and space. To allow for analysis of music documented before the advent of audio recording technology, this requires the use of transcriptions, although this comes at the cost of losing details about performance style (e.g., timbre, ornamentation, microtuning, microtiming).

Furthermore, to allow evolutionary analysis using state-of-the-art methods from evolutionary biology, we need to further reduce the information into aligned sequences. For proteins, this preserves information about amino acid types but removes information about three-dimensional structure (Fig. 2.1c). For tunes, this preserves pitch information but removes rhythmic information (Fig. 2.1d). This approach was already implicit in the melodic alignment approach developed by tune family scholars. Here, tunes were transposed into a common tonic, and time signatures, phrases, and rhythms were stretched and compressed as necessary to align notes sharing similar pitches (Bayard 1954; C. Seeger 1966). The intuition of early tune family scholars to emphasize alignment of pitches, rather than rhythms or global stylistic features, is supported by recent research that has demonstrated quantitatively that pitch is greatly superior to rhythm and to global stylistic features both for the purposes of tune family identification in particular and for melodic similarity in general (Urbano et al. 2011; van Kranenburg, Volk, and Wiering 2013). However, it is still possible to use various techniques to preserve some rhythmic information, such as by distinguishing rhythmically accented, unaccented, and ornamental notes (see Fig. 2.1h and below)².

² Since this method uses only pitch sequences with minimal rhythmic information, the term "pitch sequence evolution" may appear more precise than the term "melodic evolution". However, because "melody" is often used synonymously with "pitch

Just as DNA can be modeled as a sequence constructed from an “alphabet” of 4 nucleic acids (C, G, A, or T) or a protein can be modeled as a sequence constructed from an alphabet of 20 amino acids (Fig. 2.1e), a melody can be modeled as a sequence constructed from an alphabet of 12 pitch classes representing the 12 notes of the chromatic scale (Fig. 2.1f). This compresses melodies into a single octave, losing information about pitch range in addition to the information about microtonality, rhythm, etc. already lost. However, given that octave equivalence is a near-universal phenomenon among humans (Brown and Jordania 2013), this is a small loss compared to the gain in comparability across different ranges (e.g., different sexes, instruments, etc.). Transposing melodies to a common tonic of "C" also helps to improve comparability (although there may sometimes be some ambiguity as to what constitutes the tonic³).

2-3. Sequence alignment

By aligning melodies known to share common ancestry, we can identify sites that are conserved, where a different pitch has been substituted, or where a pitch has been inserted/deleted (“indel”, represented using dashes). Such alignments were traditionally done manually for a handful of melodic variants already known to be

sequence" and because pitch sequence evolution has been shown to very closely approximate melodic evolution even when rhythm is ignored (van Kranenburg, Volk, and Wiering 2013; Savage and Atkinson 2015), I will use the more concise and descriptive term "melodic evolution" throughout this dissertation.

³ Such ambiguity can sometimes be mitigated by using consistent rules, such as assuming that the final note is the tonic. When using automated algorithms to find related melodies, inconsistent tonic assignment can result in masking relationships between melodies. One way of circumventing this problem is to run the algorithm multiple times using different tonic assignments, although this is more computationally intensive and increases the false positive rate.

related by descent, but my method allows this to be automated to find groups of related melodic variants from within vast samples.

2-3-1. Automatic alignment

The sample of 4,125 Child ballad melodic variants analyzed in Chapter 3 is far too large to manually align all 8,505,750 possible pairs of melodies. Instead, an automated alignment algorithm is required. Quentin Atkinson and I have demonstrated how the Needleman and Wunsch's (1970) global pairwise alignment algorithm (originally designed for automatically aligning pairs of proteins) can be modified to automatically compare pairs of melodies (Savage and Atkinson 2015). Briefly, this algorithm attempts to find the alignment between two sequences that maximizes similarity between the sequences without requiring too many gaps (indels) to be opened. This requires researchers to manually pre-specify weighting values for a "gap opening penalty" (GOP) and "gap extension penalty" (GEP). Researchers also have the option of specifying values by which to weight non-identical matches to account for the fact that some kinds of amino acid changes are more likely than others and hence certain mismatches be treated as more similar than others (just as some melodic changes are likely to be more common than others). The precise values such parameters should take vary even within molecular genetics research depending on the goals of the study and the precise evolutionary mechanisms of the amino acids in question, and so adapting this algorithm to melodic evolution required testing of a range of parameter values and comparing the resulting automatic alignments to manual alignments performed by experts.

To test these parameter values, Atkinson and I used a set of 26 folk songs from four tune families (two British-American [Bayard 1954], two Japanese [町田；竹内 1965]) that had previously been manually identified and aligned. We tested 80 different parameter combinations, including not only different GOP (ranging from 0.8 to 16) and GEP (0.2-8), but also whether or not to include differences of mode (i.e., treating major

and minor versions of the same scale degree [e.g., major third "E" vs. minor third "e"] as the same or different), rhythmic stress (ignoring or including unstressed notes) or lyrics (ignoring or including non-text-carrying melisma).

Our automated alignment performed fairly well in capturing the manual judgments of expert musicologists. Including unstressed notes and non-text-carrying notes always improved alignment accuracy regardless of the other parameters. Interestingly, however, the best-performing combination of the other parameters depended on the goals of the alignment. The best-performing parameter combination in terms of tune family identification (correctly grouping 100% of the tunes in terms of overall similarity to other tunes and identifying 85% of these tunes as forming distinct tune families) ignored differences in mode and used GOP and GEP values of 12 and 6, respectively. In contrast, the best-performing parameter combination in terms of alignment within individual tune families (automated alignments highly correlated with manual ones at $r = .83$) did not ignore differences in mode and used GOP and GEP values of 0.8 and 0.4, respectively. Thus, future research should not assume that there is one "best" parameter combination, but should continue to explore different automated alignment parameters and try to use the combination most suitable for its specific research goals.

2-3-2. Manual alignment

Although automated alignment makes it possible to compare on massive scales beyond the capabilities of unassisted humans, it is unlikely to ever be able to match expert manual alignment in terms of accuracy. Thus it is advisable when possible to manually correct automatic alignments (just as automatic alignments of molecular genetic sequences benefit from manual correction). Manual correction also allows researchers to incorporate musical information ignored by the sequence alignment algorithms (e.g., octave, rhythmic position).

At this stage, there is no formal method for manual melodic alignment: researchers must use their musical intuitions, just as scholars of tune family evolution have done for decades (Bayard 1954; Bronson 1959-72; 町田 ; 竹内 1965; Marett 1985). All final melodic alignments in this dissertation - even for the 172 highly related pairs in Chapter 3 that were initially identified automatically - were performed manually.

2-4. Measuring sequence similarity

A simple evolutionary measure for comparing sequences is percent identity (PID). This is calculated based on the number of aligned sites (i.e., amino acids, DNA nucleotides, musical notes, etc.) that are identical (ID) divided by the sequence length (L). There are several possibilities for how to operationalize sequence length in cases where the sequences have unequal lengths due to insertion/deletion. We have chosen to use the average length of both sequences, as this appears to be the most consistent measure of percent identity (May 2004):

$$PID = 100 \left(\frac{ID}{\frac{L_1 + L_2}{2}} \right)$$

For example, in the virus example (Fig. 2.1g), 8 amino acids are identical (ID = 8), and both sequences are 10 amino acids long ($L_1 = L_2 = 10$), giving a PID of **80%**. In the musical example (Fig. 2.1h), 15 notes are identical (ID = 15), the top sequence is 20 notes long ($L_1 = 20$), and the bottom sequence is 17 notes long ($L_2 = 17$), giving a PID of **81%**.

PID can be used to describe similarities between sequences, establish objective cutoffs for evolutionary analysis (e.g., limiting analysis to highly related pairs with >85% identity; Dayhoff, Schwartz, and Orcutt 1978), or calculate whether similarities between sequences are significantly higher than expected by chance for random

sequences of similar length and sequence composition. To do this, random distributions can be created by randomly reshuffling sequences 100 times and recalculating PIDs using the reshuffled sequences. If fewer than 5 out of 100 random PIDs are greater than or equal to the real observed PID (i.e., $P < .05$), this can be taken as evidence that the two proteins or two melodies are significantly more similar than chance (R. F. Doolittle 1981; Savage and Atkinson 2015).

More complex measurements of similarity can also be used that incorporate information about known evolutionary transition probabilities (e.g., certain types of amino acid mutations are more likely than others). For music, we showed previously that ignoring changes of mode (e.g., treating minor and major scale degrees as identical) improved tune family identification (Savage and Atkinson 2015: 165), and other researchers have proposed different methods of weighting melodic similarity including harmonic similarity and melodic distance (Mongeau and Sankoff 1990; Müllensiefen and Pendsch 2009; van Kranenburg, Volk, and Wiering 2013). In the future, more complex measures incorporating information about musical evolution may be useful, but in this dissertation I focus on simpler PID measurements that have already shown success.

2-5. Measuring mutation rates

Evolutionary rates can be measured in a variety of ways (Baer, Miyamoto, and Denver 2007; Duffy, Shackelton, and Holmes 2008; Dayhoff, Schwartz, and Orcutt 1978). Generally, rates of biological evolution are calculated using aligned molecular sequences in the form of a number of changes per sequence site per unit of time. The unit of time may be in absolute time (e.g., per year), per generation, per cell division, or other units. The number of changes may be measured as the short-term number of spontaneous mutations (mutation rate) or the long-term number of fixed substitutions (substitution rate). These rates vary a great deal among and within species and are difficult to measure precisely, so the exact choice of measurement depends on the

specific goals and assumptions of the research project.

Because musical evolution has so far rarely been investigated quantitatively, I have chosen to focus in this dissertation on the simplest measure of evolutionary rates in terms of observed mutations per year (where the term "mutation" includes both unconscious copy-errors and conscious innovations). For example, in the virus example (Fig. 2.1g), 2 out of the 10 sites display mutation (amino acid substitution) over the 1 year between 2012 and 2013, giving an average mutation rate of **0.2 per site per year**. In the musical example (Fig. 2.1h), 5 out of the 20 sites display mutation (2 notes are substituted [red arrows], 3 notes are deleted [blue arrows]) over the 1 year between 1965 and 1966, giving an average mutation rate of **0.25 per site per year**.

It is also possible to calculate mutation rates for certain subsets of sequences. For example, DNA sequences tend to have faster mutation rates at non-protein coding sites, since mutations at such sites have less deleterious functional consequences (i.e., there is less purifying selection). Likewise, calculating separate mutation rates for ornamental (italics) vs. non-ornamental sites in Fig. 2.1h shows a much higher musical mutation rate for ornamental sites. All three ornamental sites in the top melody are deleted to give an ornamental mutation rate of **1 per site per year** (3 changes / 3 sites / 1 year), which is almost 10 times greater than the non-ornamental mutation rate of **0.12 per site per year** (2 changes / 17 sites / 1 year). This suggests that, in music as well as in genetics, more functional sites may be more resistant to change - a hypothesis that is explored further in Chapters 3-4.

It is interesting to note that the absolute evolutionary rates shown in the examples of Fig. 1 are fairly similar for the virus example and the music example (0.2 and 0.25 per site per year, respectively). Obviously, such similarities are the products of vast differences in evolutionary mechanisms involved. However, it does suggest that there may be cases where cultural evolution can operate on time scales comparable to biological evolution.

In the future it may be useful to compare different measures of evolutionary rates to better explore the mechanisms of musical evolution. For example, measuring musical mutation rates over repeated singing by the same singer may be most analogous to biological rates per cell division, while measuring musical mutation rates over transmission from teacher to student may be most analogous to biological rates per generation⁴.

2-6. Measuring transition rates

In addition to measuring average mutation rates for entire sequences or subsets of sequences, it is possible to calculate the rates of different types of mutations. For example, mutations can be broadly categorized as either substitutions, insertions, or deletions. In biological evolution, substitutions are much more common than insertions or deletions ("indels"). Indeed, in Fig. 2.1g both of the virus sequence changes are substitutions, with no indels observed. On the other hand, deletions (blue arrows) actually outnumber substitutions (red arrows) three to two in the musical example (Fig. 2.1h). My analyses in Chapters 3-4 further support the hypothesis that indels generally outnumber substitutions in musical evolution, and propose an explanation for why this may be. This suggests that there are major differences between musical and biological evolution due to the details of their mutational mechanisms.

More fine-grained differences can also be shown by calculating the rates of different types of substitutions. For example, both the amino acid substitutions observed in Fig. 2.1g (Q to L and T to P) require only a single nucleotide substitution in the underlying

⁴ Other analogies are possible (e.g., variation in different verses of the same performance may be analogous to differential gene expression in different cells), and some musical phenomena may have no analogue in biological evolution (e.g., conscious improvisation).

DNA codon. In contrast, amino acid substitutions requiring multiple nucleotide substitutions are hardly ever observed (Dayhoff, Schwartz, and Orcutt 1978). Likewise, both of the note substitutions shown in Fig. 2.1h (e to D and F to e) involve small melodic distances of a 2nd. In Chapters 3-4, I show that this trend toward musical substitutions of small melodic distances is consistent across a selection of cultures and genres.

Averaging the frequencies of different types of substitutions across larger samples capturing many hundreds or thousands of evolutionary changes allows the construction of detailed transition rate matrices. Figure 2.2 shows one matrix commonly used in genetics, calculated from an analysis of 1,572 amino acid mutations observed in 71 groups of highly related proteins (>85% identity).

		ORIGINAL AMINO ACID																			
		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
REPLACEMENT AMINO ACID	A	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
	A	9867	2	9	10	3	8	17	21	2	6	4	2	6	2	22	35	32	0	2	18
	R	1	9913	1	0	1	10	0	0	10	3	1	19	4	1	4	6	1	8	0	1
	N	4	1	9822	36	0	4	6	6	21	3	1	13	0	1	2	20	9	1	4	1
	D	6	0	42	9859	0	6	53	6	4	1	0	3	0	0	1	5	3	0	0	1
	C	1	1	0	0	9973	0	0	0	1	1	0	0	0	0	1	5	1	0	3	2
	Q	3	9	4	5	0	9876	27	1	23	1	3	6	4	0	6	2	2	0	0	1
	E	10	0	7	56	0	35	9865	4	2	3	1	4	1	0	3	4	2	0	1	2
	G	21	1	12	11	1	3	7	9935	1	0	1	2	1	1	3	21	3	0	0	5
	H	1	2	18	3	1	20	1	0	9912	0	1	1	0	2	3	1	1	1	4	1
	I	2	2	3	1	2	1	2	0	0	9872	9	2	12	7	0	1	7	0	1	33
	L	3	1	3	0	0	6	1	1	4	22	9947	2	45	13	3	1	3	4	2	15
	K	2	37	25	6	0	12	7	2	2	4	1	9926	20	0	3	8	11	0	1	1
	M	1	1	0	0	0	2	0	0	0	5	8	4	9874	1	0	1	2	0	0	4
	F	1	1	1	0	0	0	0	0	1	2	8	6	0	4	9946	0	2	1	3	28
	P	13	5	2	1	1	8	3	2	5	1	2	2	1	1	9926	12	4	0	0	2
	S	28	11	34	7	11	4	6	16	2	2	1	7	4	3	17	9840	38	5	2	2
	T	22	2	13	4	1	3	2	2	1	11	2	8	6	1	5	32	9871	0	2	9
	W	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	9976	1
	Y	1	0	3	0	3	0	1	0	4	1	1	0	0	21	0	1	1	2	9945	1
V	13	2	1	1	3	2	2	3	3	57	11	1	17	1	3	2	10	0	2	9901	

Figure 82. Mutation probability matrix for the evolutionary distance of 1 PAM. An element of this matrix, M_{ij} , gives the probability that the amino acid in column j will be replaced by the amino acid in row i after a given evolutionary interval, in this case

1 accepted point mutation per 100 amino acids. Thus, there is a 0.56% probability that Asp will be replaced by Glu. To simplify the appearance, the elements are shown multiplied by 10,000.

Figure 2.2 An evolutionary transition rate matrix for amino acid substitutions⁵

⁵ Source: Dayhoff, Schwartz, and Orcutt (1978: 348)

In Chapter 3 I calculate an analogous musical transition rate matrix (Fig. 3.3) based on an analysis of 932 observed mutations in 172 pairs of highly related Child ballad melodic variants (>85% identity). These transition rate matrices are important because they provide data showing which types of evolutionary changes are more or less likely (see Ch.3). These data may help us to understand why music evolves as it does.

2-7. Conclusion

In this chapter I have shown that various aspects of musical microevolution can be measured quantitatively by adapting techniques from molecular genetics, particularly techniques for analyzing protein evolution. In the following chapters, I will apply these methods to larger and more diverse musical samples to test the generality of the trends shown in this chapter's *Scarborough Fair* example.

Summary

In this chapter I introduce a new method for quantifying aspects of musical evolution. This method builds off the tune family concept but adds quantitative rigour by adapting tools from molecular genetics. In particular, I highlight analogies between protein evolution and melodic evolution. The former can be modeled as sequences constructed from an "alphabet" of 20 amino acids, while the latter can be modeled as sequences constructed from an "alphabet" of 12 notes, corresponding to the equal-tempered chromatic scale. This makes it possible to adapt automated sequence alignment algorithms from molecular genetics to any music - Western or non-Western - that can be approximated by standard staff notation, and to make automated quantitative comparisons on scales far beyond the capabilities of unassisted humans. I demonstrate the process of measuring musical evolution using the example of a pair of related melodic variants of *Scarborough Fair* (Child ballad no. 2), and show the analogous process from protein family evolution using a pair of related variants of the human avian influenza H7N9 "bird flu" virus.

3. Large-scale analysis: 4,125 Child ballad melodic variants

In Chapter 2, I described how methods for measuring biological evolution can be adapted to measure musical evolution, using short examples. In this chapter, I test these methods on a larger sample to see if the rates and mechanisms of musical evolution follow general rules, as they do for biological evolution.

3-1. Background

Rates of biological evolution are governed by the three general evolutionary mechanisms discussed in Chapter 1: 1) inheritance, 2) variation, and 3) selection (Baer, Miyamoto, and Denver 2007). For example: 1) average mutation rates in RNA viruses (e.g., influenza) are very high because inheritance of RNA sequences is more error-prone than DNA replication (Duffy, Shackelton, and Holmes 2008), 2) transition rates among different amino acid types vary depending on mutational distance - amino acid transitions requiring multiple nucleotide substitutions are much less likely than those requiring only one (Dayhoff, Schwartz, and Orcutt 1978), and 3) purifying selection against deleterious mutations results in low rates of evolution at functional sites (e.g., certain protein-coding regions; Nei, Suzuki, and Nozawa 2010). Analogous general constraints have been identified in cultural evolution (Dawkins 1976; Richerson and Boyd 2005; Pagel, Atkinson, and Meade 2007; Lieberman et al. 2007; Rogers and Ehrlich 2008; Currie et al. 2010; Currie and Mace 2014). For example, functional components of Polynesian canoe design evolve more slowly than ornamental ones (Rogers and Ehrlich 2008).

Cultural evolutionary theory applied to music cognition leads to analogous predictions about rates of musical evolution. 1) Written transmission via direct copying of musical notation should evolve more slowly than oral transmission via singers teaching and imitating one another, due to the greater potential for error in oral transmission. 2) Substitutions between small mutational distances (e.g., 2nds) should be more common

than between large ones (e.g., 7ths), because smaller distances require smaller physical deviations in vocal/instrumental production and are less perceptually noticeable (Honing et al. 2015). 3) Notes with stronger functional roles (e.g., final notes, notes carrying stressed syllables) should evolve more slowly than less-functional ones (e.g., ornamental notes, unstressed notes), due to purifying selection against deleterious variation (e.g., interfering with the sense of melodic closure by failing to end on the tonic, or interfering with the meaning of the lyrics by deleting notes carrying important syllables; Bronson 1969; Kaneshiro 1990).

3-2. Musical sample

Early collectors such as Cecil Sharp and Alan Lomax believed that careful scientific comparison of folk songs would reveal general laws of musical evolution (Sharp 1907; Lomax 1968)¹. Particular attention was paid to the evolution of the "Child ballads", a canon of 305 families of British-American narrative songs that were deemed by Francis Child to be the most traditional (Child 1882-98/1904; Nettl 2015: 357-358). Bertrand Bronson (1959-72) compiled 4,125 variant Child ballad melodies notated between 1575-1972 (Fig. 3.1).

Through this full compilation, an abridged version with a comprehensive introduction (Bronson 1976), and a series of articles later compiled into a single book (Bronson 1969), Bronson attempted to qualitatively trace their histories and the forces that shaped the evolution of these Child ballads. In particular, Bronson argued that dynamic interaction between tunes and texts are crucial evolutionary mechanisms. Bronson offered impressive historical documentation of textual and melodic links, and expressed a desire for rigorous quantitative statistics like a "coefficient of change"

¹ Sharp (1907: x) wrote that "the main thesis of this book is the evolutionary origin of the folk-song", while Lomax entitled one of his major Cantometric articles "The evolutionary taxonomy of culture" (Lomax and Berkowitz 1972).

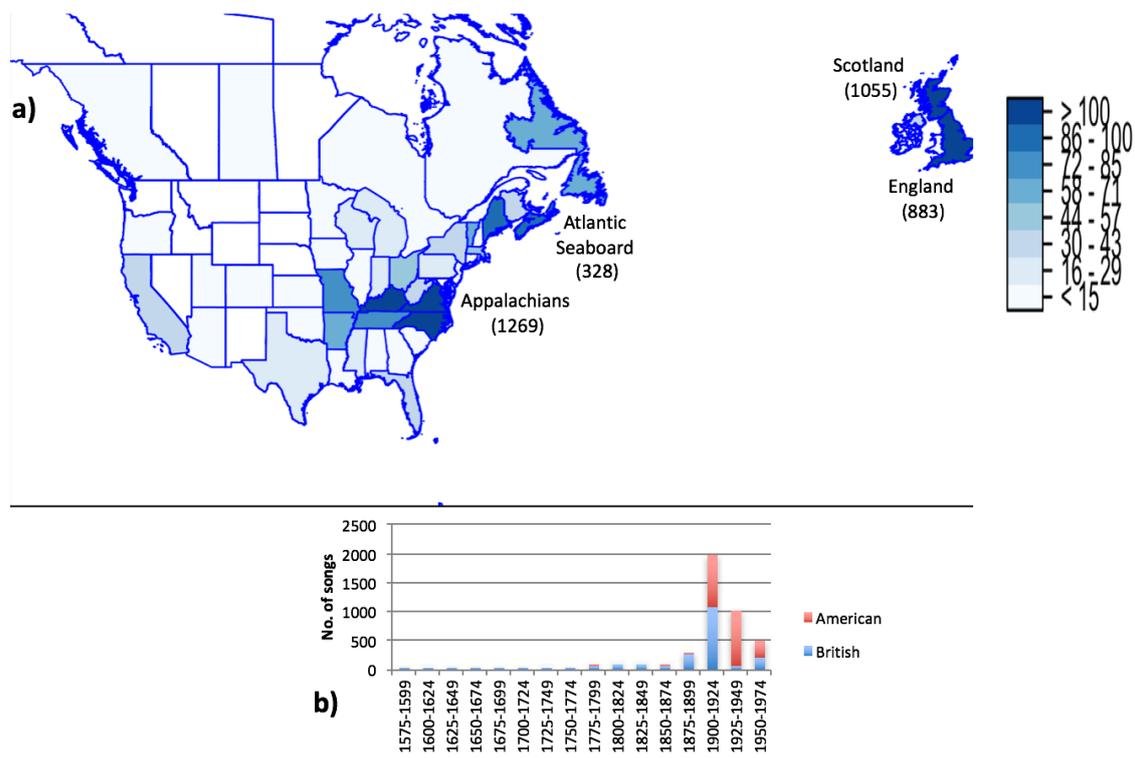


Figure 3.1 Geographic and temporal distributions of the sample of 4,125 Child ballad melodic variants²

(Bronson 1969: 61) analogous to a biological mutation rate. However, the actual quantitative analysis offered was limited to mechanical sorting of highly reduced skeleton melodies (containing only stressed notes from the 1st, 2nd, and 4th phrases) by crude 1960's punch-cards (cf. Fig. 3.2), and Bronson's exhaustive groupings of these melodies into tune families was explicitly subjective.

² Geographic (a) and temporal (b) distributions of the full sample of 4,125 Child ballad melodic variants compiled by Bronson (1959-72). Pre-20th century records are scarce because systematic documentation only began in the 20th century after the advent of audio recording technology.

a)

In Scar-let Town where I was born There was a fair maid dwellin' Made
 ev' - ry heart cry 'Well - a - day !' Her name was Bar - b'ra Al - len. All
 in the mer - ry month of May, When green buds they were swellin', Young
 Jemmy Grove on his death-bed lay, For love of Bar - b'ra Al - len.

b)

Figure 3.2 A sample Child ballad melodic variant and its coding on Bronson's IBM punch-card³

³ a) The original melody published by Lucy Broadwood (1904:265). Stressed notes coded in Bronson's skeleton melody are circled in red. b) Bronson's (1969:233) punch-card coding of this skeleton melody and its metadata. My brief interpretation of this coding follows (Bronson's full explanation and further examples are shown on Bronson 1969:181-184). *Metadata*. Child no.: 84 ["Barbara Allen"], Authority: JFS [*Journal of the Folk-Song Society*], Volume: 1, Date: [1]904, Collector: Bro[adwood], Singer: Gra[hame], Region: 1 [England], No. of phrases: 8, Phrasal scheme: [A]BABCDCB, Refrain scheme: none, Burden: none, Time signature: 3/4, Range: P[lagal], Mode: 3 [Ionian], Final note: 1 [tonic], Upbeat: N [dominant below tonic]. *Skeleton melody* (stressed notes from 1st, 2nd, and 4th phrases). 1st phrase: N1P2 [GCBD in my notation (cf. Ch. 2, p. 42)], 2nd phrase: 3O2W1 [EADC], 4th phrase: 3O2W1 [EADC].

The remainder of the twentieth century saw little progress in attempts to quantify musical evolution, with many skeptical of the idea of general laws of music evolution (see Ch. 1). Only in the last decade have theoretical and methodological advances in cultural evolution and the digital humanities made it feasible to rigorously test hypotheses about musical evolution on a large scale (van Kranenburg et al. 2007; MacCallum et al. 2012; Mauch et al. 2015; Savage and Atkinson 2015; Windram, Charlston, and Howe 2014).

3-3. Methods

Here I apply the methods developed in Chapter 2 to test the three preceding evolutionary hypotheses through a large-scale quantitative analysis of melodic evolution.

3-3-1. Coding

I manually coded all 4,125 melodic variants directly from the staff notations compiled by Bronson (1959-72), along with metadata about recording location, date, and other information (cf. Fig. 3.2b)⁴. For consistency, only the first appearance of the melody was coded, ignoring repeated verses whether or not they contained minor melodic variations. Melodies usually consisted of between four and eight phrases, each consisting of approximately 10 notes (mean melodic sequence length = 47.4 notes). The assignment of tonic (reference pitch coded as "C") followed Bronson's choice, which usually but not always corresponded to the final note. A small number (40) of obvious inconsistencies in Bronson's tonic assignment were corrected to avoid missing some highly related variants⁵.

⁴ See supplementary spreadsheet for full codings and metadata.

⁵ Noted in the "Comments" column of the Supplementary Information spreadsheet.

3-3-2. Similarity/alignment

All 8,505,750 pairwise similarities among the 4,125 melodic variants were automatically calculated using the methods described in Chapter 2 (Fig. 3.3).

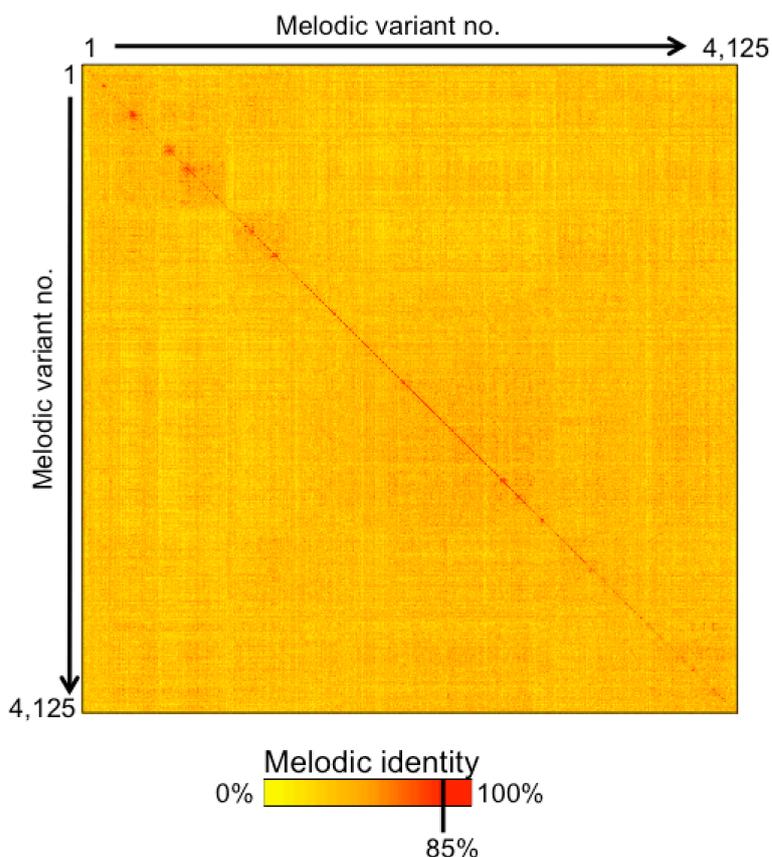


Figure 3.3 Seriated heatmap visualizing the 8,505,750 pairwise similarities among the 4,125 melodic variants⁶

Percent identity calculations revealed 434 variants (i.e., 10.5% of all 4,125 Child ballad melodic variants) that were highly similar to at least one other variant by greater than 85%. I chose this 85% threshold because it was used in similar analyses of protein

⁶ Only 172 pairs displaying greater than 85% identity (dark red) were used to calculate mutation rates, in order to avoid errors due to successive mutations and alignment error.

evolution to minimize chances of miscounting successive mutations (Dayhoff, Schwartz, and Orcutt 1978) and to avoid alignment error, which is particularly important in melodic evolution given the high rate of insertion/deletion (see Chapter 4).

These 434 variants included 254 variants that formed 127 unique pairs, as well as 180 variants falling into 45 larger groupings containing between 3-15 variants that all showed greater than 85% identity to one another. To ensure consistency in the analysis when comparing against the 127 unique pairs, I used only the most similar pairs within each of these 45 groups, giving a total of 172 highly related pairs (encompassing a total of 15,786 notes) used to calculate evolutionary rates⁷. The automated alignments of these 172 highly related pairs were manually checked against the original score notation and corrected where necessary based on rhythmic information (which is not incorporated in the automated sequence alignment).

3-3-3. Mutation rate calculation

In some pairs, it is likely that the more recent variant directly descends from the older variant (e.g., variants known to be transmitted from parents to children or teachers to students, or known to be reprinted from older editions). In cases where the chain of

⁷ Of these 172 pairs, 149 were part of the same Child ballad text family (i.e., had similar lyrics), while the remaining 23 represented nearly identical melodies accompanying unrelated texts. While similar methods could be used to investigate the parallel evolution of variant lyrics and their coevolution with melodies, the present analysis focuses only on melodic evolution without regard for lyrics and without regard for whether the singers themselves believe the melodies/lyrics to be related. Future analysis of such factors and the extension of the current study to include larger families and less related variants in addition to these highly related melodic pairs should help to better understand the mechanisms described here.

transmission is unknown, it is unclear whether more recent variants are directly descended from older variants or whether both variants share a more ancient common ancestor (or ancestors) or an intermediate form that may or may not have been recorded.

Because of this uncertainty, I chose to adopt the simpler assumption and modeled the older variant as the direct ancestor for the purpose of calculating evolutionary rates. Thus, mutation rates per site per year (μ) were calculated from aligned sequences as in Chapter 2 by assuming that the site of the older sequence represented the ancestral state, with elapsed time calculated as the number of years intervening between the two recording dates (mean time = 23.4 years). For ambiguous dates given by Bronson as ranges (e.g., 1792-1794), the average age was used (e.g., 1793). For variants recorded during the same year, a time of 0.5 years was used, and the variant appearing first in Bronson's compilation was treated as the older one⁸. Significance of predicted differences between average mutation rates was evaluated using paired t-tests (one-tailed).

The assumption of direct ancestry is likely to systematically overestimate the true absolute mutation rate, since there are likely some situations where the true ancestral form was more ancient. However, this does not bias my conclusions, since my hypotheses are about relative rates (e.g., stressed notes more resistant to change than non-stressed notes), not absolute ones.

⁸ Because the year of recording was consistently recorded, but not necessarily the date, and because Bronson's ordering within tune families was generally based on a combination of known and assumed chronology

3-3-4. Transmission fidelity

Pairs of related variants were classified as transmitted by oral (n = 135 pairs) or written (n = 37 pairs) transmission based on whether or not the more recent variant was recorded from a live performance. This operationalization was chosen because singers tend to learn their songs from other singers, whereas notations printed in collections without attribution to a particular live performance tend to be copied from earlier notation (Bronson 1959-72).

3-3-5. Functional role

Because lyrics in my sample were not usually directly matched with their notes⁹, coding of functional position followed the standard approach of being based on rhythmic accent rather than syllable accent (Bronson 1969). Notes falling on the downbeat of all bars and on the strong middle beat of duple (4/4, 2/4, 6/8, or 12/8; Savage et al. 2012) bars were coded as rhythmically accented (in bold), as these beats usually correspond to accented syllables. All other sites (notes or gaps) were treated as unaccented. Grace notes (*appoggiatura* and *acciaccatura*) were coded as ornamental (in italics). Assignment of stressed and final notes was based on the older melody, while any site in either the older or younger melody containing a grace note was treated as ornamental (because all melodies contained stressed and final notes but not all melodies contained ornamental ones).

Only 34 of the 172 pairs contained ornamental notes in one or both variants, thus only these pairs were used to calculate evolutionary rates for ornamental notes (these 34 pairs contained 92 sites where one or both notes was ornamental; 51 of these ornamental sites changed). All other functional positions were found in all pairs, and

⁹ Generally, melodies for a single verse were printed devoid of lyrics and then lyrics for all verses were printed below the melody.

thus rates for final, accented, and unaccented notes were calculated using all 172 pairs. Re-running the analyses of all functional positions using only the 34 pairs containing ornamental notes to ensure consistency replicated the same patterns of rate variation.

3-3-6. Mutational distance

For each pair, a 13x13 note transition matrix was constructed to show transitions among the 12 notes ("A"- "G") and gaps ("-"; see Chapter 2, especially section 2.6). These transitions were then averaged across all 172 pairs to give a full transition rate matrix (Fig. 3.4).

Substitutions were grouped by melodic distance according to standard musical theory. Raising or lowering the pitch by 1-2 semitones were classed as 2nds, 3-4 semitones as 3rds, 5 semitones as 4ths, 6-7 semitones as 5ths, 8-9 semitones as 6^{ths}, and 10-11 semitones as 7^{ths} (note that the ambiguous decision of whether tritones [6 semitones] should be classed as 4ths or 5ths does not affect my results, since no tritone substitutions were observed). This required manually checking the original score notation octave to determine whether a substitution was rising or falling (e.g., a substitution from C to D could represent rising by a 2nd or falling by a 7th). Substitutions of an octave (12 semitones) or more were transposed to the equivalent distance within the octave to be consistent with the perceptual principle of octave equivalency¹⁰.

¹⁰ Note that losing information about octaves makes it more difficult to investigate questions about melodic range, including the distinction between plagal vs. authentic ranges that Bronson (1959-72, 1969) believed to be important.

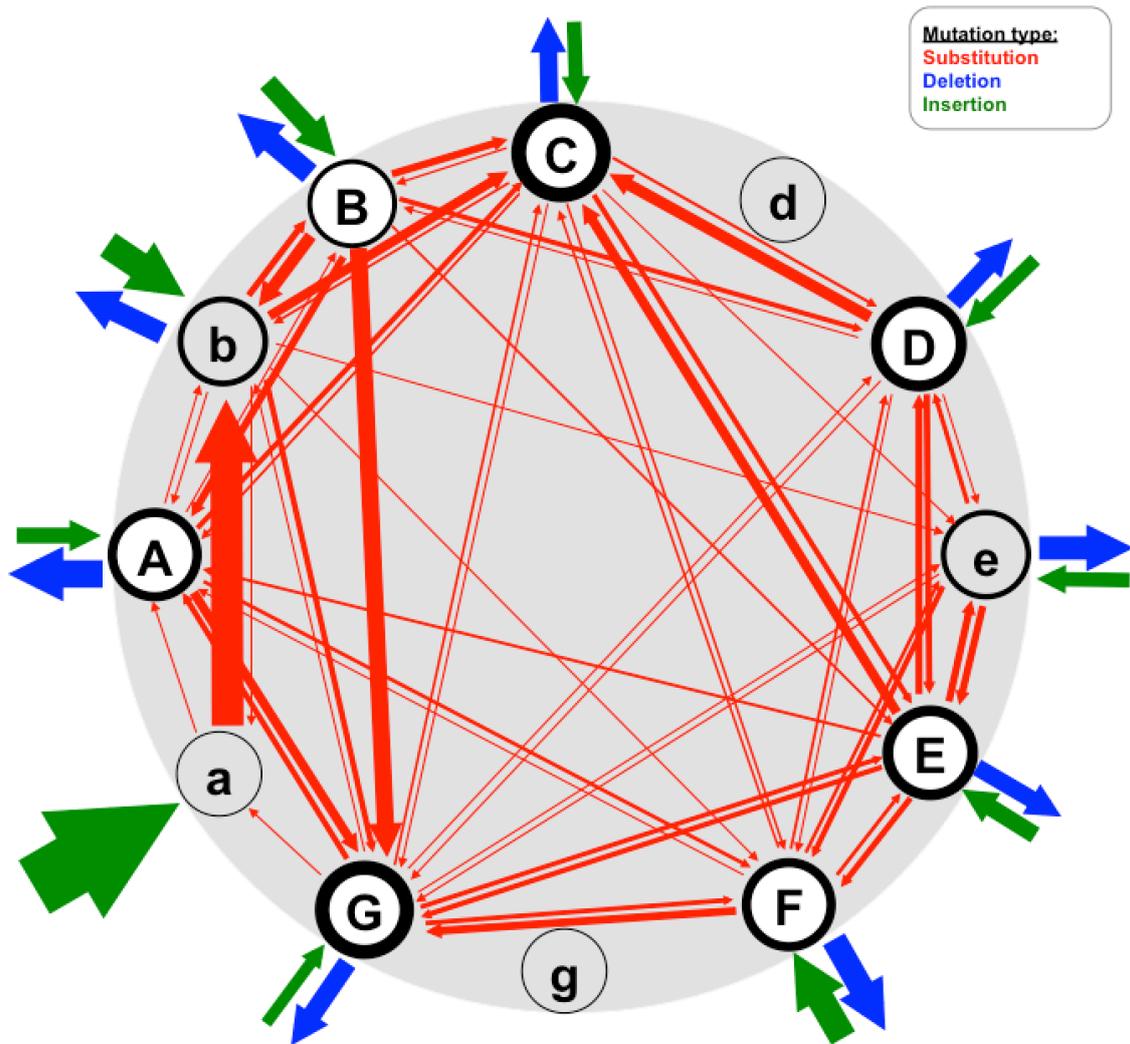


Fig. 3.4 Transition probabilities among the 12 musical notes¹¹

¹¹ Arrow widths are proportional to transition probabilities, while the width of the circle outlining each note is proportional to the square root of that note's frequency. Deletions (blue arrows) and insertions (green arrows) are more common than substitutions (red arrows). The notes "d" (semitone above the tonic) and "g" (tritone above the tonic) were very rare, and no transitions involving them were observed. In general, small mutational distances (i.e., substitutions around the outside of the circle) were more common than large ones (i.e., substitutions crossing the middle of the circle), as shown more clearly in Fig. 4.5b.

3-4. Results

3-4-1. Transmission fidelity

As predicted, written transmission evolved more slowly on average than oral transmission (Fig. 3.5a; average mutation rate (μ) = .018 and .077 per site per year, respectively, $P < 1 \times 10^{-5}$). For example, the slowest non-zero mutation rate of any pair ($\mu = 9.99 \times 10^{-5}$ per site per year) involved only a single change in a 72-note melody over the course of 139 years of written transmission. This appeared to be sustained by periodic reprinting of identical versions every few decades between 1790 and 1904, with the change only appearing during the final 25 years between 1904 and 1929 (Bronson 1959-72: 214 [vol. IV]).

3-4-2. Mutational distance

Also as predicted, substitutions were much more common between small melodic distances than large ones (Fig. 3.5b). Frequency of substitutions was strongly inversely correlated with melodic distance with the smallest melodic intervals (2nds) outnumbering the largest intervals (7ths) by a factor of over 100. Spearman's correlation coefficients were calculated between mutational distance measured in 2nds through 7ths (i.e., 2-7) and total number of substitutions, giving a strong and significant correlation of $r_s = -.94$ ($P < .01$; $n = 6$).

Measuring melodic distance in raw semitones (i.e., 1-11) gave only slightly weaker correlations of $r_s = -.84$ ($P < .001$; $n = 11$) due to the interaction between melodic distance and tonal relationships (see Fig. 3.4), but were still very strongly and significantly correlated. This suggests that the correlation between mutational distance and substitution frequency holds regardless of the way mutational distance is categorized.

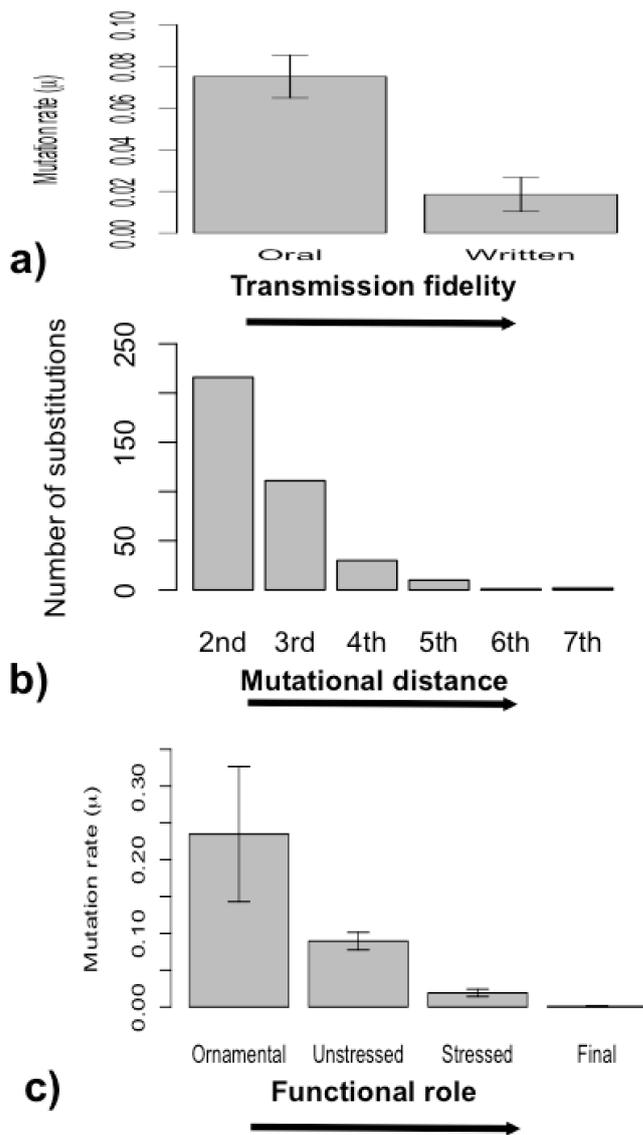


Fig. 3.5 Transmission fidelity, mutational distance, and functional role predict rates of musical evolution¹²

¹² **a)** Melodies evolve more slowly through written transmission ($n = 37$ pairs) than oral transmission ($n = 135$ pairs; $P < 1 \times 10^{-5}$). **b)** Substitutions are more common between small mutational distances (e.g., 2nds) than large ones (e.g. 7ths; $r_s = -.94$, $P < .01$). **c)** Final notes ($n = 172$ pairs) are more resistant to change than stressed notes ($n = 172$ pairs, $P < .001$), which are in turn more resistant than unstressed notes ($n = 172$ pairs, $P < 1 \times 10^{-7}$), which are more resistant than ornamental notes ($n = 34$, $P = .053$). All error bars represent the standard error of the mean.

3-4-3. Functional role

Figure 3.5c confirms my predictions regarding the effect of functional role on rates of musical evolution. Mean rates vary by a factor of almost 300 between the most-stable final notes ($\mu = .00086$ per site per year) to the least-stable ornamental notes ($\mu = .24$). Ornamental positions were most likely to change, almost always by insertion or deletion. This reflects the fact that singers are free to add or remove ornamental embellishments largely without affecting the lyrics or overall melodic contour. On the other hand, only two out of the 172 final positions changed. In one case, the entire final 6-note phrase was deleted as a unit. In the other, the final phrase changed key, modulating to the relative minor. In both cases, the new version still ended on a tonic, so these exceptions prove the rule that there is strong selection against violating musical closure by ending on a note other than the tonic.

3-4-4. Confirmatory analyses

To determine whether my findings could have been biased by the composition of the sample or assumptions of the analyses, I performed a number of confirmatory analyses.

It is possible that the assumption of direct ancestry may in some cases mistakenly identify the older site as ancestral when the ancestral state may in fact be represented by the newer variant. This should not affect my conclusions, since my hypotheses do not posit directional trends. Regardless of which sequence is treated as older, melodic distance of substitutions is always the same, functional position is usually the same, and assignment of oral vs. written transmission is usually the same. However, to ensure that my results were robust to this assumption, I re-ran the analyses reversing the assumption so that the newer variant was instead assumed to represent the ancestral state.

To ensure that the observed trends were not biased by the geographic or temporal

composition of the sample, I also re-ran the analyses separately for sub-samples separated by geography and time period (cf. Fig. 3.1). For geography, "British" (n = 98 pairs, including England, Scotland, and Ireland¹³) and "American" (n = 74 pairs, including USA and Canada) variants were analyzed separately. For pairs containing one British and one American variant, classification was based on the younger variant, as this gave a more even split (using the older variant would have given sub-sample sizes of 107 and 65 pairs, respectively).

For time, the samples were split into two time periods based around the median date of the older variant (1907). Thus, the older subsample consisted of pairs whose older variant was recorded during or before 1907 (n=91) and the younger subsample consisted of pairs whose older variant was recorded after 1907 (n=81).

All of these analyses confirmed my predictions, replicating my original results in terms of both the direction of the differences and their significance. In other words, rates of musical evolution in our sample followed the same patterns of inverse correlation with transmission fidelity, mutational distance, and functional role regardless of geography, time period, or the ancestry assumptions of our analysis. All of these differences were significant ($P < .05$) across all analyses, with the exception of ornamental sites. In all of my analyses, ornamental sites evolved more than twice as rapidly as unaccented sites on average, but this difference was not significant in any of my analyses (including my main analysis), due to the small relative sample size of ornamental sites (which were only present in 34 pairs, whereas all other types of functional sites are present in all 172 pairs). Thus, all confirmatory analyses exactly replicated the patterns of our main analysis and their statistical significance.

¹³ Note that Ireland has been politically independent since 1922.

3-5. Discussion

My analyses confirmed all three predictions of general rules of musical evolution paralleling the three general mechanisms of transmission fidelity, mutational distance, and functional role in biological evolution. These predictions held regardless of geographic location, time period, or the assumptions of the ancestry relationships between variants. This suggests that my findings are not specific to the contexts of this sample but are general characteristics of melodic evolution in British-American folk song. Since my predictions are based on general mechanisms of music cognition that are likely to be universal (Brown and Jordania 2013; Savage, Brown, et al. 2015), I hypothesize that they should also apply universally across cultures and genres. In Chapter 4, I explore this hypothesis using a number of case studies from different cultures and genres.

Further exploratory analyses of the transition rate matrix (Fig. 3.4) revealed several dynamics specific to musical evolution. Evolution in this musical sample is dominated by insertion/deletion ("indels") rather than substitution (564 vs. 368 sites, respectively; see Fig. 3.4), whereas the opposite is true of biological evolution (Baer, Miyamoto, and Denver 2007; Duffy, Shackelton, and Holmes 2008). The main reason indels are rare in biology is that the nature of the genetic code is such that indels that do not encompass exact multiples of three DNA nucleotides result in "frame shifts" that completely change the types of amino acids produced downstream. In fact, music might be predicted to observe analogous frame shifts of meter, such that insertion or deletion of notes would disrupt the series of strong and weak accents. However, the fluid nature of musical rhythm means that it is easy for musicians to add or remove ornamentation without disturbing the overall meter, by lengthening or shortening the duration of the surrounding notes (as demonstrated again in "Scarborough Fair" in Chapter 2).

Melodic substitutions (Fig. 3.4) are affected by tonal relationships, which are analogous to but different from the chemical relationships that affect amino acid

substitutions. The notes of the diatonic major scale (upper-case letters) were all more common than their minor variants (lower-case letters), and substitutions between major and minor scale degrees were rare (only 77 out of all 368 substitutions), even to small melodic distances. For example, although substitutions in Scarborough Fair to "d" (i.e., semitone above the tonic) or "g" (tritone above the tonic), respectively, would also have been 2nds, those scale degrees are neither part of Scarborough Fair's Dorian scale nor the scale of almost any traditional British-American music. In fact, substitutions involving "d" or "g" were not observed once throughout my analysis (these notes themselves appeared in a handful of melodies, but were not involved in any mutations). I did observe substitutions between major and minor scale degrees, but these were usually between the major and minor versions of the 3rd or 7th scale degrees (e/E or b/B), all of which are common throughout the British-American folk repertoire. In some cases, these occurred via a sudden tonal shift throughout the entire melody (e.g., all minor 3rds ["e"] of a melody simultaneously majorized [to "E"]), analogous to sound shifts in linguistics or concerted evolution in biology (Hruschka et al. 2015). The details of tonal relationships are likely to depend partly on universal cognitive constraints on scale construction and partly on culture-specific patterns of the types of scales used (Deutsch 2013; Brown and Jordania 2013; Savage, Brown, et al. 2015).

One intriguing trend in my analysis was the fact that deletions outnumbered insertions (318 vs. 246 sites, respectively). This trend was consistent regardless of whether the transmission mode was through oral (219 vs. 190 sites) or written transmission (99 vs. 56 sites). This is surprising because traditional theories of musical evolution in particular and evolution in general posit progressive evolution from simple to complex (Spencer 1875; Sachs 1943; Nettl 2015; Currie et al. 2010; McShea and Brandon 2010), which should predict the opposite pattern of more insertions than deletions. However, a predominance of deletions is consistent with the findings of cultural transmission chain experiments, which show a gradual simplification of content over the course of transmission (Bartlett 1932; Mesoudi and Whiten 2008). Early tune family scholars were ambivalent about the role of insertion vs. deletion, with some case studies

showing substantial deletions and other case studies showing substantial insertions (Bayard 1954; Bronson 1969; 町田 ; 竹内 1965).

However, it is important to note that my finding of a predominance of deletions over insertions is the only result from my analysis invoking directionality. Thus, unlike my other findings, it is not robust to the ancestry assumptions described in the methods section (since reversing the ancestry assumptions as done in the confirmatory analyses would reverse the result to favour insertions over deletions). Thus, my data suggesting a tendency toward simplification should be treated as suggestive but not conclusive, and require future studies to properly investigate (see Chapter 4).

The similarities and differences I have identified between musical and biological evolution evoke the heavily debated question: how analogous are cultural and biological evolution (Dawkins 1976; Richerson and Boyd 2005; Fracchia and Lewontin 1999; Rahaim 2006)? My analysis shows that they are analogous enough that methods can be profitably adapted between the two, but not enough that this can be done blindly. Although the observed average absolute rates of musical evolution (on the order of 10^{-2} per site per year) were much faster than most organisms, they were comparable to rates of RNA virus evolution, which range from approximately 10^{-2} - 10^{-5} per site per year (Duffy, Shackelton, and Holmes 2008).

A crucial difference is that, unlike genes, cultural evolution is the result of conscious innovation as well as random mutation. Most of the changes identified in this analysis represented small, isolated changes at functionally unimportant sites that could easily be the result of unconscious copy-errors, especially through the error-prone process of oral transmission. However, a few changes, such as major insertions, deletions, or substitutions of entire phrases, seem almost certain to have been intentional. Such conscious innovation or "guided variation" can be difficult to distinguish from (and can work in tandem with) the effects of selection, highlighting the need for better understanding of the role of individual agency, and for complementary analyses, such

as controlled laboratory studies (Mesoudi and Whiten 2008; Kirby, Cornish, and Smith 2008; Claidière, Kirby, and Sperber 2012; Leroi et al. 2012).

3-6. Conclusion

Given the importance of artistic creativity in human evolutionary history, understanding the dynamics of the cultural evolution of creative arts such as music represents a difficult but important challenge (Richerson and Boyd 2005; Fogarty, Creanza, and Feldman 2015). My analysis offers specific mechanisms and quantitative evidence to show that even a creative art like music is subject to strong evolutionary constraints. In the next chapter I will explore whether the principles I have identified for British-American folk song generalize to other cultures and genres.

Summary

In this chapter, I test hypotheses about general trends in musical evolution by applying sequence alignment methods developed in Chapter 2 to a large sample of 4,125 British-American "Child ballads" notated between 1575-1972. I automatically identified and manually analysed 172 pairs of highly related (>85% identity) melodic variants encompassing a total of 15,786 notes. Mutation rates varied greatly (over 100-fold) in ways that followed my predictions: 1) written notation evolves more slowly than oral transmission, 2) functional notes are more resistant to change than ornamental notes, and 3) substitutions are more likely to occur between small melodic distances than large ones. This confirms the hypothesis that even a creative art form such as music is subject to evolutionary constraints analogous to those governing the evolution of genes, languages, and other non-artistic domains of culture. Furthermore, in contrast to the predictions of Spencerian evolutionary progress, this sample tended to decrease rather than increase in complexity, with deletions modestly outnumbering insertions.

4. Cross-cultural and cross-genre case studies

In the previous chapter, I showed that the evolution of highly related British-American folk song variants follows several general rules. But do such rules apply to more complex examples from different cultures and genres? In this chapter, I will explore the generality of these proposed rules of melodic evolution using diverse case studies drawn from British-American and Japanese folk, art, and popular traditions to. These case studies involve not simply highly related pairs with almost identical melodies, lyrics or instrumentation as in the previous two chapters, but diverse melodies that have been adapted to completely different lyrics and/or instrumentation to the point where their connections to the original melodies are almost unrecognizable in some cases. After detailed descriptions of the mechanisms of each case study, I will quantitatively compare the patterns across the case studies to explore the degree to which trends are consistent across cultures/genres (these comparisons are summarized in Table 1.1).

4-1. Case study 1 (Folk: British-American): Splitting of *Lady Cassiles Lilt* (1620) into *Edward* (1931) and *The Bonnie House o' Airlie* (1960)

My first case study will be drawn directly from Bronson's (1959-72) corpus of Child ballads analyzed in Chapter 3, but involving a more complex example than the highly related variants analyzed in that chapter. Throughout his compilation of 4,125 melodic variants for the 305 families of Child ballad texts, Bronson noted the appearance of several large tune families that encompassed many different texts. The largest of these was one he labeled the "Cassilis" family that was common in the US Appalachians, where it accompanied many unrelated texts (e.g., Child #4 [*Lady Isabel and the Elf Knight*], #13 [*Edward*; see Fig. 4.1], #200 [*Geordie*], #216 [*Clyde's Water*], and many more). However, the oldest documented appearance of this tune family was not in America, nor even accompanying a Child ballad text, but in a 1620 Scottish instrumental melody entitled *Lady Cassiles Lilt* (Fig. 4.1).



Figure 4.1 Melodic evolution in British-American folk song pt. I (*Lady Cassiles Lilt* becomes *Edward*)³⁷

The widespread Cassilis family variants are generally made up of four phrases that repeat for each stanza, like most English ballads. The *Edward* variants in Figure 4.1 are slightly different in being made up of five phrases, where the addition of the final fifth phrase is achieved by repeating both the melody and the text of the preceding fourth phrase. However, the original *Lady Cassiles Lilt* is a so-called "double strain" melody, in which the full 8-phrase melody is made up of two different four-phrase strains. Only the second of these strains gave rise to Bronson's Cassilis family, with the first strain being completely deleted between the 1620 *Cassiles* and its first documented appearance with the text of *Edward* in 1918.

³⁷ The 1620 melody for *Lady Cassiles Lilt* is from the instrumental manuscript of John Skene in the National Library of Scotland (Bronson 1959-72: 201 [vol. III]). The 1918 melody for *Edward* (Child ballad no. 13) was recorded by Cecil Sharp from the singing of Mrs. Mary Gibson in North Carolina, USA (Bronson 1959-72: 241 [vol. I]). The 1931 melody (also for *Edward*) was recorded by Vance Rudolph from the singing of Mrs. Emma L. Dusenbury in Arkansas, USA (Bronson 1959-72: 242 [vol. I]). Cf. Ch. 2 for explanation of how musical notations (top) are coded as aligned sequences (bottom).

There is at least one group of melodies, however, that retained parts of both the first and second strains of *Lady Cassiles Lilt*, (Fig. 4.2). Here, the entire 8-phrase tune was adapted to the text of *The Bonnie House o' Airlie* (Child #199) in 1894, after which phrases 3-6 were deleted to create a 4-phrase version recorded in 1960.

Thus, over the course of three centuries of evolution, the melody of *Cassiles* diverged into at least two lineages so different that they retained only 6 of the original 85 notes in common ("CAGF", "D", and "C" from what were originally the 7th and 8th phrases). Yet it is possible to trace the sequence of insertions, deletions, and substitutions of each individual note and/or phrase that gave rise to these differences (Figs. 4.1 and 4.2).

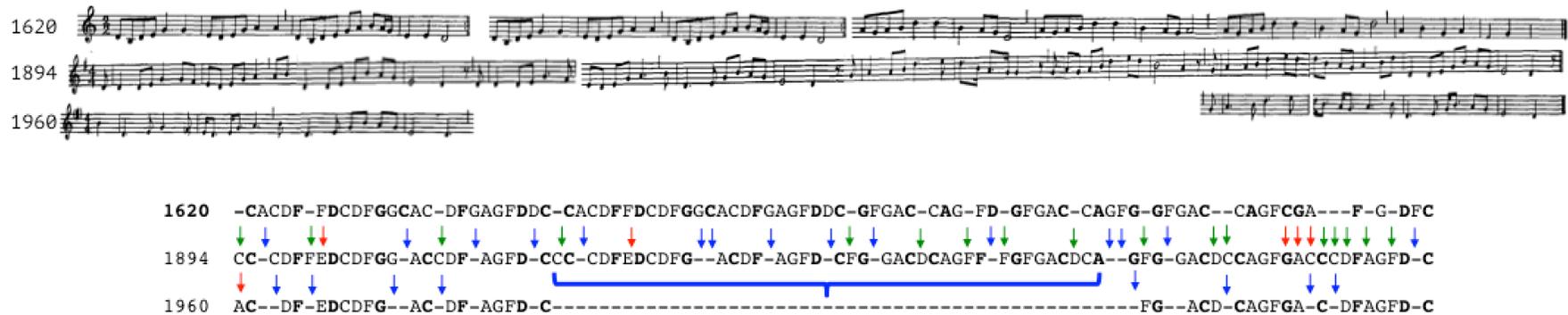


Figure 4.2 Melodic evolution in British-American folk song pt. II (*Lady Cassiles Lilt* becomes *The Bonnie House o' Airlie*)³⁸

³⁸ As in Fig. 4.1, the 1620 melody for "Lady Cassiles Lilt" is from the instrumental manuscript of John Skene in the National Library of Scotland (Bronson 1959-72: 201 [vol. III]). The 1894 melody for "The Bonnie House o' Airlie" was published by George Eyre-Todd in *Ancient Scots Ballads* (Bronson 1959-72: 196 [vol. III]). The 1960 melody for "The Bonnie House of Airlie" was sung by Scottish singer Isabel Sutherland and published by Selection Records Ltd. in New York, USA (Bronson 1959-72: 196 [vol. III]).

4-1-1. Simplification by phrase deletion

In both cases, half of the original 8-phrase tune was deleted to condense a double-strain tune into a single-strain one. However, different halves were deleted in each case. In one case (Fig. 4.1), this major deletion was accompanied by the addition of a single phrase at the end by repetition of the previous phrase.

As a result, deletions strongly outnumbered insertions (124 to 27) over the course of *Cassiles* splitting into *Edward* and *Airlie*. This is consistent with a general trend for deletions to outnumber insertions found in Chapter 3, and contradicts general assumptions of a tendency for music to evolve from simple to complex. Insertions and deletions also greatly outnumbered substitutions (11), which is also consistent with the findings and mechanisms discussed in Chapters 2 and 3.

4-1-2. Adaptation to new text by note insertion/deletion

The adaptation of the melody to different texts is facilitated by the conventions of poetic meter. English ballads tend to be made up of four-line stanzas in which the first and third lines contain four stressed syllables and the second and fourth contain either three or four. Thus, a melody that fits the rhythmic stresses of one text can often be adapted with minor rhythmic alterations to fit another. For example, the first phrase of the second *Cassiles* strain contains four rhythmic stresses, which is the same number of stresses in the corresponding phrase of *Edward* ("What **blood** is **that** all **on** your **shirt**?") and *Airlie* ("The **Duke** o' Mont-**rose** has **writ**-ten to Ar-**gyle**").

However, the number of unstressed syllables and notes is more variable, and this requires more flexibility in inserting/deleting notes as necessary to accommodate different texts. For example, the *Edward* line above contains 8 syllables (four stressed, four unstressed), while the *Airlie* line contains 11 (four stressed, seven unstressed). Therefore, the corresponding *Edward* melodic phrase requires only 8 notes

(FGACCAGF), while the *Airlie* melody requires 11 notes to accommodate the 11 syllables (FGGACDCAGFF). The original *Cassiles* instrumental phrase contained 10 notes (GFGACCAGFD), thus requiring a combination of both insertions and deletions of notes to accommodate the new texts (Figs. 4.1 and 4.2). Such interactions between melodies and lyrics represent a major functional mechanism of folk song evolution (Bronson 1969).

4-1-3. Rhythmic stress and mutation rate

The example of *Cassiles* evolving into *Edward* and *Airlie* is consistent with the findings in Chapter 3 that stressed notes are slightly more likely to mutate than unstressed ones (the average unstressed to stressed mutation rate ratio of 1.9 is more than the neutral ratio of 1 if stress had no effect on mutation rate). However, this effect is not as strong as in the other Child ballad examples in Chapter 3, where stressed notes tended to be more than four times more resistant to change than unstressed ones.

I suspect two reasons for this weaker effect: 1) the massive deletions involved in the *Cassiles* example affect both stressed and unstressed notes equally, thus masking potential differences in the rest of the tunes. 2) The switch from instrumental tune to song text requires a change from a melody with accented downbeats to a song with iambic poetic meter (i.e., the first syllable tends to be weak followed by a strong second syllable). Thus, there is a contradiction between the strong instrumental downbeat and the weak song opening syllable. One way to resolve this is to delete the stressed opening note (as occurs in the *Cassiles* to *Edward* deletion discussed above), increasing the overall mutation rate for stressed notes.

4-1-4. Melodic distance and mutation rate

The role of melodic distance in this case study is consistent with the analyses of Chapter 3 in showing that almost all of the observed substitutions involve small

melodic distances (mean substitution interval size = 2.5 semitones). Ten out of the 11 substitutions were either 2nds (e.g., G to A) or 3rds (e.g., A to C), with the remaining substitution constituting a 4th (C to G).

4-1-5. Cassiles summary

With some caveats, the general evolutionary principles developed in Chapters 2 and 3 apply to the splitting of the 1620 Scottish instrumental melody *Lady Cassiles Lilt* into the almost completely different variants of *Edward* and *The Bonnie House o' Airlie* sung in the USA in the 20th century. The absolute and relative mutation rates observed in this process are quantified in the first two columns of Table 4.1.

I will now describe similar analyses of case studies of melodic evolution in different cultures/genres and compare the resulting rates and mechanisms (in the remaining columns of Table 4.1).

4-2. Case study 2 (Folk: Japanese): Merging of *Hirado Bushi* and *Komoro Magouta* into *Esashi Oiwake*

For my second case study, I will describe the evolution of the Japanese folksong *Esashi Oiwake*. I chose this example because: 1) it is often considered the most famous and most sophisticated Japanese folksong (it is sometimes called the "king of Japanese folk song" (「民謡の王」), 2) it is part of a large tune family whose evolution has already been qualitatively documented in detail (町田；竹内; Hughes 2008: 108-118), and 3) because I have personal experience learning it and performing it at the annual national competition (Figs. 4.3).



Figure 4.3 Me performing at the *Esashi Oiwake* national competition³⁹

4-2-1. Background

In contrast to the example of *Cassiles* splitting into two songs discussed in the first case study, *Esashi Oiwake* evolved through a merging of two formerly independent melodies. One of these melodies had its origins as an unaccompanied, non-metric work song sung solo by pack-horse drivers (馬子) as they led their horses through the mountains of Shinano (now Nagano prefecture, central Japan). *Komoro Magouta* (小諸馬子唄) represents a surviving melody thought to be close to this original style. This melody became gradually more elaborately ornamented and acquired *shamisen*

³⁹ I (center) was one of several hundred performers who passed the regional qualifying competitions to be eligible to perform at the national competition held in Esashi, Hokkaido, during September 19-21, 2015. My teacher, Matsunaga Tatsuo (left) sang the unpitched interjections (ソイ掛け) between phrases, while Suetake Tadao (right) played the *shakuhachi* accompaniment. Unfortunately, I was not among the 50 singers to advance to the grand final the following day. Source:

<https://youtu.be/3fu7GONIM8Q>

accompaniment as it was transmitted between a variety of singers including pack-horse drivers, prostitutes (飯盛女), and sailors to become the main melody (本唄) of *Echigo Oiwake* (Echigo is now Niigata prefecture, northeast Japan) and eventually also the main melody of *Esashi Oiwake* (the town of Esashi is on the northern-most Japanese island of Hokkaido).

The other melody that now appears as a prelude (前唄) and coda (後唄) before and after the main melody also originated as an unaccompanied work song, although in this case a metric one sung by groups of whalers in Kyushu (southwestern Japan). Hirado Bushi (平戸節) represents a surviving melody similar to this ancestral form. It followed a similarly convoluted route to Echigo, where it was added to the main melody of *Echigo Oiwake* as a coda (合の手), since it was easier for audiences to sing along with than the more complicated main melody. Eventually, *Esashi Oiwake* came to include the coda not only after the main melody but also as a prelude (前唄). In a famous 1912 Tokyo concert, Hirano Genzaburo performed *Esashi Oiwake* accompanied by *shakuhachi*, which gradually came to supplant the *shamisen* as the usual preferred form of accompaniment. At some point during this process the metric rhythm of the original whaling song came to conform to the non-metric rhythm of the main melody, so that all parts of *Esashi Oiwake* are now sung without any clear beat (Koizumi Fumio (小泉 1984/2009) named his canonical non-metric type "Oiwake" after this song).

A simplified overview of the full evolution of *Esashi Oiwake's* melodic form is shown in Fig. 4.5. Detailed analysis of individual note changes are shown in Figs. 4.6 (prelude) and 4.7 (main melody).

In the course of its evolution, each phrase has tended to become longer and more ornamented, to the point where it approaches the physical limitations of the singer's breath capacity. Indeed, singers in competitions are automatically disqualified if they fail to sing the first 25-second phrase in a single breath (a fate I narrowly avoided).

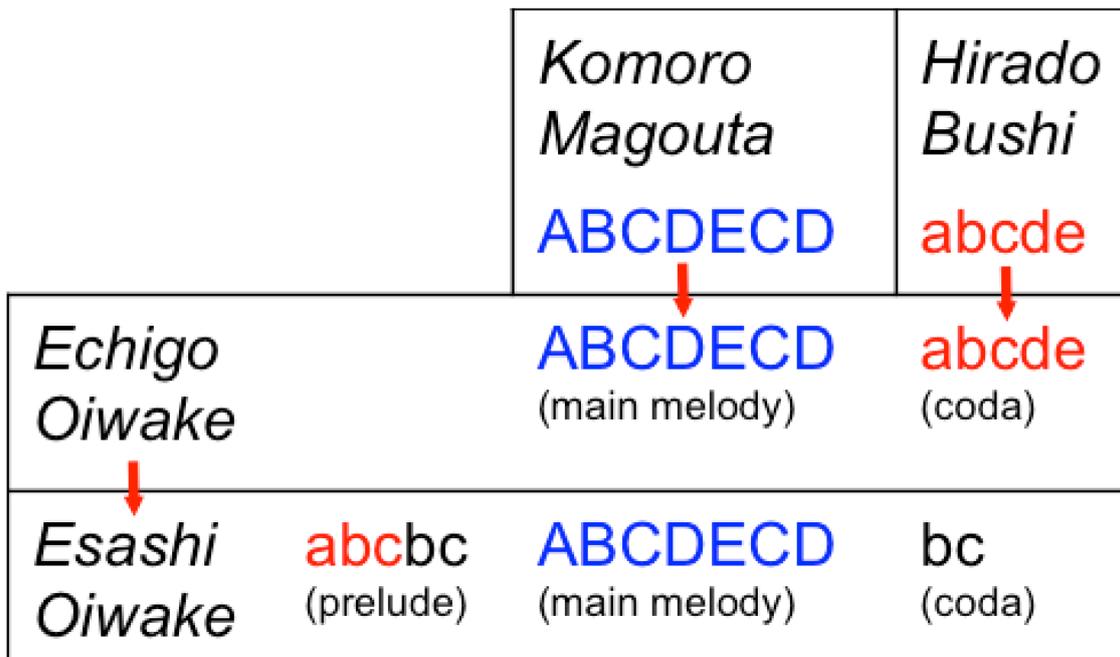


Figure 4.5 Melodic evolution in Japanese folk song pt. I (simplified overview of evolution of *Esashi Oiwake* melodic form)⁴⁰

Ironically, the full song has now become too long for most performance contexts, with the entire combination of prelude, main melody, and coda taking approximately 8 minutes. Thus, most performances, including the national competition, focus only on the main melody, which takes approximately 2.5 minutes to sing, and is the only part of the song to have been formally codified into prescriptive notation. Performances of the full song with prelude and coda are generally reserved for special occasions, such as guest performances by previous champions.

After the collapse of the fish stock in Esashi at the end of the 19th century, local leaders

⁴⁰ Based on Machida and Takeuchi (町田；竹内 1965). Here each letter represents a single *phrase* (not note), with lower case letters representing phrases originating from *Hirado Bushi* and capitals representing phrases originating from *Komoro Magouta*. Detailed note-level alignments and mechanisms for these evolutions are shown in Fig. 4.6 (red) and Fig. 4.7 (blue), respectively.

desperate to save their town from collapse turned to the famous folksong and decided to leverage its cultural capital into financial capital for the town (this process included the formal standardization in 1909 of the previously diverse melodies into a single notated "correct" (正調) main melody). So far, this effort has succeeded - the town of Esashi remains financially viable thanks in large part to the success of the *Esashi Oiwake Association*. The association is formally administered by the town's tourism department and attracts hundreds of singers (including myself) to the town for the annual competition and other events, managing to collect sizeable revenue from the registration fees and ranking examinations (analogous to the belt ranking systems in martial arts) as well as the general economic revenue provided by visiting tourists.

4-2-2. Synchronic vs. diachronic comparison problems

Unfortunately, unlike British-American folk song, Japanese folk song melodies were not documented before the 20th century, severely limiting our ability to directly trace its evolution over several centuries in the diachronic manner shown above for *Cassiles*. In theory, it should be possible to reconstruct the "proto-melody" that gave rise to 20th century melodic variants of the Oiwake tune family through careful synchronic comparison of large numbers of related members of this tune family (Boilès 1973). Ideally, this would also be combined with knowledge of general mechanisms of musical evolution (analogous to the comparative method used by historical linguists to reconstruct proto-languages; Campbell 2013) as well as advanced statistical techniques developed by evolutionary biologists for dealing with uncertainty in phylogenetic reconstruction (Bouckaert et al. 2014). As with linguistic/biological evolution, this would allow for a more rigorous and nuanced understanding of the factors governing musical change.

Unfortunately, such advanced phylogenetic reconstruction of musical tune families is too complicated to be practical within the constraints of this dissertation. Instead, I will rely for this case study on the simplifying assumptions of Machida and Takeuchi's

analysis, which assumes that the ancestral forms of *Esashi Oiwake* can be best approximated by the simpler contemporary forms of the Oiwake family. This assumes a degree of evolutionary stasis, a concept that has been highly criticized (Stock 2006b). However, Machida and Takeuchi present a great deal of historical, musical, lyrical, and ethnographic evidence to suggest that in this case the assumption of stasis is at least partly justified: although other related variants have undoubtedly changed since the proto-Oiwake melodies, they appear to have changed less than has *Esashi Oiwake*. Thus, for the purposes of this case study, I will adopt the simplifying assumption that the evolution of *Esashi Oiwake* can be approximated as a linear sequence. In the future, the accuracy of this assumption should be checked using the more sophisticated evolutionary modeling techniques described above (this caveat also applies to a lesser degree to the other case studies discussed in this chapter).

4-2-3. Rates and mechanisms

In the previous case study of British-American folk song, the number of notes per phrase generally corresponded to the number of syllables, which varied depending on the lyrics. In contrast, Japanese folk song lyrics tend to have less variable numbers of syllables (usually 26 syllables organized into four lines of 7-7-7-5). However, the number of notes per phrase ends up being highly variable because there is a stronger tradition of using ornamental melisma (in which a single syllable is extended over many different notes), which can be easily inserted or deleted without affecting the lyrics. Among other things, this melisma makes it even easier to adapt the same tune to different lyrics in Japanese than in British-American folk songs. Indeed, all of the songs shown in Figs. 4.5-4.7 have completely different lyrics. In fact, even for the single song *Esashi Oiwake*, there are many completely different sets of lyrics that are considered acceptable, in contrast to the single rigidly prescribed melody.

As predicted, stressed notes were on average more resistant to change than unstressed ones. However, while this difference was strong in the main melody (unstressed : stressed ratio = 6.4), the difference was much smaller for the prelude (1.5). As with *Cassiles*, part of the explanation for this discrepancy probably lies in the fact that the major phrase deletions of the prelude serve to mask differences in the rest of the song. In addition, rhythmic stress assignments here are based on downbeats determined by the first note after a phrase-line (van Kranenburg, Volk, and Wiering 2013; Savage and Atkinson 2015), but in the case of *Esashi Oiwake* the transcription of the non-metric melody of *Esashi Oiwake* into a 2/4 meter seems dubious, and this metric ambiguity may also be serving to mask any effects of rhythmic stress.

4-2-4. Esashi Oiwake summary

Once again, the general evolutionary principles developed in Chapters 2 and 3 apply with some caveats to the evolution and merging of two stylistically and geographically distinct unaccompanied work songs into the famously long and complexly ornamented *Esashi Oiwake*. Unlike the previous British-American example in which *Cassiles* diverged into shorter, simpler tunes through deletion, *Esashi Oiwake* became longer and more complex over time through the merging of shorter tunes and the gradual accumulation of inserted ornamentation, to the point where its length became limited by physical constraints on breathing.

4-3. Case study 3 (Art: Japanese *gagaku*): Vestigial 1,000-year-old Chinese melodies in modern *Seigaiha*

Although cultural evolutionary theory is particularly useful for tune family evolution in folk musics, it can also be useful for classical and popular musics. For example, Heather Windram and colleagues have recently applied phylogenetic methods to reconstructing the evolutionary divergence of a single Western classical music composition, Orlando Gibbons' *Prelude in G* (1613) into a set of variant notations over

the course of approximately one century of hand-copying (Windram, Charlston, and Howe 2014). One interesting finding of their analysis was the coexistence of both "silent" and "audible" mutations, and the ways in which silent mutations can pave the way for audible ones, analogous to "silent" and "functional" genetic mutations. For example, in Fig. 4.8, versions 1 (left) and 2 (right) sound different, but the top and bottom variants of version 1 sound identical despite differences in the way the rhythms are notated.

Ex.1 Gibbons, Prelude in G, variants in bar 20, left hand

<p>Version 1</p>  <p><i>Parthenia</i> Lcm 2093 (no tie) Och Mus. 89 NYp Drexel 5612 B Ms. Ly A2 Lbl Add. 23623(i) Lbl Add. 23623(ii)</p>	<p>Version 2</p>  <p>Och Mus. 47 Cfm Mu Ms 653 HADolmetsch II e.17 Tn MS N-3/35 (tie replaced by dot of addition at start of next bar)</p>
 <p>Lbl Add. 31403 Pc Rés 1186 bis I (tie in T voice from previous bar)</p>	 <p>Lbl Add. 22099 (split at half bar over two systems)</p>

Figure 4.8 "Silent" and "audible" mutations in Gibbons' *Prelude in G*⁴³

⁴³ From Windram et al. (2014: 524). Versions 1 (left) and 2 (right) sound different, with Version 2 having three audible insertions of eighth notes. However, the top and bottom variants of Version 1 sound identical despite the "silent" mutation where a half note becomes notated as two tied quarter notes. Such silent mutations can eventually results in functional consequences (e.g., failing to copy the tie results in the appearance of a new note).

In this case study, I want to explore a more extreme form of evolution of notated classical music in a non-Western genre: Japanese *gagaku* (雅楽), which is often described as "the world's oldest continually performed orchestral music" (S. G. Nelson 2008: 36). Specifically, I will build on Alan Marett's (1985) analysis of ~1,000 years of documented changes in the notation of the piece *Seigaiha* (青海波) from the oldest *togaku* (唐楽) repertoire. There are some methodological issues involved in interpreting *gagaku* notation and performance practice that have resulted in some controversy around the conclusions of Marett and Laurence Picken's school of *gagaku* scholars with whom he is associated (Marett 1985; S. G. Nelson 2008; Hughes 2010). Of particular relevance to this dissertation, the degree to which the older notations represent full descriptive notations of the melody as opposed to a skeleton notation to which unwritten, orally transmitted melodic aspects were added is unclear. However, for the purposes of this short case study I will simply accept Marett's transcriptions and analysis in order to explore whether his analysis can be usefully expanded and compared with the other case studies in this chapter through the use of evolutionary sequence alignment techniques.

4-3-1. Background

Gagaku is a ritual court music that is the oldest documented Japanese music (S. G. Nelson 2008). Some *gagaku* music accompanies song or dance, while some is purely instrumental. The instrumentation has changed over the years, but the core ensemble has generally included winds (e.g., *ryuteki* [flute], *hichiriki* [reed pipe], *sho* [mouth organ]), strings (e.g., *biwa* [lute], *koto* [zither]), and percussion (e.g., *taiko* [drum], *shoko* [gong]). All the non-percussion instruments play more or less the same melody in heterophony, although as we shall see this same melody has become wildly different in different instruments.

The oldest *gagaku* repertoire is the *togaku* repertoire, which was imported from the Chinese Tang dynasty during the 7th-9th centuries. Although this repertoire later died

out in China, it has continued in Japan all the way to the present day, albeit with major changes (including those introduced through a revival following a virtual extinction during the 15th-16th century wars that destroyed the Japanese imperial court). One of the most striking changes is the fact that, although the core notes of the earliest melodies remain detectable in modern notation, they are now almost completely inaudible. There are at least three reasons for this: 1) The melodies have been best preserved in the lowest notes of the *aitake* chords played by the *sho* mouth organ (only the lowest notes are explicitly notated - the *aitake* have developed in a parallel oral tradition), which are perceptually masked by the higher notes in the chords and by the more melodic-sounding flute and *hichiriki*. 2) The melodies preserved in the more prominent flute and *hichiriki* have accumulated so many additional notes in between the original ones that there is little resemblance remaining. 3) The tempo of *gagaku* appears to have slowed dramatically by at least a factor of four, such that the notes are now so far apart and the former melodies so long that they violate psychological principles of perceptual grouping. Instead, what used to be brief ornamental additions have now slowed down enough to be perceived as a true melody, while the former melody remains with little or no melodic function, analogous to a vestigial organ or limb (e.g., human appendix, wings in flightless birds). This phenomenon has striking parallels to the development of European motets from a slowed down Gregorian chant *cantus firmus* (Hughes 2010).

This phenomenon has been demonstrated by Marett (1985) for the evolution of the piece *Seigaiha*. By transcribing notations from the 10th to 20th centuries for the flute, mouth organ, and other instruments into standard Western staff notation and aligning them (Figs. 4.9 and 4.10), Marett showed that the bottom note of the modern *sho* part was "virtually identical" (Marett 1985: 416) to ancient flute versions, while the relationship of the modern and ancient flute parts was "not immediately discernible" (Marett 1985: 420). Analyzing Marett's alignments using the quantitative methods developed in Chapter 2 allows us to investigate these statements more precisely.

4-3-2. Rates and mechanisms

The creation of the 29-note 20th c. *sho* lower-note melody from the 26-note 10th c. flute part involved only six note changes (4 insertions [green arrow], 1 deletion [blue], 1 substitution [red]), retaining a melodic identity of 87% through a mutation rate of 0.0002 per site per year (Fig. 4.9 and Table 4.1). During the same time period, the flute part more than tripled in length by accumulating a staggering 63 insertions and 3 substitutions, retaining a melodic identity of only 40% through a mutation rate of 0.0025 per site per year - a rate more than ten times faster than the rate observed for the *sho* from the same shared ancestral melody in the same 1,000-year period (Fig. 4.10 and Table 4.1).



Figure 4.9 Melodic evolution in Japanese *gagaku* pt. I (modern *sho* part from *Seigaiha*)⁴⁴

⁴⁴ From Marett (1985: 412/423). The 10th c. flute is from *Hakuga no fue-fu* (HFF; compiled by Minamoto no Hiromasa), while the 20th c. *sho* (mouth organ) is from 芝 (1969).



Figure 4.10 Melodic evolution in Japanese *gagaku* pt. II (modern flute part from *Seigaiha*)⁴⁵

The average melodic distance of the four substitutions observed in Figs. 4.9 and 4.10 is 1.5 semitones (i.e., in between a minor and major 2nd). Of these four substitutions, three (one D to d; two D to e) represent the smallest possible melodic distance of one semitone, while the fourth (D to F) represents a slightly larger but still relatively small minor 3rd. D is the only note to undergo substitution in this example, consistent with some historical variability in the intonation of this scale degree in *gagaku* (Terauchi 2011). However, not all Ds are substituted, unlike some of the modal shifts observed in British-American folk song in Chapter 3, where all of the third scale degree changed from minor to major or vice-versa.

⁴⁵ From Marett (1985: 423-424). As in Fig. 1, the 10th c. version is from HFF, while the 20th c. version is from 芝 (1969). The 14th c. version is from Chū Ōga ryūteki yōroku-fu (CORYF, written by Yamanoi no Kagemitsu; also known as Ōga Kagemitsu no ryūteki yōroku-fu; cf. 遠藤 1996).

As predicted, rhythmically stressed sites were on average more resistant to change than unstressed ones (unstressed : stressed ratio = 15). Interestingly, in this case this rhythmic stress effect did not seem to apply to substitutions (three of the four substitutions occurred on stressed notes). Instead, the higher rate of unstressed notes was driven by the fact that the predominant evolutionary mechanism was the addition of unstressed ornamental notes (although over time some of these notes eventually became stressed as the metric structure accommodated the slowing melody; Marett 1985; S. G. Nelson 2008; Hughes 2010).

4-3-3. Seigaiha summary

The general principles of melodic distance and rhythmic stress developed above also apply to the divergent evolution of the modern *sho* and flute melodies of the Japanese *gagaku* piece *Seigaiha* from their common ancestral flute melody notated 1,000 years earlier. During the same 1,000-year period, the original melody evolved at vastly different rates in these two instruments, such that there is little similarity remaining in the two resulting melodies even though they continue to be performed simultaneously. The original flute melody remains largely unchanged as a vestigial, unheard structure at the bottom of the *sho* chords, while the modern flute melody more than tripled its original length by accumulating ornamentation and slowing down to the extent that this ornamentation came to function as a new melody in its own right.

4-4. Case study 4 (Popular: Contemporary Western) Subconscious plagiarism in George Harrison's *My Sweet Lord*

In both popular and classical musics, there is often artistic and legal pressure to be original. Composers thus often try to avoid directly copying entire melodies from previous work, even if they borrow uncopyrightable aspects such as smaller melodic motives or stylistic features (e.g., chord changes, instrumentation, rhythmic patterns). Thus, in many cases the techniques for studying melodic evolution developed here

may be more applicable to classical and popular musics using local sequence alignment algorithms to identify evolution/borrowing of individual motives (Urbano et al. 2011; Smith; and Waterman 1981) rather than entire melodies.

However, there are still many applications for studying global evolution of entire melodies, including cover song identification and plagiarism detection (Robine et al. 2007; Müllensiefen and Pendzich 2009). In this case study, I want to show how the method I have developed for measuring musical evolution can be usefully applied to one of the most famous plagiarism cases: the US\$1.6 million judgement that the Beatles' George Harrison was liable for subconscious plagiarism of the Chiffons' 1962 hit *He's So Fine* when composing his 1970 hit *My Sweet Lord* (Judge Owen 1976). Although researchers in the field of music information retrieval (MIR) have developed a number of techniques for automatically identifying potential musical plagiarism (some of which have been applied to the *My Sweet Lord* example, e.g., Robine et al. 2007; Müllensiefen and Pendzich 2009), my approach adds the unique benefit of evaluating whether observed melodic similarities are significantly higher than might be expected for stylistically similar works.

4-4-1. Background

Musical copyright law is highly complex, but it essentially recognizes the lyrics and melodies of the written score as the copyrightable essence of a musical composition, excluding stylistic and performance features such as chords, instrumentation, vocal timbre, and small ornamental/microrhythmic variation in the recorded performance (Cronin 2015; Fruehwald 1992). For *My Sweet Lord*, there was no question of lyrical plagiarism, as the lyrics were completely different from *He's So Fine*. Instead, the melodies sounded similar enough that the crucial question of the copyright case was whether this degree of similarity was due to illegal copying or simply by chance due to the similar motives and scale structures common to the style of much popular music at the time.

George Harrison admitted to having heard *He's So Fine* (as most people would have, since it was a number one hit on the pop charts), but claimed to have composed *My Sweet Lord* without consciously drawing on it. The judge accepted Harrison's story, but maintained that the two songs were nevertheless so similar as to be "virtually identical except for one phrase" (Judge Owen 1976: 180). The judge went on to conclude even more strongly:

"it is clear that My Sweet Lord is the very same song as He's So Fine with different words, and Harrison had access to He's So Fine. This is, under the law, infringement of copyright, and is no less so even though subconsciously accomplished." (Judge Owen 1976: 180-181)

4-4-2. Melodic similarity

Using my methods, it is possible to quantify the melodic similarity beyond the vague "virtually identical" into the more precise percent melodic identity developed in Chapter 2. As one of the most famous cases, it will be particularly informative to know the percent melodic identity of these two tunes as a benchmark for comparing the many similar copyright cases⁴⁶.

Fig. 4.11 shows my own melodic alignment of *He's So Fine* and *My Sweet Lord*. This analysis confirms that there are indeed statistically significant similarities between the two. They share a melodic identity of 54% (ID = 28, L₁ = 59, L₂ = 44) that is extremely unlikely to be due to chance resemblances given the types of scales and lengths of the tunes ($p < .00001$).

⁴⁶ Cronin (2016) has an excellent overview of many high-profile examples (involving Led Zeppelin's *Stairway to Heaven*, Duke Ellington's *Satin Doll*, John Williams' soundtrack to *E.T.*, Rogers & Hammerstein's *There Is Nothing Like A Dame*, Justin Bieber's *Somebody to Love*, The Black Eyed Peas' *Boom Boom Pow*, etc.).

and "My sweet lord" share the same number of syllables (three) with similar stress patterns, Harrison inserts an appoggiatura to lengthen the corresponding melody to four notes (GEED), while the three syllables of "He's so fine" are accommodated with only three notes (GED).

As in the previous case studies, note deletions (27) and insertions (12) vastly outnumber substitutions (4). As with the British-American folk songs analyzed in Ch. 3, there is a tendency toward simplification through deletion, but this is accompanied by a lesser degree of insertion. Interestingly, while Harrison's melody is simpler in terms of the number of notes, it is more complicated in various other dimensions, such as the use of ornamentation (e.g., the appoggiatura shown above) and more thickly textured chords.

The average melodic distance of the four substitutions observed in Fig. 4.11 is 3.5 semitones (i.e., in between a major and minor 3rd). Three of these four substitutions represent a substitution of a G by a minor 3rd above (b) or below (E), while the final substitution represents a substitution of an E by a perfect 4th above (A). While these are somewhat larger than the intervals observed in other case studies (e.g., 1.5 semitone average for *Seigaiha*), 3rds still represent relatively small intervals.

As predicted, rhythmically stressed sites were on average more resistant to change than unstressed ones (unstressed : stressed ratio = 6.1). This suggests that rhythmic stress plays a role in musical evolution even when this evolution is happening subconsciously. (Stress in this case study is assigned based on syllable stress, rather than downbeats, both since syllable information is available and because the heavy syncopation of both parts makes this a more appropriate measure of rhythmic stress.)

4-4-4. *My Sweet Lord* summary

The general principles of melodic distance and rhythmic stress developed above in

cases of conscious copying and evolution of folk and classical melodies also apply to subconscious copying found in a high-profile copyright case in popular music. The techniques I have developed have shown promise both in adding quantitative precision to vague statements about melodic similarity (i.e., *My Sweet Lord* and *He's So Fine* being "the same song with different words") and in confirming that observed similarities (54%) are significantly greater than expected by chance for stylistically similar songs ($P < .00001$). Such techniques could well have important applications in other ongoing or future copyright disputes, as would a better understanding of the nuances and mechanisms of musical evolution in different cultures and genres.

4-4-5. Appendix: No significant melodic similarity between *Blurred Lines* and *Got to Give It Up*

As an example of the reverse case - where evolutionary analysis may help *disprove* claims of copyright infringement - I want to briefly present an analysis of a high-profile copyright case currently under appeal: *Blurred Lines*.

In 2015, a jury award Marvin Gaye's heirs US\$7.4 million for its finding that Robin Thicke and Pharrell Williams' massive hit *Blurred Lines* (2013) was guilty of plagiarizing Marvin Gaye's *Got To Give It Up* (1977)⁴⁸. One of the primary pieces of evidence was testimony by musicologist Judith Finell who, when asked whether she thought that Thicke and Williams copied *Got To Give It Up*, replied "Yes...musically there's no other explanation for so many similarities"⁴⁹. The jury's decision is currently under appeal on the grounds that they were allowed to consider similarities in extra-melodic information such as instrumentation (e.g., shared use of cowbell) and

⁴⁸ <http://mcir.usc.edu/inplay/Pages/williams.html>

⁴⁹ <http://mcir.usc.edu/inplay/Pages/documents/williamsfinelldepo.pdf>, p.48. Here Finell is referring to a "constellation of 8 similarities" (p.57) that includes aspects like instrumentation, timing, and vocal style as well as melody.

vocal timbre (e.g., shared use of falsetto) rather than strictly melodic similarities contained in the musical notation.

It is difficult for me to manually apply my new melodic sequence alignment techniques as I have done in the above case studies because Finell's testimony does not appear to provide any melodic alignments of the type shown here, nor provide enough information to construct such alignments. Furthermore, there is not enough melodic similarity between the two songs that I can identify to confidently create such an alignment myself. This is where the automated algorithms introduced in Chapter 2 are useful for their objective power.

Fig. 4.12 shows the melodies of the first two verses of each song and their coding as unaligned melodic sequences using the standard technique developed in Chapter 2 (including transposing them to the same tonic). Applying the automated melodic sequence alignment algorithm from Chapter 2 to align these sequences gives a value of 19% melodic identity⁵⁰. By comparing this against a baseline distribution of melodic similarity generated by randomly reordering these sequences shows us that the observed degree of 19% melodic identity is not statistically significant ($P = .49$), and is easily found in any two random melodies of these lengths that use these scales (stylistic features such as scale choice and melody length are not copyrightable).

⁵⁰ Note that this value of 19% melodic identity is also almost certainly an overestimate of the true melodic identity, since automatic alignment ignores rhythmic and other structural information and thus tries to maximize similarity even when that results in finding melodic matches that are musically implausible. For comparison, automated alignment of *He's So Fine* and *My Sweet Lord* returned a value of 60% melodic identity rather than the true value of 54% found above through manual alignment.

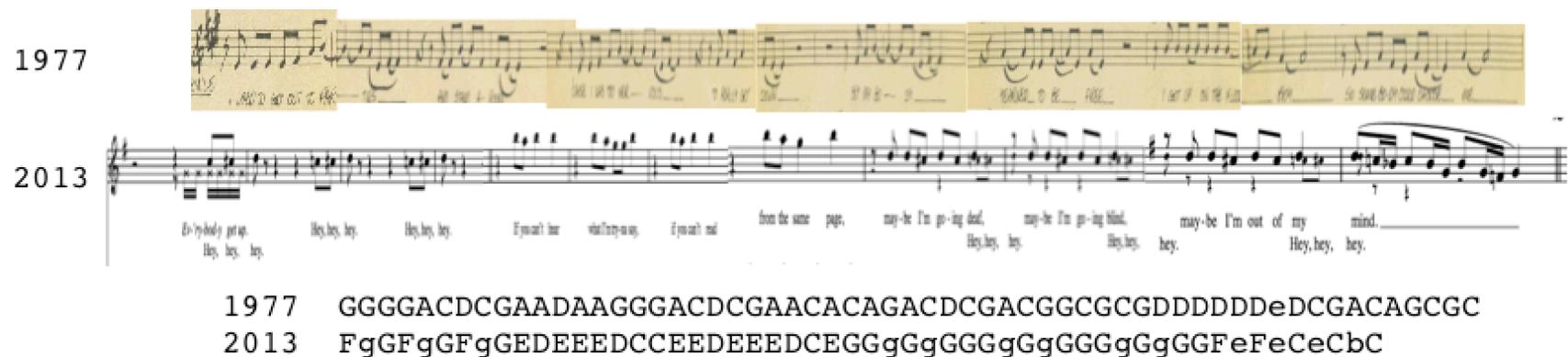


Figure 4.12 Unaligned melodic sequences for *Got To Give It Up* and *Blurred Lines*⁵¹

This analysis provides quantitative support to the claims of the defendants and independent experts alike that the jury's initial verdict was "unfounded, illogical, and a miscarriage of justice"⁵². However, a more comprehensive analysis would ideally be based on the plausibility of a manual melodic alignment of official notation for both songs provided by Finell or another musicologist who believes they can make a case for significant melodic similarities between the two songs. It is also conceivable that a more nuanced

⁵¹ The first two verses for each song are shown transcribed into melodic sequences in a common tonic using the method described in Chapter 2. The melody for *Got To Give It Up* (1970) is taken from the copyright registration listed at <http://mcir.usc.edu/inplay/Pages/williams.html>. The melody for *Blurred Lines* (2013) was taken from <http://www.musicnotes.com/sheetmusic/mtd.asp?ppn=MN0118109>, as no full notation could be found in court documents.

Automatic alignment of these tunes gives a non-significant value of 19% melodic identity ($P = .49$).

⁵² <http://mcir.usc.edu/inplay/Pages/williams.html>

melodic analysis that includes rhythmic as well as pitch information may reveal evidence for significant melodic similarities, although I find this unlikely for this particular case.

4-5. General comparison across case studies

The rates and types of mutations for each case study analyzed above are compared in Table 4.1 below. Comparison among and within case studies gives an indication of the degree of variability in different evolutionary parameters. All averages mentioned below are weighted means across these columns from Table 4.1.

4-5-1. Absolute mutation rates highly variable

The overall average musical mutation rate in these case studies is 0.02 per site per year. However, average absolute mutation rates vary almost 400-fold from the slowest-evolving (*Seigaiha sho* part) to the fastest (My Sweet Lord). Indeed, even within the same piece, different lineages and different instruments can vary greatly (e.g., mutation rates for the *sho* and flute parts of *Seigaiha* differ by over 10-fold).

It is not possible to calculate absolute mutation rates for Esashi Oiwake because of the lack of pre-20th century documented recordings (musical "fossils") with which to calibrate the time dimension. However, it seems likely that the common ancestor of these melodies diverged during the Edo period (1603-1868), during which many Japanese folk songs are thought to have emerged (Hughes 2008). This would give an estimated rate of approximately 0.004 to 0.02 per site per year, which falls towards the middle of the distribution of other mutation rate values given in the table.

This rate variability is consistent with findings that rates of linguistic change vary greatly within and between families, such that there is no single universal "glottoclock" that can be used to independently date language divergence (Campbell 2013; Atkinson

Table 4.1 Comparison of evolutionary parameters within and between case studies⁵³

	<i>Cassiles</i> to <i>Edward</i>	<i>Cassiles</i> to <i>Airlie</i>	<i>Oiwake</i> (prelude)	<i>Oiwake</i> (main melody)	<i>Seigaiha</i> (<i>sho</i>)	<i>Seigaiha</i> (flute)	<i>My</i> <i>Sweet</i> <i>Lord</i>
Time (years)	411	440	?	?	1000	1000	8
Initial melody length (notes)	85	85	69	90	26	26	59
Mutations	74	86	87	143	6	66	43
Average mutation rate (per note per year)	0.0021	0.0023	?	?	0.0002	0.0025	0.0911
Insertions	11	17	23	94	4	63	12
Deletions	58	63	44	46	1	0	27
Substitutions	5	6	20	13	1	3	4
Indel vs. substitution ratio	13.8	13.3	3.4	10.8	5.0	21.0	9.8
Mean substitution size (semitones)	2.6	2.5	3.9	4.46	1.0	1.7	3.5
Unstressed vs. stressed mutation rate ratio	1.6	2.1	1.5	6.4	6.8	23.8	6.1

and Gray 2005). It is also consistent with an emerging consensus from evolutionary biology that even the so-called "molecular clock" used to calculate genetic divergence is also actually much more variable than previously believed (Ho and Larson 2006).

⁵³ Question marks signify that absolute mutation rates could not be calculated for *Esashi Oiwake* because of the lack of pre-20th c. notation. See text for details.

4-5-2. Bias toward small substitutions

Overall, note substitutions were strongly biased towards small mutational distances. The average mutational distance of substitutions was 2.8 semitones (i.e., a minor 3rd) across all case studies, and was less than 5 semitones (i.e., a perfect 4th) in each case study. In each case, the average size was lower than the tritone (6 semitones) that would be predicted if note substitutions were random and not influenced by mutational distance. Instead, this bias toward small intervals is consistent with my earlier predictions in Chapter 3 that smaller intervals are more likely to be substituted and to be passed down to future generations because such changes are more easily produced and less easily perceived as being different. Such biases also have parallels in linguistics and biology, where sound changes to phonetically similar sounds are most likely (Campbell 2013) and amino acids are most likely to mutate to ones requiring only a single nucleotide change (Dayhoff, Schwartz, and Orcutt 1978).

4-5-3. Stressed notes more stable than unstressed

On average, stressed notes were approximately 7 times more resistant to change than unstressed notes were. This trend was consistent for all examples, although the differences were less pronounced for the folk songs containing major deletions of entire phrases (i.e., *Cassiles* to *Edward* and the *Esashi Oiwake* prelude). Presumably, this is largely because deletions of entire phrases affected stressed and unstressed notes equally, masking any differences (see the case studies above for further discussion).

This stress bias is consistent with purifying selection against functional change also observed in linguistics and biology. Although these case studies are not large enough to make a quantitative comparison of ornamental or final note stability as done in Chapter 3, they seem to tentatively conform to the same patterns. For example, the final note was unchanged in all but one example (*Esashi Oiwake* main melody), and most of the numerous insertions in the Japanese folk and *gagaku* examples were originally

ornamental (although these ornamental notes gradually came to assume more functional roles over time).

4-5-4. Predominance of insertion/deletion over substitution

The average ratio of indels (insertions/deletions) to substitutions was approximately 11 to 1. This strong preference for indels was consistent across all examples, and was also consistent with the findings of Chapter 3. This bias toward indels is strikingly opposite to the situation in biology, where substitutions vastly outnumber indels. As explained in Chapter 3, this is likely explained by the flexible rhythms of music that allow rhythms to be modified to accommodate insertion/deletion of ornamentation without disrupting the meter, in contrast to the fixed 3-nucleotide DNA codons that cause "frame shifts" of any genetic indels that don't encompass multiples of 3 nucleotides.

4-5-5. No clear trend toward complexification or simplification

The simplest method of measuring a trend toward complexity or simplification is to count whether the number of notes in the melody increases (via insertion) or decreases (via deletion). These case studies gave no indication of any general trend in either direction. Deletions outnumbered insertions in four out of the seven columns in Table 4.1, while the opposite was true for the remaining three. Even within one individual song, *Esashi Oiwake*, the prelude became simplified through deletion of two entire ending phrases, while the main melody became more complex through the accumulation of many small ornamental insertions throughout the melody. This suggests that, if there is any general trend toward complexity or simplification, it is much more nuanced and context-dependent than the strong general trends identified above involving melodic distance and rhythmic stress.

4-5-6. Possible role of transmission fidelity

It is difficult to compare the different types of transmission fidelity in these case studies in the manner done in Chapter 3 with oral vs. written transmission. However, the large variation in absolute mutation rates among cases studies is consistent with differences in transmission fidelity. Specifically, the remarkable fidelity with which 87% melodic identity was maintained over 1,000 years in the *sho* part of *Seigaiha* with a mutation rate of .0002 per site per year seems very likely to be aided by its preservation in written notation. The faster - but still relatively slow - rates of the British-American folk song seem to fit with a combination of oral and written transmission suggested by its history of documentation, and the slightly faster rate suggested by the Japanese folk song example is consistent with that repertoire being transmitted almost entirely orally until the introduction of limited written notation and audio recordings in the 20th century. Finally, the extremely high rate of evolution in *My Sweet Lord* is consistent with the idea that the transmission fidelity in this example was so low that its composer was not even consciously aware that he was copying a pre-existing work at all.

On the other hand, the fact that different instruments within the same *gagaku* piece displayed wildly different mutation rates suggests that written notation alone does not guarantee low mutation rates. Interestingly, *gagaku* is currently taught through a combination of written and oral transmission, but the nature of earlier transmission systems remains controversial (S. G. Nelson 2008). In *gagaku* and other genres, a thorough understanding of the evolution of the transmission systems may help to better understand the evolution of the melodies themselves.

4-6. Conclusion

Through these four case studies spanning melodic evolution in folk, classical, and popular traditions of Western and non-Western music, I have quantitatively explored the generality of the evolutionary mechanisms predicted and identified in highly related British-American Child ballads in Chapter 3. Using a series of complex and

diverse examples, I showed that the same principles of melodic distance, rhythmic function and transmission fidelity operated consistently in almost all case studies, while there was little evidence of any consistent trends in absolute mutation rate or directional evolution. In the future, more detailed quantitative analyses of large, comprehensive samples will be needed to confirm the suggestions of these limited case studies.

Summary

In this chapter I apply the method of measuring musical evolution developed in Chapter 2 to explore the generality of the British-American folk song evolution findings in Chapter 3 through the following four diverse case studies, for which the history of musical evolution has already been qualitatively documented: 1) the divergence of the Scottish 17th c. *Lady Cassiles Lilt* into nearly unrecognizable 20th c. American descendants, 2) the merging of work songs from distant prefectures into the Japanese folk song *Esashi Oiwake*, 3) the simultaneous performance of vestigial, inaudible 1,000-year-old Chinese melodies and their radically changed descendants in the Japanese *gagaku* piece *Seigaiha*, and 4) the legal cases finding George Harrison's *My Sweet Lord* (1970) and Robin Thicke and Pharrell Williams' *Blurred Lines* (2013) guilty of plagiarism.

Although the precise mechanisms differ and absolute rates of evolution vary almost 400-fold within and between these case studies, several patterns are consistent with the predictions and findings of Chapter 3. These patterns include: 1) the relative ease of mutations to nearby pitches, 2) the relative predominance of insertions/deletions over substitutions, 3) the relative stability of functional notes (e.g., rhythmically stressed or vs. unstressed), and 4) the relative stability of written over oral traditions. Both increases and decreases in complexity were observed, with no clear trend favouring one direction.

5. General conclusion and future directions

In this dissertation, I have attempted to answer old questions about the nature of musical evolution using new theoretical and methodological tools from evolutionary biology. In Chapter 1, I argued that music can be said to "evolve" and that evolutionary theory can help us understand the phenomenon of musical change and have useful practical applications. In Chapter 2, I demonstrated how methodological tools from evolutionary biology can be used to measure musical evolution, allowing us to quantitatively test hypotheses that previously tended to be debated qualitatively. In Chapter 3, I tested several such hypotheses on a large sample of 4,125 British-American Child ballads, finding strong support for general rules of musical evolution governing the mechanisms of transmission, variation and selection. In Chapter 4, I explored the generality of these findings using several diverse case studies to demonstrate the general nature of the approach and identify general trends that may be characteristic of musical evolution near-universally.

While this dissertation represents a useful contribution to musicology, there are several limitations deserving future study. In particular:

5-1. Methodological sophistication

The method of measuring melodic evolution is based on fairly simplistic models that assume a direct ancestor-descendant relationship between closely related variants. This is likely to be an over-simplification of the complexities of transmission. In some cases, this may closely approximate reality, as editors and singers may learn directly from other singers, published notations or recordings, introducing both copy-errors and intentional changes in the process. However, in many cases, recorded variants may not be directly descended from one another but instead share a more ancient common ancestor that may or may not have been recorded. Furthermore, singers may be

exposed to multiple versions of a melody and create hybrid melodies incorporating different parts from different versions.

The problem of reconstructing evolution with a combination of sampled and unsampled ancestors has analogies in virus evolution, and tools developed for this problem may be useful in future attempts to build more-nuanced phylogenetic models of musical evolution (Gavryushkina et al. 2014). Likewise, the problem of reconstructing non-tree-like evolutionary hybridization also has theoretical and methodological parallels in virology (Duffy, Shackelton, and Holmes 2008) that may be useful in future studies. However, I know of no unified methodology currently capable of dealing with both sampled ancestors and hybridization under a single framework that could be appropriately and efficiently adapted to the current study of melodic evolution. Given the current pace of methodological development, however, there is promise that this problem will be resolved in the near future.

5-2. Cross-cultural generalizability

Although I have tested hypotheses about general rules of musical evolution on a diverse cross-cultural sample of case studies, logistical considerations limited my ability to perform large-scale testing of these hypotheses on only a single genre (British-American Child ballads). In the future, I hope to test the predictions of these hypotheses against large samples from different cultures (e.g., Japanese folk songs; NHK 1944).

5-3. Beyond melody

This dissertation focuses on melodic evolution because of its historical role as the strongest candidate for a quantifiable unit undergoing descent with modification over

time. Furthermore, the analogies between melodies represented by sequences constructed from a 12-note "alphabet" and proteins represented by sequences constructed from a 20-amino acid "alphabet" make it relatively easy to quantify melodic evolution by adapting tools from molecular genetics.

However, music is far more than simply sequences of notes, just as humans are far more than simply genetic sequences. Many of the Child ballads analyzed in Ch. 3 have gone extinct. In many cases, lyrics presumably played a role at least as strong as melody: particularly disturbing lyrics involving things like rape, incest, and/or infanticide (e.g., "Prince Heathen"). Likewise, did Simon and Garfunkel's simplified, easier-to-learn melody play a role in Scarborough Fair's phenomenal popularity, or was its success due to extra-melodic factors such as instrumental arrangement, addition of new lyrics, vocal style, or the prestige of the singers themselves? If the success of musical variants can be predicted from general principles, it could have important implications for the music industry and on sustainability initiatives such as UNESCO's policies on intangible cultural heritage.

A comprehensive theory of musical evolution will have to extend the theories and methods developed in this dissertation to many more domains. These include not only the domains of rhythm, performance style, texture, instrumentation, dance, etc. focused on by Alan Lomax's (1968) Cantometrics Project, but also the roles of non-acoustic domains of "behavior" and "concept" emphasized in ethnomusicology since Alan Merriam's (1964) book, *The Anthropology of Music*.

Measuring the cultural evolution of closely related melodies is a fundamental step towards this goal, but it is only the first of many. While this dissertation has illuminated some general mechanisms of *how* music evolves, crucial questions about *why* the musicians made each specific change (including the degree to which changes

are made consciously) remain for future research⁵⁴. Only by integrating quantitative and qualitative evidence ranging from the specific details of minute melodic variation through to the grand patterns of global variation in musical style can we create a comprehensive general theory of musical evolution. This challenge may never be fully attained, but each step closer we get increases our ability to understand, preserve, and promote the beautiful musical diversity that is all around us, and that represents the common "intangible cultural heritage of humanity" (UNESCO 2003).

⁵⁴ One way to pursue this might be through more detailed versions of the type of autoethnographic case study I presented in Chapter 1.

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