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SONIFICATION OF PHYLOGENETIC TREES: LISTENING TO EVOLUTION

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ABSTRACT

A phylogenetic tree is a visual representation of the evolutionary relationships linking organisms or species, analogous to a genealogy for members of a family. In phylogenetic trees, nodes represent ancestors, leaves represent species, and edges represent time or the amount of character or genetic change. The visualization and the comparison of such hierarchical structure can be very challenging, especially when the number of species is high. In this work, we suggest a new approach for getting insights into the main structural features of phylogenetic trees. We define simple rules for the sonification of a phylogeny and apply them to the simplified tree of Boroetheria, a group of mammals comprising, among others, human, mouse, rabbit, whale and cat. This approach appears to be very promising for better apprehending tree structures.

RÉSUMÉ

Un arbre phylogénétique est une représentation graphique des relations évolutives entre organismes ou entre espèces, analogue à un arbre généalogique pour des individus. Dans les arbres phylogénétiques, les nœuds représentent les ancêtres, les feuilles représentent les espèces, et les branches montrent le nombre de différences (morphologiques, génétiques) accumulées au cours du temps. La visualisation et la comparaison de telles structures hiérarchiques sont des enjeux de taille, en particulier lorsque le nombre d'espèces est élevé. Nous proposons dans cette étude de considérer les caractéristiques structurelles clés des arbres phylogénétiques par une nouvelle approche. Nous définissons pour cela des règles simples de sonification d'une phylogénie et l'appliquons à l'arbre simplifié des Boréoeuthériens (Boroetheria), un groupe de mammifères composé, entre autres espèces, des humains, des souris, des lapins, des baleines et des chats. Cette approche semble très prometteuse pour mieux appréhender les structures d'arbres.

1. INTRODUCTION

Using sound to communicate information is the *raison d'être* of auditory displays. One subtype of auditory displays is *sonification*, where sounds are generated from complex data in a systematic, objective and reproducible manner with the aim of facilitating data interpretation and communication[1-2].

The use of sonification in biology (reviewed in [3]) dates back to the eighties. It was applied to DNA sequences [4], to protein sequences [5] and even to protein structures ([6] and references therein). In all cases, the conversion of these data into audio proved to be useful for getting a better sense of the patterns in the data that was not obvious with visual inspection.

The examples above rely on the conversion of a single object, usually a sequence, into sound. But these biological objects have been shaped by an evolutionary process that started more than 4 billion years ago when life emerged on earth [7]. It is this process that we propose to encode into a sequence of chords.

In evolutionary biology, the comparison of sequences helps resolve evolutionary relationship between living species. The principle is straightforward: two species that diverged a long time ago will carry sequences (DNA and protein) that diverge more than species that diverged recently. By comparing sequences for multiple species, it is possible to reconstruct the evolutionary history of all these species. These relationships are usually represented by trees referred to as *phylogenetic trees*.

Apart from their reconstruction, working with phylogenies in biology can be challenging. The main reason is that trees of more than a few hundred species cannot be easily represented graphically. Solutions to this problem have been proposed recently, by transforming the tree into a fractal structure [8] and making it explorable in a Google-maps-like manner. Doing so, however, one loses an important feature of phylogenetic trees, namely branch lengths. Another obvious difficulty with phylogenetic trees, and any tree-like structure, is their diffusion to blind people. For these reasons, alternative (non-visual) methods for representing phylogenetic trees could be very useful.

In this paper, we suggest a first model to convert phylogenetic trees into a chord sequence. Sonification of phylogenetic trees requires the use of rules that respect both the hierarchical nature of the tree and its temporal nature (branch lengths).

We constrained the sonification model to be systematic and repeatable, but also to be bijective: the tree-generated chord sequence can be unequivocally converted back to the initial tree. Our sonification assigns a chord to each node, from the root to the tips of the tree. The chord is a group of notes simultaneously played. For each node, it is obtained by modification of the parental chord, following simple rules described in the next section. Such a process of inheritance with modification is analogous to the transmission of genes from ancestors to descendants in evolution. Consequently, and still analogous to evolutionary processes, closely related nodes and tips have chords that are less different than nodes that diverged for a longer time. Once each node and tip has a chord assigned to it, two options for playing these chords are suggested: one follows the evolutionary direction (from root to tips); the other follows the graphical representation of the tree. Pros and cons of each option are discussed.

2. METHODS

We detail here how a chord is assigned to each node of any phylogenetic tree. We then describe two options for the order and rhythm at which to play these chords.

2.1. Definitions

A binary tree (in our case a phylogeny) is a directed graph where all nodes have one parent node and two descendant nodes. Nodes are linked by *edges*. If a node has no parent node, it is the *root*. If it has no descendants, it is a *tip*. Nodes and tips are hereafter referred to as *nodes* for simplicity.

2.2. Onsets

In the audio, the order of the onsets is given by the projection of the tree nodes on a vertical axis or on a horizontal axis, depending on the playing option chosen. The musical time origin coincides with the projection of the root, in the horizontal reading (first option), or with the projection of the lower tip, in the vertical reading (second option).

2.3. Chords

To each node is associated a chord containing the same notes as the parent node, plus one additional note. This note depends on the node position in the tree, upper or lower, relative to its parent. As a result, a node with N ancestors is associated to a chord with $N+1$ notes and only the root corresponds to a single note, arbitrarily chosen: C in this study.

2.4. Pitch

In the binary trees considered here, the two descendants of each parent node are called *upper* and *lower* nodes, depending on their graphical position in the tree. The additional note associated to the upper node is chosen to be one third below the lowest pitch note assigned to its parent node, while the additional note of the lower node is chosen to be one fifth below that of its parent node. These two notes follow the lowest pitch note of the parent node in the sequence of Figure 1a. This sequence is constructed so that the musical interval between two successive notes is a minor or a major third, and the interval between two notes separated by one note is a fifth. Such a sequence has a period of 24 notes, in which all notes of the chromatic scale appear twice.

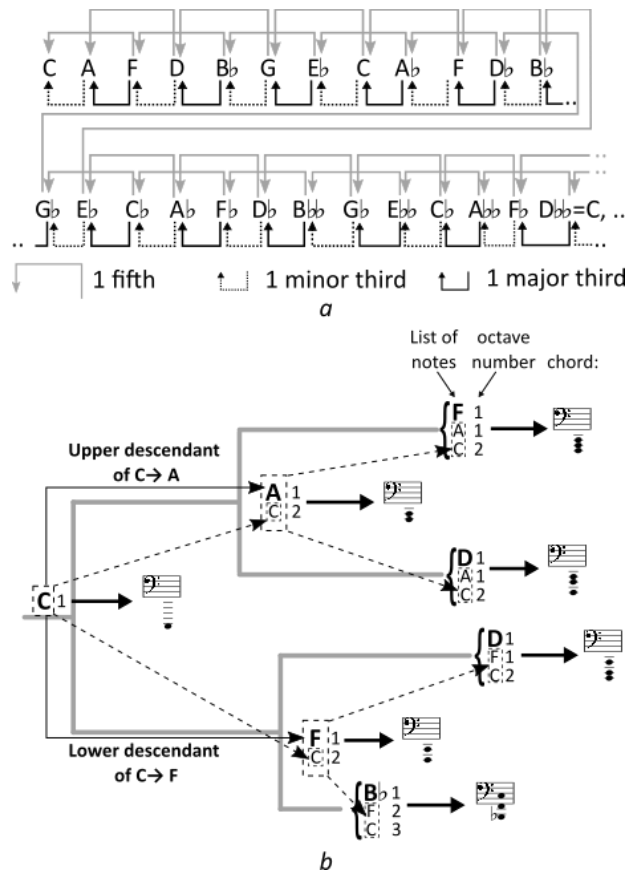


Figure 1. a- Periodic sequence of notes associated to successive nodes in a phylogenetic tree. Starting from C, the two following notes, A and F, are attributed to the upper and lower descendants. The interval between two consecutive notes forms a minor or a major third, while the interval between every second note forms a fifth. b- Example of symmetric tree with three generations of nodes (solid gray). For each chord, the additional note (bold) is deduced from the lower note of the parent chord (solid black arrow) and the sequence of Fig.1a. The other notes (light) are inherited from the parent node (dashed black arrows). For each chord, the octave numbers are chosen so that the pitches of the notes form a growing sequence.

Then, for each chord, the notes are ranked: the lowest one is the one added at the current node and is followed by the notes composing the parent chord, in the same order. In this sequence of notes, the octave numbers are the minimum numbers so that their pitches form a growing sequence. The octave number of the lowest note is arbitrarily set to 1, so that its fundamental frequency lies between 32Hz (C1) and 62Hz (B1). This choice leads to chords with a potentially large number of notes in the frequency range where human hearing is particularly sensitive [9]. Further, with such a method, distant nodes correspond to high pitch notes, which human hearing is less sensitive to. Therefore their contribution to the current chord is relatively small.

With such a method, the chord associated to each node mirror all its ascending nodes and therefore occurs only once. In consequence, a tree leads to one and only one audio extract, as soon as the root is assigned a note. As an example, see Fig. 1b, in a symmetrical tree, if the root corresponds to C, the nodes of third generation are associated to the following four triads:

- F1 A1 C2, which is a major F chord,
- D1 A1 C2, which is a D7 chord with absent third,
- D1 F1 C2, which is a Dm7 chord with absent fifth,
- B♭1F2 C3, which is a B♭9 chord with absent third.

Therefore, nodes with more ancestors are associated to chords with more notes. In consequence, for large phylogenetic trees, the chords are composed of a widely varying number of notes.

This coding system is illustrated in Figure 2 with a very simple phylogenetic tree of five tips. Its root is arbitrarily associated to C. The two reading options are given by the vertical and the horizontal staves. We believe that such a coding system allows the listener to identify the tree structure from the audio extract.

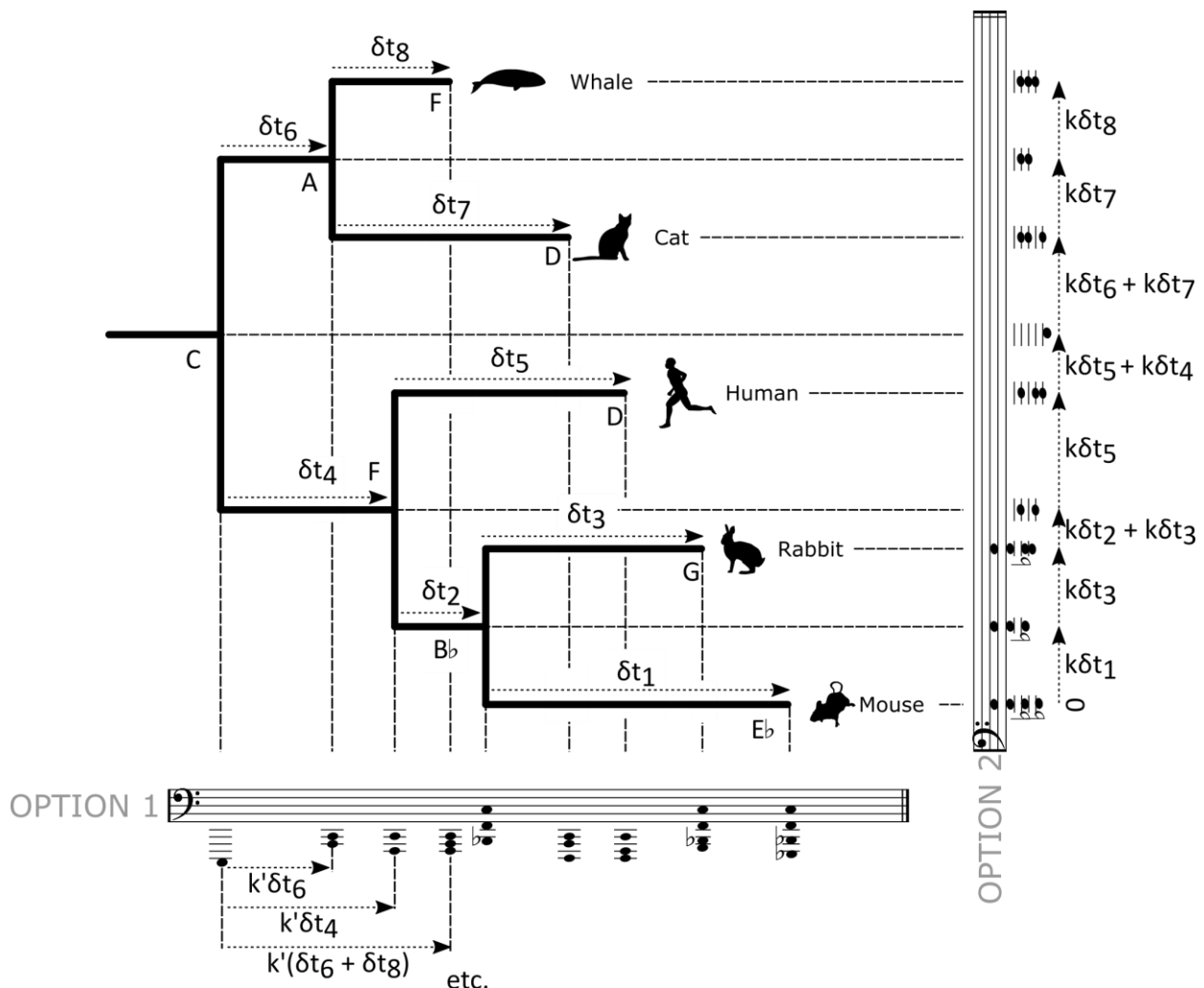


Figure 2. Conversion of the phylogenetic tree of Boroetheria (a group of mammals) to a chord sequence. The two reading options lead to different orders of chords. The dashed lines indicate the onsets of the chords associated to the nodes and tips of the tree. The notes of each chord are shown on the vertical and horizontal staves. The duration of the chords are proportional to the length of branch separating them. In this example, the topology of the tree is correct but the branch lengths have been randomly sampled.

2.5. Rythm

In each chord, the notes have equal duration. What changes is the duration of the chords. In both options, vertical and horizontal readings, this duration is the sum of the branch lengths separating the corresponding nodes, as shown in Fig.2. For simplicity, the durations between the first chord (representing the root) and the following chords are given for the horizontal option, while for the vertical option, the arrows show the duration of each chord. Branch lengths being continuous variables, the rhythm of the audio was not shown on the stave directly. Note however that its total duration can be adjusted by modifying the k and k' constants.

2.6. Bijectivity

Let us consider an audio sequence derived from a binary tree using the preceding rules. Each chord is composed of a sequence of notes, corresponding to a unique list of ancestors. Accordingly, its position in the tree is unequivocal. In consequence, only one topology of tree can be associated to the given audio. In addition, the lengths of its branches are determined by the chord durations. Therefore the tree corresponding to the audio considered is unique and the sonification model is bijective between the sets of binary trees and resulting audio sequences.

2.7. Audio

As an example, the phylogenetic tree of Boroetheria (cf.Fig.2) is converted to audio using the coding method and the two reading options. The two resulting sequences of chords are synthesized using virtual piano sounds with the visual programming language Pure Data.

3. CONCLUDING REMARKS AND PERSPECTIVES

The horizontal reading should be preferred when possible for multiple reasons: the chords are played in the same order as the nodes in the evolutionary timescale, and the graphical representation chosen for the tree has no impact on the rhythm of the chords sequence, which is desirable. However, for 'ultrametric trees', all tips lie at the same distance to the root. In the horizontal reading they would thus be all played simultaneously. To avoid this, vertical reading may be preferred in this case.

This first attempt of sonification of a phylogenetic tree is promising. More work is needed in order to better evaluate alternative coding methods, and to test the ability of evolutionary biologists that are used to manipulate phylogenies to discriminate between alternative topologies or recognize similarities

between trees, based solely on their music representation.

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