



Rhythm Zoo: Music Composition Modeled on Genetic Networks

Anna Lindemann¹ and Eric Lindemann²

¹University of Connecticut, USA, Email: aklindemann@gmail.com

²Synful, USA, Email: eric@synful.com

Abstract

Inspired by the cyclical patterns of gene expression found in developing organisms, and the resonance these patterns have with rhythmic and harmonic cycles in music, our ongoing creative work focuses on the use of hierarchical Random Boolean Networks (RBNs) for musical creation. RBN models are widely used in scientific research to study the genetic networks underlying biological systems. A hierarchical RBN consists of multiple, interconnected sub-networks that run at different time scales. As a result, the sub-networks disrupt and influence each other's cyclical behaviors. In biology, these patterns of interference, which manifest in genetic networks, are what define biological structure: for instance, which part of an organism will become a head versus a tail. Inspired by the way that disruption creates biological structure, we use hierarchical systems of musical RBNs to create musical form and compose “musical organisms.”

Keywords

Music, Biology, Random Boolean Network (RBN), Generative Art, Genetic Networks

A Case for Biological Art

Life on earth is filled with beauty, diversity, complexity, and even absurdity—many of the qualities artists often strive to capture in creative work. We believe that artists can learn from the billions of years that life on earth has had for creative exploration by taking inspiration from the processes that develop these qualities in living organisms.

DNA acts as the code for biological development and has been a source of inspiration for the development of a wide range of artworks, including music. Susumu Ohno and Midori Ohno's 1986 paper “The all pervasive principle of repetitious recurrence governs not only coding sequence construction but also human endeavor in musical composition” compares repetitions found in DNA sequences with the repetitions found in music, and suggests the possibility for creating music based on DNA as well as DNA based on music [1]. Other composers, musicians, and musician-biologist collaboratives have developed a variety of approaches to creating music based on DNA sequences as well as music based on protein amino acid sequences [2, 3, 4, 5].

In our work inspired by biological development we have been interested in the *interactions* between specific DNA sequences (i.e. genes). These gene interactions form what is known as genetic networks (Figure 1). One of the in-

credible and inspiring aspects of biological development is the process of converting DNA sequence information into complex, hierarchical structure with repetition at different scales. An organism is composed of a variety of large-scale structures, some of which can be repeating structures like ribs and limbs. Each of these structures can be composed of a variety of tissues, which in turn can be composed of many cells of a particular cell type. Each cell, in turn, is composed of varied, but repeated, molecules. Similarly, a musical composition possesses complex, hierarchical structure with repetition at different scales. A musical work might follow a sonata form or a rondo form composed of repeating sections and phrases. Within each of these larger sections, different rhythmic patterns, harmonic cadences, and melodic motifs can recur.

Our work extends Susumu Ohno and Midori Ohno's comparison of “repetitious recurrence” in music and biology to include the “repetitious recurrence” found in the complex hierarchical structures of both music and biology. With “Rhythm Zoo” we create “musical organisms” with musical form that is at once familiar and novel. We achieve this by creating algorithmically generated music modeled on the gene network dynamics that generate structure in living organisms.

“Rhythm Zoo” evolves from a nine-year investigation of biological systems as models for music composition, and is influenced by our backgrounds in evolutionary developmental biology, digital signal processing, music synthesis, art-science performance, and music composition.

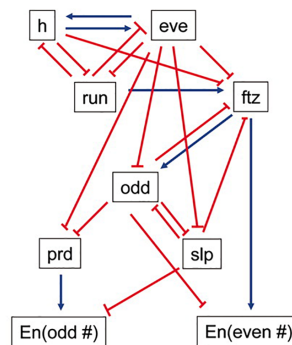


Figure 1. This is an example of a gene network [6]. Each node in the network represents a gene (e.g. ‘ftz’). At any given time, a gene can be expressed (ON) or unexpressed (OFF). The expression of a gene is dependent on influences from other genes, represented by the interconnecting lines. A gene can inhibit (turn OFF) the expression of another gene (red lines) or promote (turn ON) the expression of another gene (blue arrows). The interconnectivity of the network results in complex patterns of gene expression that are critical to defining structure and pattern in developing organisms. This particular gene network is important in defining body segments in the beetle *Tribolium castaneum*.

Using Random Boolean Networks

Many breakthroughs in genomic sequencing have been made in the past half century, including the completion of the Human Genome Project in 2003. But even for species where the entire genome has been sequenced, much of the interconnectivity of the genome (i.e. the genetic network) remains unknown. Uncovering genetic networks is especially challenging for species like humans where experimental manipulation of genes is problematic.

Random Boolean Networks (RBNs) were first introduced by Stuart Kauffman in 1969 as simplified, computational representations of genetic networks [7]. RBNs have since been widely used in scientific research to simulate and study gene network dynamics in the absence of and in conjunction with wet lab experimental data.

An RBN is a randomly generated network containing a random number of nodes with random interconnections. The number of connections and the type of connections (promotion or inhibition) in the network are critical to the network demonstrating behaviors similar to those found in the gene networks of living organisms. Given an initial state, with certain genes expressed (ON) and others unexpressed (OFF), an RBN will pass through a number of expression states and then fall into a rhythmic pattern. Figure 2 shows the state space of a 13-gene RBN where 8,192 possible initial states fall into one of 15 rhythmic patterns.

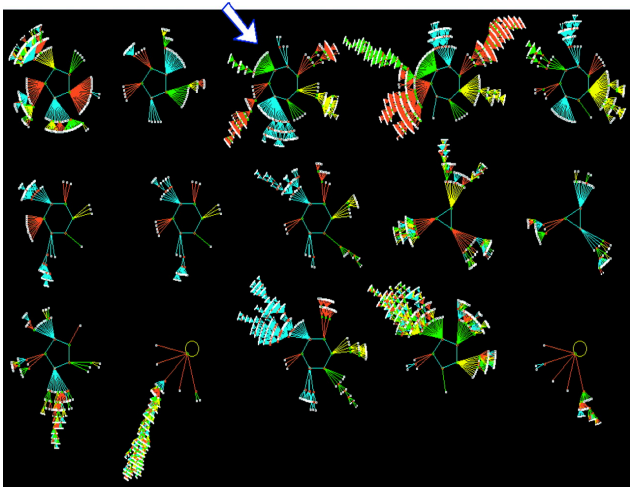


Figure 2. This figure diagramming a 13-node network is reproduced from a paper by Stefan Bornholdt [8] and adapted from an image by Andrew Wuensche [9]. The network has $2^{13} = 8,192$ possible initial states. Each state flows into one of 15 attractor cycles (the polygons at the center of each of the clustered paths). The number of edges for each polygon corresponds to the number of “beats” for that attractor cycle. For example, the attractor cycle identified by the white arrow has 7 edges or “beats.” This network can generate cycles with 1, 3, 5, 6, or 7 beats. From a network with only 13 nodes (genes or musical pitch states) springs the possibility for rhythmic and metric complexity.

In our “Rhythm Zoo,” genes within an RBN are associated with musical tones (e.g. a piano note or a particular drum in a percussion ensemble) that are sounded when the genes are expressed. In biological networks, most expressed genes ultimately make proteins that give structure to a cell. However, some expressed genes, called transcription factors, serve purely as regulators of other genes. In our musical networks, some musical genes create musical structure (they produce sounds), while other musical genes act as musical transcription factors. These musical transcription factors are silent, but they act as regulators of other sound-producing genes.

The “Rhythm Zoo” has focused on hierarchical RBN systems with a number of RBN sub-networks and limited interconnections between sub-networks. This hierarchical approach is critical to creating complex “repetitious recurrence” at different structural scales. Key to this hierarchical approach is that each sub-network runs at a different time-scale (e.g. one sub-network may be evaluated 100 times per second while another only once per second). This results in the disruption of one sub-network by another, creating abrupt shifts in musical texture and revealing large-scale musical structure. In one significant network configuration, one or more slow sub-networks, with silent regulatory musical genes, are connected to fast sub-networks with sound-producing genes.

Animals from the Rhythm Zoo

Our RBN system produces “musical organisms,” some examples of which can be found online in our “Rhythm Zoo”: <http://www.askewmusic.com/RBNMusic.html>. Our “musical organisms” are simulated in Matlab and sonified using a variety of music synthesis techniques.

“RBN Free Jazz,” [10] one of the “musical organisms” featured online, was generated algorithmically using our RBN system and using sampled piano, bass, and drums without edits or post-production. At 18 seconds into the piece, a dense poly-rhythmic structure in the piano with an equally chaotic drum part gives way to a simple driving repeated pattern in the piano accompanied by a strong backbeat in the drums on 2 and 4. These changes occur without human intervention. This demonstrates the capacity of our multi-periodic RBN system to produce musical structure with dramatic shifts in texture and complexity.

Our RBN system was also used to create the score for *Beetle Bluffs* (2013) [11], an animated film by Anna Lindemann, developed in collaboration with the Harvard Museum of Comparative Zoology. The film illuminates the evolution of an adaptive color pattern found across nine Cuban beetle species. As a beetle’s color pattern evolves in the film from 3m26s to 6m48s, the musical textures also evolve. The five incremental steps in the evolutionary process illustrated in the film were generated musically as a result of five instances of human modification to initial parameters defining a single musical RBN hierarchy. The music was realized using sampled synthesized sounds.

Conclusion

To our knowledge, our use of RBNs makes our project the first work of generative art modeled on the mutual interference of multiple genetic networks running at different time cycles. In biology, the patterns of interference that result from the disruption of one genetic sub-network by another are what define biological structure: for instance, which part of an organism will become a head versus a tail, or how many legs an organism will grow. Inspired by the way that disruption creates biological structure, we use hierarchical systems of musical RBNs to create musical form. This ability to generate macro-scale structure algorithmically is a novel and significant contribution to the world of generative art.

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