

Computational Analysis of Selection and Mutation Probabilities in the Evolution of Chord Progressions

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Abstract. We build a model of cultural evolution and study the properties of the process in which new chord progressions are repeatedly generated by referencing and modifying past chord progressions. As an extension of the models for biological molecular evolution, this model represents a stochastic process in which references are selected from an accumulating pool of chord segments and new chord segments are created by mutation including insertion, deletion, and substitution of chord symbols. We used a dataset of Japanese popular music and analyzed this evolutionary process by inferring the model parameters. A number of suggestive results regarding the evolution of the creative culture were obtained, including a strong recency bias, large mutation rates and large dynamic changes in mutation probabilities, and correlations between fluctuations and mutation probabilities and between the diffusedness of mutant chord segments and their mutation probabilities. Model-based predictions of new chord progressions were also made.

Keywords: cultural evolution; evolutionary model; symbolic music processing; chord progression; prediction of evolution; accumulating artifact pool

1 Introduction

Cultural development is a key aspect of human’s intelligence, and musical culture provides a fruitful venue for studying its creative role. Quantitative studies on music evolution have revealed some interesting macroscopic phenomena. These include directional changes (trends) in average features continuing for decades [1–3] or centuries [4–6], punctuational short time periods with rapid changes [1, 4, 7], concurrent and transient cluster structure [1, 3, 4], and frequency-dependent selection bias [5, 8]. Since individual musical pieces are produced by creators who learn to create music from previous

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creators or musical pieces, revealing the microscopic processes of knowledge transmission and modification is essential for understanding the mechanisms underlying these phenomena [9].

Transmission processes of musical knowledge can be classified into two types, direct and indirect. In direct transmission, a song or other musical data serves as a reference and is replicated for producing a new one. For example, folk songs are typically transmitted in this way [10]. Some models of direct transmission of musical scale [11] or music sampling [8] have been proposed for testing musicological hypotheses. Direct transmission of music is also studied in laboratory experiments [12, 13]. In indirect transmission, on the other hand, knowledge for music creation is learned from a collection of past music or through teaching, and the acquired knowledge is used for creating (rather than replicating) new musical pieces. A dominant part of art music and popular music is considered to be created by indirectly transmitted knowledge, and there is some evidence from studies on automatic music composition showing the relevance of statistical learning [14]. Cultural evolution models incorporating indirect knowledge transmission have been studied to explain empirical laws found in music data [5, 15].

Here we focus on the evolution of chord progressions in popular music. Chord progressions outline how accompaniments are played and are of prime importance in the composition process of tonal music. In popular music, they are usually notated together with the melodies, forming a type of musical score called lead sheet. Unlike melodies, chord progressions are very often reused with possible modifications, and there are books [16] and websites [17] listing commonly used chord progressions, suggesting that direct transmission is at work. It is commonly known and has been shown by a corpus analysis [18] that patterns of chord progressions have changed significantly over the last decades while new chord progressions have continuously been invented. Therefore, chord progressions are scientifically and practically interesting objects to study how a creative culture evolves by knowledge transmission and modification.

To reveal the basic characteristics of the transmission and modification processes of chord progressions, we construct a stochastic model of evolution and analyze a dataset of chord progressions in popular music songs. We view a chord progression as a sequence of chord symbols and consider chord segments (L -grams) as the unit of knowledge transmission. The process of creating a new chord segment by (i) choosing a reference from the ‘artifact pool’ of previously created chord segments (i.e. selection) and (ii) possibly modifying it (i.e. mutation) is akin to that of biological molecular evolution, where nucleotides or amino acids correspond to chord symbols.

We thus build a model similar to the models of molecular evolution [19, 20], with extensions to incorporate essential factors of the cultural evolution. First, we formulate a model where created artifacts (chord segments) are accumulated in the artifact pool unlike individuals that are removed upon death from the population in biological models. Second, we incorporate in the selection process the recency and frequency-dependent biases, which are often relevant in cultural evolution [21, 22]. Third, we consider in the mutation process insertions and deletions of chord symbols, which are often ignored in molecular evolution models [20], as well as substitutions. These features also make our model different from the one previously used for chord progression data [23], enabling us to harvest a number of suggestive results. Another study analyzed folk songs

and estimated note-wise mutation probabilities using a dataset without time information [10]. With the use of mathematical model and data with proper time information, we here analyze more detailed properties of the evolutionary process such as dynamic changes of mutation probabilities, correlations between evolutionary parameters, and the characteristics of new chord segments that later become commonly used.

2 Method

2.1 Data representation

We consider a dataset of chord progressions represented in a standard popular music notation, transposed to the natural key (C major or A minor), and labelled with a year of creation. The set of distinct chords in the data is denoted by Ω (e.g. $\Omega = \{C, Am7, FM9, \dots\}$). From each progression, we extract L -grams (also called chord segments), which are segments of L consecutive chords, where we remove repetitions of chords. An L -gram so obtained is assigned a time stamp, which is the same as the year of creation of its source progression. The collection of all L -grams obtained from progressions created in year t is denoted by $S_t^{(L)} = \{w_i | t_i = t\}$ and its index set by $I_t^{(L)} = \{i | t_i = t\}$, where i is used as an index for L -grams and $w_i = (w_{i\ell})_{\ell=1}^L$ ($w_{i\ell} \in \Omega$) denotes the corresponding L -gram. We also define $S_{<t}^{(L)} = \bigcup_{s=1}^{t-1} S_s^{(L)}$, where we take the starting time $t = 1$ as the earliest year of creation in the data. For simplicity of notation, we define $S_t = S_t^{(L)}$, $S_{<t} = S_{<t}^{(L)}$, $S_t^+ = S_t^{(L+1)}$, $S_t^- = S_t^{(L-1)}$, etc. For the result in Sec. 3, we consider the case $L = 4$.

2.2 Evolutionary model

We consider that each L -gram $w \in S_t$ is stochastically generated by selecting a reference segment w' from past data and possibly mutating it. Three mutation modes are considered: substitution, deletion, and insertion. In the substitution mode, a reference w' is taken from the set $S_{<t}$ of L -grams and mutated by changing one or more component chords, from w'_ℓ to w_ℓ , according to the symbol-wise substitution probability $\pi_{\text{sub}}(w_\ell | w'_\ell)$. The substitution probability from L -gram w' to w is defined as

$$P_{\text{rep/sub}}(w|w') = \prod_{\ell=1}^L \pi_{\text{sub}}(w_\ell | w'_\ell), \quad (1)$$

where we also include the pure replication case ($w_\ell = w'_\ell$ for all ℓ) in this probability. In the deletion mode, a reference w' is taken from the set $S_{<t}^+$ of $(L+1)$ -grams and mutated by removing one of its components. Since a removal of the first or last chord in $w' \in S_{<t}^+$ produces an L -gram in $S_{<t}$, we exclude such a case. Then, the deletion probability can be defined as

$$P_{\text{del}}(w|w') = \frac{1}{L-1} \sum_{\ell=2}^L \delta(w, w'_{1:(\ell-1)} w'_{(\ell+1):(L+1)}), \quad (2)$$

where $w_{\ell:\ell'} = w_\ell w_{\ell+1} \cdots w_{\ell'}$, and $\delta(w_1, w_2) = 1$ if $w_1 = w_2$ and 0 otherwise. In the insertion mode, a reference w' is taken from the set $S_{<t}^-$ of $(L-1)$ -grams and mutated by inserting a chord a after one of its chords w'_ℓ according to the symbol-wise insertion probability $\pi_{\text{ins}}(a|w'_\ell)$. The insertion probability is defined as

$$P_{\text{ins}}(w|w') = \frac{1}{L-1} \sum_{\ell=1}^{L-1} \pi_{\text{ins}}(w_{\ell+1}|w'_\ell) \delta(w, w'_{1:\ell} w_{\ell+1} w'_{(\ell+1):(L-1)}). \quad (3)$$

Note that the mutation probabilities considered here are among the simplest choices and we can generalize them to more elaborated models. For example, while we assumed that the symbol-wise substitution probabilities are context free, that is, the probability is independent of the preceding or succeeding chord symbols, it is possible to include context dependence by extending the probability $\pi_{\text{sub}}(w_\ell|w'_\ell)$ to such forms as $\pi_{\text{sub}}(w_\ell|w'_{\ell-1}, w'_\ell)$ and $\pi_{\text{sub}}(w_\ell|w'_{\ell-1}, w'_\ell, w'_{\ell+1})$. Similarly, we can extend the insertion probability so that it also depends on the succeeding chord symbols. These refinements generally increase the complexity (the number of parameters) of the model and require a larger amount of data to reliably infer the parameters.

In the generative process, one of the mutation modes is first chosen according to the mutation mode probability $P(b) = \lambda_b$ where $b \in \{\text{rep/sub}, \text{del}, \text{ins}\}$. We again note that the pure replication case is included in the mode $b = \text{rep/sub}$. Next, in this case, a reference segment w is chosen from $S_{<t}$ according to the selection probability $P_{\text{sel}}(w|S_{<t})$. We incorporate two biases in the selection probability to represent potential tendencies of creators. The first is the recency bias [21], which represents the creators' tendency to more likely choose a reference that appears in a recently created song. This bias can be represented by a weighting factor $e^{-(t-t_i)/\tau}$ for a segment i , where the time constant τ represents the time scale for the bias. The second is the frequency-dependent bias [22], which represents the creators' tendency to more likely choose a reference that is more (or less) frequently used in $S_{<t}$. To formulate this bias, let $F(w; I_s) = \#\{j \in I_s | w_j = w\} / \#I_s$ denote the relative frequency of w in I_s . The frequency bias can be incorporated in a factor $[F(w; I_s)]^\alpha$ in the selection probability, where $\alpha > 1$ ($\alpha < 1$) represents a positive (negative) frequency-dependency bias.

The selection probability incorporating the two biases is then given as

$$P_{\text{sel}}(w; S_{<t}) \propto \sum_{s=1}^{t-1} e^{-(t-s)/\tau} [F(w; I_s)]^\alpha. \quad (4)$$

We note that this formulation removes a potential bias arising from the unbalanced numbers of chord segments created in individual years. Similarly, we define $P_{\text{sel}}(w; S_{<t}^+)$ and $P_{\text{sel}}(w; S_{<t}^-)$ for choosing a reference in the deletion and insertion modes, respectively, where the same α and τ are used.

We can summarize the generative probability of $w \in S_t$ as follows:

$$P(w; S_t) = \sum_{b \in \{\text{rep/sub}, \text{del}, \text{ins}\}} \lambda_b P_b(w; S_t), \quad (5)$$

$$P_{\text{rep/sub}}(w; S_t) = \sum_{w' \in S_{<t}} P_{\text{rep/sub}}(w|w') P_{\text{sel}}(w'; S_{<t}), \quad (6)$$

$$P_{\text{del}}(w; S_t) = \sum_{w' \in S_{<t}^+} P_{\text{del}}(w|w')P_{\text{sel}}(w'; S_{<t}^+), \quad (7)$$

$$P_{\text{ins}}(w; S_t) = \sum_{w' \in S_{<t}^-} P_{\text{ins}}(w|w')P_{\text{sel}}(w'; S_{<t}^-). \quad (8)$$

We can also separately define the (pure) replication and substitution probabilities as

$$P_{\text{rep}}(w; S_t) = P_{\text{rep/sub}}(w|w)P_{\text{sel}}(w; S_{<t}), \quad (9)$$

$$\begin{aligned} P_{\text{sub}}(w; S_t) &= \sum_{w' \in S_{<t}, w' \neq w} P_{\text{rep/sub}}(w|w')P_{\text{sel}}(w'; S_{<t}) \\ &= P_{\text{rep/sub}}(w; S_t) - P_{\text{rep}}(w; S_t). \end{aligned} \quad (10)$$

2.3 Inference method

The parameters of the evolutionary model, λ_b , $\pi_{\text{sub}}(a|a')$, $\pi_{\text{ins}}(a|a')$, τ , and α , can be estimated from the data by the maximum likelihood method. To estimate the first three sets of parameters, we apply the expectation-maximization (EM) algorithm by treating the mutation mode b and reference w' as latent variables for each observed w .

To estimate τ and α , we can apply a simple iterative grid search using the likelihood as the objective function. Since the optimal values of these parameters depend on the values of the other parameters and vice versa, we iterate the EM step and grid search step alternately until a convergence of the likelihood value. To evaluate their estimation variances, we can apply a Bayesian method based on Monte Carlo Markov Chain sampling. Specifically, we used the Metropolis method with a flat prior distribution and a log-normal distribution as the proposal distribution.

2.4 Posterior analysis

Given the set of model parameters estimated as in Sec. 2.3, we can apply the method of posterior analysis for analyzing possible dynamic changes in the evolutionary parameters. First, given an L -gram w at time t , its posterior probability of mutation modes $\tilde{\lambda}_b(w, t) = P(b|w, t)$ ($b \in \{\text{rep}, \text{sub}, \text{del}, \text{ins}\}$) can be obtained as

$$\tilde{\lambda}_{\text{rep}}(w, t) = \lambda_{\text{rep/sub}}P_{\text{rep/sub}}(w|w)P_{\text{sel}}(w; S_{<t})/P(w; S_t), \quad (11)$$

$$\tilde{\lambda}_{\text{del}}(w, t) = \lambda_{\text{del}}P_{\text{del}}(w; S_t)/P(w; S_t), \quad (12)$$

$$\tilde{\lambda}_{\text{ins}}(w, t) = \lambda_{\text{ins}}P_{\text{ins}}(w; S_t)/P(w; S_t), \quad (13)$$

$$\tilde{\lambda}_{\text{sub}}(w, t) = 1 - \tilde{\lambda}_{\text{rep}}(w, t) - \tilde{\lambda}_{\text{del}}(w, t) - \tilde{\lambda}_{\text{ins}}(w, t), \quad (14)$$

where the right-hand sides of these equations can be calculated using Eqs. (5) to (8) and the replication and substitution probabilities are separately defined here. Then, the mutation mode probabilities $\tilde{\lambda}_b(t)$ at time t can be estimated, for example, as

$$\tilde{\lambda}_{\text{sub}}(t) = \frac{1}{\#S_t} \sum_{w \in S_t} \tilde{\lambda}_{\text{sub}}(w, t).$$

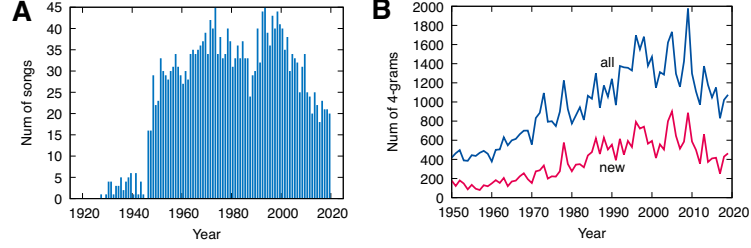


Fig. 1. A: The distribution of composition years in the dataset used. B: The yearly numbers of 4-grams (including duplications) and that of newly appeared 4-grams.

We can also calculate the posterior probability $P(w'|w, t, b)$ of reference segments $w' \in S_{<t} \cup S_{<t}^+ \cup S_{<t}^-$ in a similar way. For example, in the insertion mode,

$$P(w'|w, t, b = \text{ins}) \propto P_{\text{ins}}(w|w')P_{\text{sel}}(w'; S_{<t}^-).$$

The posterior probabilities obtained in this way can be used to estimate the mutation probabilities $\tilde{\pi}_{\text{sub}}(a|a'; t)$ and $\tilde{\pi}_{\text{ins}}(a|a'; t)$ at time t .

3 Result

3.1 Dataset

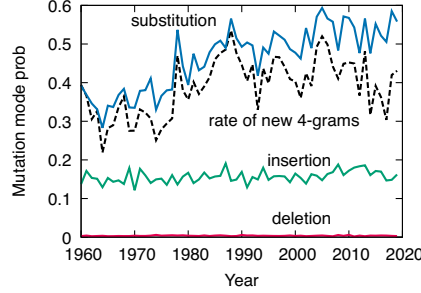
We used a dataset of Japanese popular music songs. The dataset was constructed by the author and comprised of 2419 songs. The songs were taken from top ranked songs in the Oricon yearly charts and from a compiled collection of historical popular songs [24]. The composition years spanned the range [1927, 2019] and we applied the evolutionary model for analysis in a range of years $t \geq 1960$ (Fig. 1A).

Before extracting L -grams of chords from a song, we transposed the song into the natural key, converted a consecutive repetition of the same chord into a single chord, and converted a slash chord into a normal chord by removing the bass note. The target of the analysis was 4-grams ($L = 4$). The number of distinct chord symbols was 232, from which approximately 2.9×10^9 distinct 4-grams can be created in principle. The numbers of distinct 3-grams, 4-grams, and 5-grams appearing in the dataset were 12 258, 27 237, and 44 204, respectively. Fig. 1B shows the yearly numbers of 4-grams and those of newly appeared 4-grams; the average rate of new 4-grams was 39%.

3.2 Selection biases

The inferred value of the time constant was $\tau = 2.61 \pm 0.53$. This means that the probability of a chord segment being chosen as a reference reduces by a factor of 10 in every 6.1 years, when other conditions are equal. The inferred value of the frequency-dependence parameter was $\alpha = 1.16 \pm 0.16$. The mean value indicates a slightly positive frequency-dependent bias, i.e., more common chord segments tend to be more frequently chosen as a reference than its frequency expected for random selection. However, the deviation of α from unity is small and the result is consistent with the frequency-independent bias within the range of statistical error.

λ_{rep}	λ_{sub}	λ_{del}	λ_{ins}
0.38	0.46	0.00	0.16

Table 1. Inferred values of mutation mode probabilities.**Fig. 2.** Dynamic changes of mutation mode probabilities.

3.3 Mutation modes

The inferred values of mutation mode probabilities are listed in Table 1. We found that the probability of choosing the deletion mode tended to converge to zero. To understand this result, we note that the probability of each mutation mode is of the same order, $O(K^{-L})$ for $K = \#\Omega$, if we suppose a uniform distribution over all chord symbols. The result can then be explained by the fact that there are no tunable parameters for the deletion operation whereas the substitution and insertion probabilities, $\pi_{\text{sub}}(a|a')$ and $\pi_{\text{ins}}(a|a')$, are trained so that the likelihoods of these modes will increase in the course of statistical inference. Consequently, in our model, the main mutation modes are substitution and insertion.

We see that the sum of mutation probabilities, which is equal to $1 - \lambda_{\text{rep}}$, is 62% and larger than the average rate (39%) of new segments. This value is substantially larger than the mutation probabilities in typical biological evolution and leads to distinct characteristics. For example, a significant proportion (38%) of reappeared segments are estimated to be created through a mutation process according to the present model.

A posterior analysis over time showed that the substitution mode probability had some variations across years and a general trend of increase from the 1960s to the 1990s (Fig. 2). Its temporal changes highly correlated with the rate of new segments ($\rho = 0.86$, $p < 10^{-10}$). On the other hand, the insertion mode probability had small fluctuation and no notable trend was observed.

3.4 Symbol-wise substitution and insertion probabilities

The most frequent modes of symbol-wise substitution and insertion are shown in Fig. 3 with their yearly relative frequencies obtained by the posterior analysis. For substitution probabilities (Fig. 3A), we see that there are significant changes over years and the diversity of applied substitution modes considerably increased from the early period to the late period. There is also a tendency that substitutions involving less frequent

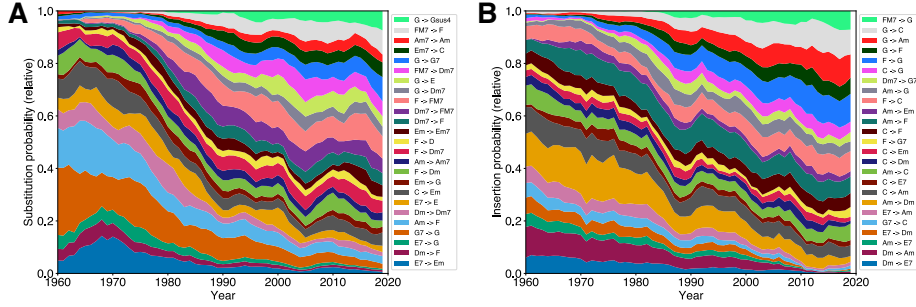


Fig. 3. Dynamic changes of symbol-wise substitution (A) and insertion (B) probabilities. In each panel, the relative frequencies of the 25 most frequent modes are shown, and a smoothing with a window of 5-year width is applied.

chords such as FM7 and Gsus4 became more frequent in later periods. From the list of substitution modes, we can find that most substitutions occur between chords with the same harmonic function. These chords often share the root tone (e.g. E7 \rightarrow Em, Dm \rightarrow Dm7, F \rightarrow FM7, and G \rightarrow Gsus4) or share constituent pitches (e.g. Dm \rightarrow F, C \rightarrow Em, and Em7 \rightarrow C). A similar relation between the substitutability of chords and the harmonic function was also found in an analysis using hidden Markov model [25].

Significant changes over years were also found in the insertion probabilities (Fig. 3B). The list of insertion modes mostly consisted of common chord transitions (see also Sec. 3.5). We see a tendency that chord transitions used in the minor key (e.g. Dm \rightarrow E7, E7 \rightarrow Am, and Am \rightarrow Dm) appear more frequently in the early period and those used in the major key (e.g. F \rightarrow G, G \rightarrow C, and FM7 \rightarrow G) in the late period.

3.5 Correlation between fluctuation and mutation probabilities

We analyzed the correlations between evolutionary parameters to examine several expectations from the evolutionary theory. On the one hand, if new chord segments are stochastically generated by substitutions, we expect that the joint probability of different chord symbols $P_{\text{var}}(a', a)$ in variants of segments related by a single substitution correlates with the joint probability of substitution $\pi_{\text{sub}}(a' \rightarrow a) = P(a')\pi_{\text{sub}}(a|a')$, where $P(a')$ is the prior probability of chord symbols. On the other hand, if we consider the implicit effect of social selection in the data, among potential creators who generate new segments with different substitution probabilities, successful creators would be those with substitution probabilities that are similar to the fluctuation probabilities of chord symbols in past data. This also suggests that the probability $\pi_{\text{sub}}(a' \rightarrow a)$ correlates with the fluctuation represented by the probability $P_{\text{var}}(a', a)$ in past data.

To examine this expectation, we analyzed the correlation between the joint substitution probability $\pi_{\text{sub}}(a' \rightarrow a)$ in a time range [2010 : 2019] and the fluctuation $P_{\text{var}}(a', a)$ observed in a time range [1927 : 2009]. The result in Fig. 4A supports the expectation and shows a positive correlation ($\rho = 0.18$, $p < 10^{-10}$). We also see a significant amount of deviation: in particular, a high fluctuation probability does not always indicate a high substitution probability.

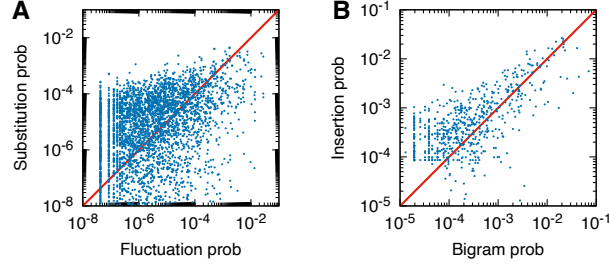


Fig. 4. Correlations between fluctuation and mutation probabilities. A: The fluctuation probability $P_{\text{var}}(a', a)$ and the joint substitution probability $\pi_{\text{sub}}(a' \rightarrow a)$. B: The bigram probability $P_{\text{bi}}(a', a)$ and the joint insertion probability $\pi_{\text{ins}}(a' \rightarrow a)$.

Similarly, we expect that the insertion probabilities are related to the corresponding fluctuation probabilities. More specifically, we expect that the joint probability of insertion $\pi_{\text{ins}}(a' \rightarrow a) = P(a')\pi_{\text{ins}}(a|a')$ correlates with the bigram probability $P_{\text{bi}}(a', a)$ of chord symbols in past data. The result in Fig. 4B supports the expectation and shows a high correlation ($\rho = 0.64$, $p < 10^{-10}$).

3.6 Diffusion of mutants

Characterizing the conditions of new mutant chord segments that will diffuse and become commonly used is important for understanding the macroscopic evolution of chord progressions. For biological evolution, where mutations are rare, a similar problem of fixation has been studied, and the fitness of the mutant and the random sampling in a finite population are studied as two major factors [26]. Our case of cultural evolution has two features that lead to an evolutionary process distinct from the typical case of biological evolution. First, as we discussed in Sec. 3.3, the mutation rate is much larger than in biological evolution so that the chance that mutants of the same form are independently generated is not negligible. Second, the evolutionary process is an accumulated process so that mutant segments will not be removed from the artifact pool.

Based on this consideration, we expect that the accumulation of independent mutants is relevant for the diffusion of a new chord segment. As a measure of diffusion of a segment w , we can use its probability of replication. More specifically, we define the diffusedness $D^{10\text{yr}}(w, t_w^*)$ of a mutant segment w first appeared in year t_w^* as

$$D^{10\text{yr}}(w, t_w^*) = \frac{1}{10} \sum_{t=t_w^*+1}^{t=t_w^*+10} \lambda_{\text{rep/sub}} P_{\text{rep}}(w, t), \quad (15)$$

where the replication probability $P_{\text{rep}}(w, t)$ is given in Eq. (9). Our hypothesis is that a mutant with a larger mutation probability $P(w; S_{t_w^*})$ has a higher chance of repeatedly introduced to the artifact pool and consequently has a higher diffusedness on average.

The relationship between the diffusedness and mutation probability analyzed for all mutant segments that first appeared in years between 1960 and 2009 is shown in Fig. 5. The observed high correlation ($\rho = 0.57$, $p < 10^{-10}$) supports our hypothesis, and

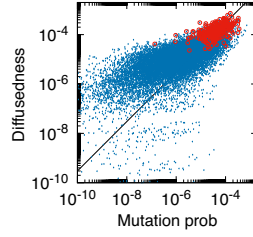


Fig. 5. Diffusedness $D^{10\text{yr}}(w, t_w^*)$ and mutation probability $P(w; S_{t_w^*})$ for mutant segments w with the year of first appearance $t_w^* \in [1960 : 2009]$. Segments that appeared four or more times within ten years after the first appearance are indicated by red circles. A linear function $y \propto x$ (black line) is shown as a guide for the eyes.

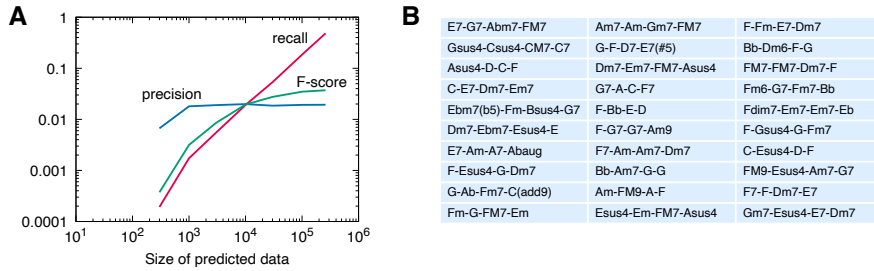


Fig. 6. Predictive ability of the evolutionary model. A: Prediction accuracies for varying sizes of predicted data. B: Most probable predictions by the evolutionary model.

the linear relation is particularly clear for mutant segments with highest diffusedness (marked in red circles in Fig. 5). The deviation from the linear relation in the small mutation probability regime can be explained by the finite size effect. We can also see that there is a variation of $O(10^1-10^2)$ in the diffusedness for those samples with a mutation probability $\sim 10^{-6}$, which indicates that the mutation probability cannot be the only factor that determines the diffusedness.

3.7 Predictions

The present evolutionary model can be used for predicting new segments to appear in the future. To examine its potential, we trained the model with a subset of the data of segments created in 1999 or before and evaluated its predictive ability using as test data the remaining data of segments created in years 2000–2019. We randomly generated 10^6 4-grams by the model and obtained approximately 2.6×10^5 segments after removing duplications and the samples already appearing in the training data. The generated 4-grams were sorted by the mutation probability in the decreasing order. We compared the predicted data with the test data by measuring the precision, recall, and F-score.

The recall achieved 48% on the whole predicted data (Fig. 6A). The precision was approximately 2%, which is much larger than the expectation value of 0.0004% by random sampling. Examples of predicted segments with highest mutation probabilities that were not included in the analyzed dataset are shown in Fig. 6B.

4 Conclusion and discussion

In this paper, we have studied the evolution of chord progressions based on a stochastic model of cultural evolution incorporating the selection and mutation processes. We summarize the main findings and discuss implications. First, the inferred selection biases showed a strong recency effect with a time constant of 2.61 yrs. This indicates that while chord segments are accumulated in the artifact pool, they will be effectively removed from the pool after some decades in the sense that their chance of being chosen as a reference will decrease significantly in that time interval. On the other hand, no significant sign of frequency dependence was observed.

Second, the analysis revealed large mutation rates and large dynamic changes in the substitution and insertion probabilities. The first feature reminds us of an interesting phenomenon known as the survival-of-the-flattest effect [27], which suggests the possibility that a chord segment with a high probability of replication can be outcompeted by segments that have lower probabilities of selection but are robust in usability against mutations. The second feature also suggests a selective advantage of chord segments that are robust in usability against mutations toward multiple directions. While the significance of this effect depends on the mutation rate and other model configurations, this observation may provide a new perspective on understanding why certain chord segments are more popular than others.

Third, the correlations found between fluctuation and mutation probabilities and between diffusedness and mutation probabilities support expectations from the evolutionary theory and may be useful for predicting the features of the evolutionary process. It is also important to seek for possible explanations for the observed deviations of $O(10^1-10^2)$ in the mutation probabilities for similar values of fluctuation probabilities.

We remark that although the present evolutionary model was built upon empirical knowledge on the process of music creation, the results of this study do not verify that the assumed process is correct. We can think of other processes of creating chord progressions, for example, a process involving data generation through statistical learning. To formulate a more realistic model, we should incorporate the multilevel structure of music, consisting of chord segments, musical piece, composer, etc.; reference and selection can occur at each of these levels. Japanese popular music is not a closed system and some chord progressions should have been imported from Western musical cultures; such migrations were treated as mutations in this study. Future work should experimentally test the model with other possibilities and address the aforementioned theoretical issues. The present evolutionary model can also be applied to analyzing the origins and relationships of chord segments in a similar way as the stochastic models of molecular evolution are applied to phylogenetic analysis.

References

1. Mauch, M., et al.: The evolution of popular music: USA 1960–2010. *Royal Society Open Science* 2(150081), 1–10 (2015)
2. Interiano, M., et al.: Musical trends and predictability of success in contemporary songs in and out of the top charts. *Royal Society Open Science* 5(171274), 1–16 (2018)

3. Singh, R., Nakamura, E.: Dynamic cluster structure and predictive modelling of music creation style distributions. *Royal Society Open Science* 9(220516), 1–18 (2022)
4. Weiß, C., et al.: Investigating style evolution of Western classical music: A computational approach. *Musicae Scientiae* 23(4), 486–507 (2019)
5. Nakamura, E., Kaneko, K.: Statistical evolutionary laws in music styles. *Scientific Reports* 9(15993), 1–11 (2019)
6. Moss, F.C., Neuwirth, M., Rohrmeier, M.: The line of fifths and the co-evolution of tonal pitch-classes. *Journal of Mathematics and Music* (2022)
7. Zivic, P.H.R., Shifres, F., Cecchi, G.A.: Perceptual basis of evolving Western musical styles. *Proceedings of the National Academy of Sciences of the USA* 110(24), 10034–10038 (2013)
8. Youngblood, M.: Conformity bias in the cultural transmission of music sampling traditions. *Royal Society Open Science* 6(191149), 1–8 (2019)
9. Cavalli-Sforza, L.L., Feldman, M.W.: *Cultural Transmission and Evolution*. Princeton University Press, Princeton (1981)
10. Savage, P.E., et al.: Sequence alignment of folk song melodies reveals cross-cultural regularities of musical evolution. *Current Biology* 32(6), 1395–1402.e8 (2022)
11. McBride, J.M., Tlustý, T.: Cross-cultural data shows musical scales evolved to maximise imperfect fifths. Preprint arXiv:1906.06171 (2019)
12. Ravignani, A., Delgado, T., Kirby, S.: Musical evolution in the lab exhibits rhythmic universals. *Nature Human Behaviour* 1(0007), 1–7 (2016)
13. Anglada-Tort, M., et al.: Large-scale iterated singing experiments reveal oral transmission mechanisms underlying music evolution. *Current Biology* 33(8), 1472–1486.e12 (2023)
14. Fernández, J.D., Vico, F.: AI methods in algorithmic composition: A comprehensive survey. *Journal of Artificial Intelligence Research* 48, 513–582 (2013)
15. Nakamura, E.: Conjugate distribution laws in cultural evolution via statistical learning. *Physical Review E* 104(034309), 1–13 (2021)
16. Scott, R.: *Chord Progressions for Songwriters*. iUniverse, Bloomington (2003)
17. Hooktheory: Popular Chord Progressions, <https://www.hooktheory.com/theorytab/common-chord-progressions>
18. de Clercq, T., Temperley, D.: A corpus analysis of rock harmony. *Popular Music* 30(1), 47–70 (2011)
19. Felsenstein, J.: Evolutionary trees from DNA sequences: A maximum likelihood approach. *Journal of Molecular Evolution* 17, 368–376 (1981)
20. Arenas, M.: Trends in substitution models of molecular evolution. *Frontier in Genetics* 6(319), 1–9 (2015)
21. Wang, D., Song, C., Barabási, A.L.: Quantifying long-term scientific impact. *Science* 342(6154), 127–132 (2013)
22. Boyd, R., Richerson, P.J.: *Culture and the Evolutionary Process*. The University of Chicago Press, Chicago (1985)
23. Warrell, J., Salichos, L., Gerstein, M.: Latent evolutionary signatures: A general framework for analyzing music and cultural evolution. Preprint bioRxiv doi:10.1101/2020.10.23.352930 (2020)
24. Shiiba, K., Kubo (ed.), S.: *Japanese Songs Vols. 3–9* (in Japanese). Nobarasha, Tokyo (1998/1999/2001/2004/2014)
25. Uehara, Y., Nakamura, E., Tojo, S.: Chord function identification with modulation detection based on HMM. In: *Proc. CMMR*, pp. 59–70. The Laboratory PRISM, Marseille (2019)
26. Kimura, M.: On the probability of fixation of mutant genes in a population. *Genetics* 47(6), 713–719 (1962)
27. Wilke, C.O., et al.: Evolution of digital organisms at high mutation rates leads to survival of the flattest. *Nature* 412, 331–333 (2001)