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Topological Analysis of Musical Transformation in Debussy's Clair de Lune

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AUTHOR BIOGRAPHY

Christina Wang is a senior at West Windsor-Plainsboro High School North in New Jersey. She is passionate about both mathematics and music and hopes to keep exploring ways to connect the two through interdisciplinary research in the future.

ABSTRACT

This study uses topological data analysis (TDA) to examine the harmonic and melodic patterns in Claude Debussy's Clair de Lune. By applying tools such as persistent homology and Betti coefficients, we uncover how Debussy shapes his music through shifting tonal centers, harmonic ambiguity, and smooth, flowing progressions. These features, central to his Impressionist style, create the soundscapes which he is well known for. To place these findings in context, we compare Debussy's work with that of Arnold Schoenberg, whose very different musical style produces contrasting topological results. The differences in the topological data generated from their works are then explained in musical terms, highlighting how Schoenberg's use of atonality and structural discontinuity diverges from Debussy's fluidity. By connecting mathematics with music, this study offers new ways to visualize and understand how composers build complex sound worlds. This analysis bridges the fields of mathematics and music, providing a novel perspective on Debussy's music and offering new tools for understanding complex musical elements through mathematical lenses.

Keywords*: Persistent Homology, Betti Coefficients, Topological Data Analysis, Harmonic Progression, Clair de Lune, Debussy, Schoenberg, Javaplex*

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INTRODUCTION

Mathematics and music are deeply intertwined disciplines, with connections spanning millen- nia. The ancient Greeks explored harmonic ratios, and Pythagoras discovered the relationship between string lengths and musical intervals, This formed the foundation of Western tuning systems. Later, the development of equal temperament in the Renaissance relied on logarithmic principles to standardize pitch spacing (Duffin, 2007).

In recent decades, computational tools have enabled new perspectives on music. Topological data analysis (TDA) examines the "shape" of data by identifying features such as connected components, loops, and voids (Carlsson, 2009). These features are quantified using Betti numbers. For example, Betti-0 counts connected components, which correspond to distinct clusters of data points. Betti-1 identifies loops, which represent cyclical relationships. Betti-2 captures voids, higher-dimensional structural gaps (Edelsbrunner & Harer, 2010).

Tymoczko (2011) introduced the concept of mapping voice leading in musical compositions to geometric spaces, demonstrating that harmonic transformations can be visualized in multi- dimensional spaces. Sethares and Budney (2014) extended this approach to analyze pitch and rhythm structures using persistent homology.

This study applies TDA to Clair de Lune by Claude Debussy, a hallmark of impressionistic music. To further demonstrate Debussy's style, we compare our results from Clair De Lune to those from Reflets dans L'eau, another piece written by Debussy, and Schoenberg's Op 11 No 1. By analyzing the similarities and differences between the three results, this research provides a mathematical lens to understand Debussy's compositional innovations.

CLAIR DE LUNE

Clair de Lune, composed by Claude Debussy in 1890 and revised in 1905, is one of the most well-known and celebrated piano pieces in the Impressionist genre (Shi, n.d.). Debussy's Clair de Lune set Verlaine's poem Clair de Lune (1869) twice for voice and piano (Bhogal, 2018). The poem can be translated into English as follows:

Your soul is a chosen landscape Charmed by maskers and revellers Playing the lute and dancing and almost Sad beneath their fanciful disguises!

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Even while singing, in a minor key, Of
victorious love and fortunate living
They do not seem to believe in their happiness, and their
song mingles with the moonlight.

The calm moonlight, sad and beautiful, Which
sets the birds in the trees dreaming And makes
the fountains sob with ecstasy

The tall slender fountains among the marble
statues!

Its title, French for "moonlight," evokes a sense of tranquility. Debussy's compositional style is often associated with the Impressionist movement, where traditional Western tonality is frequently replaced by non-functional harmony and exotic scales such as the whole-tone scale (Novak, 2015). These elements contribute to a sense of ambiguity. Fourier analysis and signal processing techniques have been used to examine the spectral properties of Debussy's pieces, allowing researchers to explore patterns of frequencies and rhythmic structures (Laneve et al., 2023). Other approaches have involved using system modeling to analyze the parametric rela- tionships amongst pitches, chord, etc (Pitombeira, 2018). However, few studies have explored "Clair de Lune" using tools from algebraic topology, such as persistent homology and barcode diagrams. These techniques, which are typically applied to data analysis and geometry, provide a novel way to examine the "shape" of musical structures over time.

MATHEMATICAL FOUNDATIONS OF BARCODES IN PERSISTENT HOMOLOGY

In this section, we will cover the points of mathematics used to derive the barcodes.

Distances

Topology is all about "closeness". In music, there are two notions of "closeness". Two notes are considered close if on a keyboard, they are near each other. For example, *C* and *C#* are perceived to be close together. Note that the 15.6 Hz "distance" from *C* to *C#* is generally perceived the same as the 24.7 Hz "distance" from *G#* to *A*.

The other notion of "closeness" is that of octave equivalence. For example, the 261.6 Hz of C is described as close to the 523.2 Hz of a higher C.

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We can combine these two notions to measure the distance between two events f and g as:

$$d_{PC}(f, g) = \min(s, 1 - s), \qquad s = |\log_2(f) - \log_2(g)| \quad \text{mod } 1.$$

This distance is called pitch-class distance (Sethares & Budney, 2014).

Simplicial Complexes and Filtrations

A simplicial complex is a combinatorial structure that generalizes the notion of a graph or a mesh. Formally, a *simplicial complex* Σ is a finite set of simplices satisfying the following properties:

- If $\sigma \in \Sigma$, then every face of σ is also in Σ.
- If $\sigma, \tau \in \Sigma$, then $\sigma \cap \tau$ is either empty or a face of both σ and τ.

A k-simplex σ is the convex hull of $k + 1$ affinely independent points $\{v_0, v_1, \ldots, v_k\}$. For example, a 0-simplex is a vertex, a 1-simplex is an edge, and a 2-simplex is a triangle. The dimension of a simplicial complex Σ, denoted $\dim(\Sigma)$, is the largest dimension among its simplices.

A *filtration* of a simplicial complex Σ is a nested sequence of subcomplexes (Carlsson, 2009):

$$\emptyset = \Sigma_0 \subseteq \Sigma_1 \subseteq \cdots \subseteq \Sigma_m = \Sigma,$$

where each Σ_i is a simplicial complex. Filtrations are central to persistent homology, as they provide a way to study the evolution of topological features over different scales.

Vietoris-Rips Complexes

To approximate homology from a point cloud, we use Vietoris-Rips complexes (Adams, Tausz, et al., 2011). Given a set of points P and a distance threshold ϵ, the Vietoris-Rips complex P_ϵ includes:

- Vertices for each point in P.
- Edges for pairs of points within distance ϵ.
- Higher-dimensional simplices for sets of points mutually within distance ϵ.

This complex captures the topology of the ϵ-neighborhoods of P. As ϵ increases, the complexes grow, forming a filtration whose persistent homology reveals stable features of the data's shape.

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Homology

Homology is a tool used to study topological spaces by analyzing their cycles and boundaries. For a simplicial complex Σ, the *chain complex* $C_*(\Sigma)$ is a sequence of abelian groups and boundary maps (Fugacci et al., 2016):

$$C_k(\Sigma) \xrightarrow{\partial_k} C_{k-1}(\Sigma) \longrightarrow \cdots \xrightarrow{\partial_{k-1}} C_1(\Sigma) \xrightarrow{\partial_1} C_0(\Sigma)$$

where $C_k(\Sigma)$ is the free abelian group generated by the k-simplices of Σ, and $\partial_k : C_k(\Sigma) \to C_{k-1}(\Sigma)$ is the boundary map defined by

$$\partial_k([v_0, \dots, v_k]) = \sum_{i=0}^{k} (-1)^i [v_0, \dots, \hat{v}_i, \dots, v_k],$$

where $[v_0, \dots, v_k]$ is an oriented k-simplex, and $\hat{v}_i$ indicates that v_i is omitted.

The kernel and image of the boundary maps define the cycle and boundary groups:

$$Z_k(\Sigma) = \ker(\partial_k),$$
$$B_k(\Sigma) = \mathrm{im}(\partial_{k+1}).$$

The k-th homology group is given by

$$H_k(\Sigma) = Z_k(\Sigma)/B_k(\Sigma).$$

The rank of $H_k(\Sigma)$, denoted β_k, is called the k-th Betti number and provides the number of k-dimensional holes in Σ. For example:

- β_0: Number of connected components.
- β_1: Number of independent loops.
- β_2: Number of voids enclosed by surfaces.

Persistent Homology

Persistent homology is a tool within topological data analysis (TDA) that captures the evolution of

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topological features across multiple scales. This approach allows us to quantify and visualize how patterns such as connected components, loops, and voids appear and disappear as we increase a distance threshold.

The foundation of persistent homology lies in constructing a *filtration*, which is a sequence of nested topological spaces indexed by a scale parameter ϵ (Fugacci et al., 2016). Each space in the filtration reflects the structure of the underlying data at a specific scale. For instance, consider a point cloud P sampled from a dataset. For each ϵ, we can construct a corresponding Vietoris-Rips complex, which encodes geometric relationships among points based on their pairwise distances. Formally, the Vietoris-Rips complex P_ϵ consists of:

$$P_\epsilon = \{\sigma \subseteq P \mid \mathrm{diam}(\sigma) \leq \epsilon\}$$

where σ represents a simplex, and $\mathrm{diam}(\sigma)$ is the largest distance between any two vertices of σ. As ϵ increases, additional simplices are added, creating a sequence of complexes:

$$P_0 \subseteq P_\epsilon 1 \subseteq P_\epsilon 2 \subseteq \ldots .$$

This filtration provides the foundation for tracking the birth and death of topological features across scales.

To formalize this process, we define homology groups $H_n(P_\epsilon)$ for each dimension n. These groups capture the n-dimensional features of P_ϵ: H_0 describes connected components, H_1 en- codes loops, and H_2 identifies voids enclosed by surfaces. The inclusion of complexes in the filtration induces maps between homology groups:

$$H_n(P_{\epsilon_i}) \rightarrow P_{\epsilon_{i+1}} .$$

These maps allow us to track how features persist or vanish as the filtration evolves.

The persistence of a topological feature is quantified by its birth and death scales. A feature is said to be "born" at scale ϵ_{birth} when it first appears and "dies" at scale ϵ_{death} when it merges with another feature or becomes redundant. The lifetime of a feature, $\epsilon_{\text{death}} - \epsilon_{\text{birth}}$, reflects its significance: longer-lived features are considered more intrinsic to the data, while shorter-lived ones are often treated as noise.

To visualize this information, we use *barcodes* and *persistence diagrams*. A barcode is a collection of horizontal bars, each representing a topological feature. The length of a bar corresponds to the persistence of the feature, providing an intuitive summary of the data's topology across scales. Persistence diagrams, on the other hand, plot features in a two-dimensional plane, where the x-coordinate represents ϵ_{birth} and the y-coordinate represents ϵ_{death}. Features with higher persistence lie farther from the diagonal $y = x$, emphasizing their importance.

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The computational efficiency of persistent homology is achieved through reductions of bound- ary matrices in simplicial complexes. These matrices encode relationships between simplices, and their reduction via column operations identifies the boundaries and cycles that contribute to homology. Algorithms such as the persistence algorithm in Javaplex utilize these reductions to efficiently compute birth and death pairs for topological features.

Persistent homology extends homology by analyzing how homological features evolve across a filtration of spaces. A filtration is a nested sequence of simplicial complexes:

$$\emptyset = X_0 \subseteq X_1 \subseteq \cdots \subseteq X_m = X.$$

Persistent homology tracks the birth and death of features as the filtration parameter changes, summarizing this evolution in a barcode.

IMPLEMENTATION WITH JAVAPLEX

JavaPlex (Tausz et al., 2011) is a software library for computing persistent homology. Given input data, such as a point cloud or a simplicial complex, JavaPlex constructs the corresponding filtration and computes the persistence intervals. The output includes barcodes and persistence diagrams, providing a visual and numerical summary of the topological features in the data. Some examples are included in the official documentation of Javaplex (Adams, Tausz, et al., 2011).

The pipeline for computing barcodes in JavaPlex typically involves the following steps:

1. Define the simplicial complex or point cloud.
2. Construct a filtration (Tausz et al., 2011).
3. Compute the persistence intervals for each homological dimension.
4. Visualize the barcodes or persistence diagrams.

We will now show an example using the C-major scale (Commons, n.d.).

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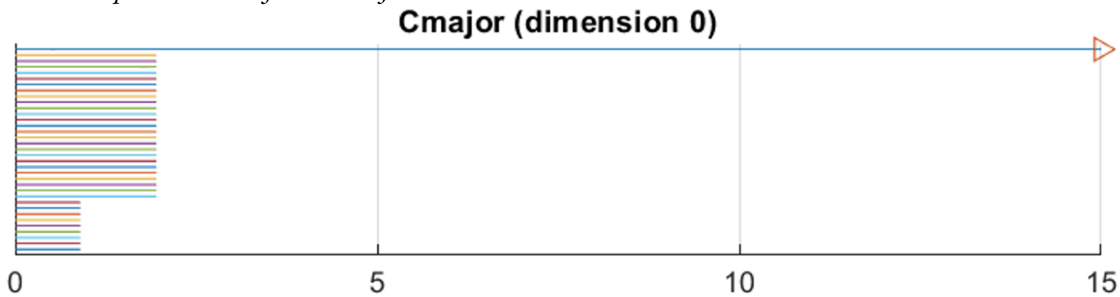
Figure 1

Barcode representation of the C-major scale



Note. Illustrate the merging of pitch classes as ϵ increases.

Initially, when ϵ is small, the barcode reflects seven distinct notes: C, D, E, F, G, A, and B. Although an octave contains eight notes, the high C is identified as equivalent to the low C under the pitch-class metric, causing them to merge immediately at $\epsilon = 0$. As ϵ increases to 0.08, the smallest intervals, E-F and B-C (both half steps), begin to merge. At $\epsilon = 0.16$, the remaining five connected components—representing whole-step intervals—combine into a single entity, reducing β_0 to 1 for all larger values of ϵ (Sethares & Budney, 2014).

RESULTS

It is worth noting that in the following barcodes, information from only the first 500 notes are used due to the calculation limit of the program. However, 500 notes is enough to capture all the important melodies and harmonies in the music.

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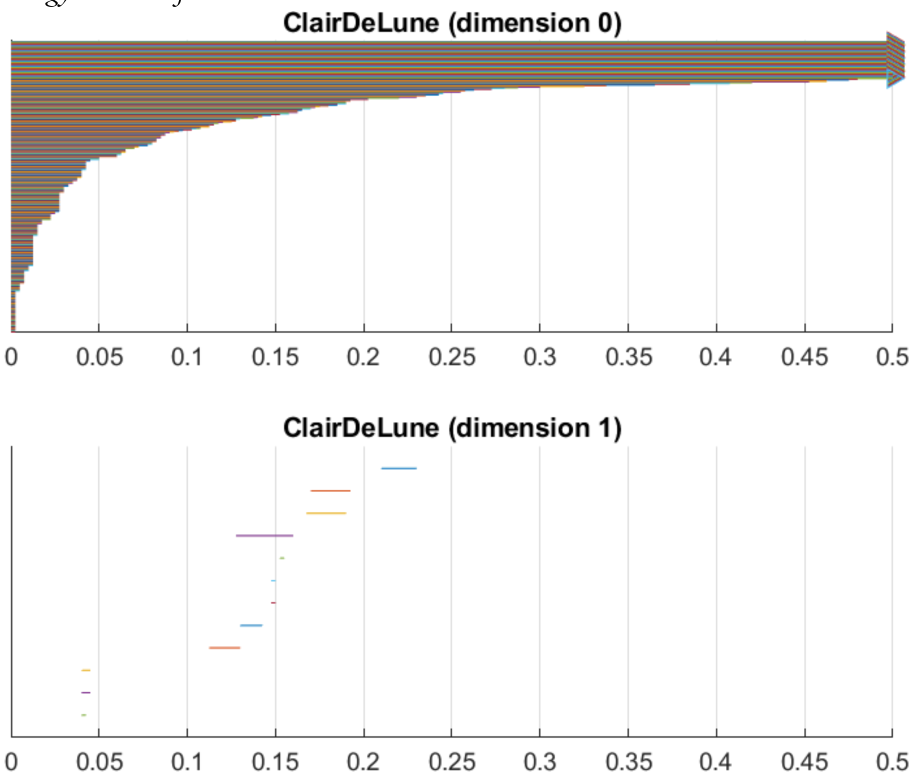
Figure 2

Persistent homology barcode of Clair de Lune.



Note. The diagram illustrates the merging of pitch components over increasing filtration values, capturing the tonal structure and harmonic relationships in the piece.

The persistent homology barcode for Clair de Lune (Figure 2) reveals structural patterns in the piece's pitch relationships. The dimension-0 barcode, which tracks connected components, exhibits rapid merging at small filtration values. This suggests a highly cohesive pitch structure, where tonal centers quickly connect to form a unified harmonic framework (Sethares, 2013; Tymoczko, 2011). A long-persisting component indicates a strong tonal or modal foundation, characteristic of Debussy's harmonic language (Robert, 2011).

The dimension-1 barcode, representing loops and cycles in the pitch space, contains a few short-lived features. These transient loops correspond to brief moments of harmonic ambi- guity or modulatory passages, yet no large-scale cyclic structures emerge. This is consistent with Clair de Lune's harmonic language, which, while rich in color, remains centered around tonal and modal relationships (Pomeroy, 2012). The short-lived cycles likely reflect Debussy's use of extended harmonies and non-functional chord progressions, which introduce momentary ambiguity without entirely departing from tonal coherence.

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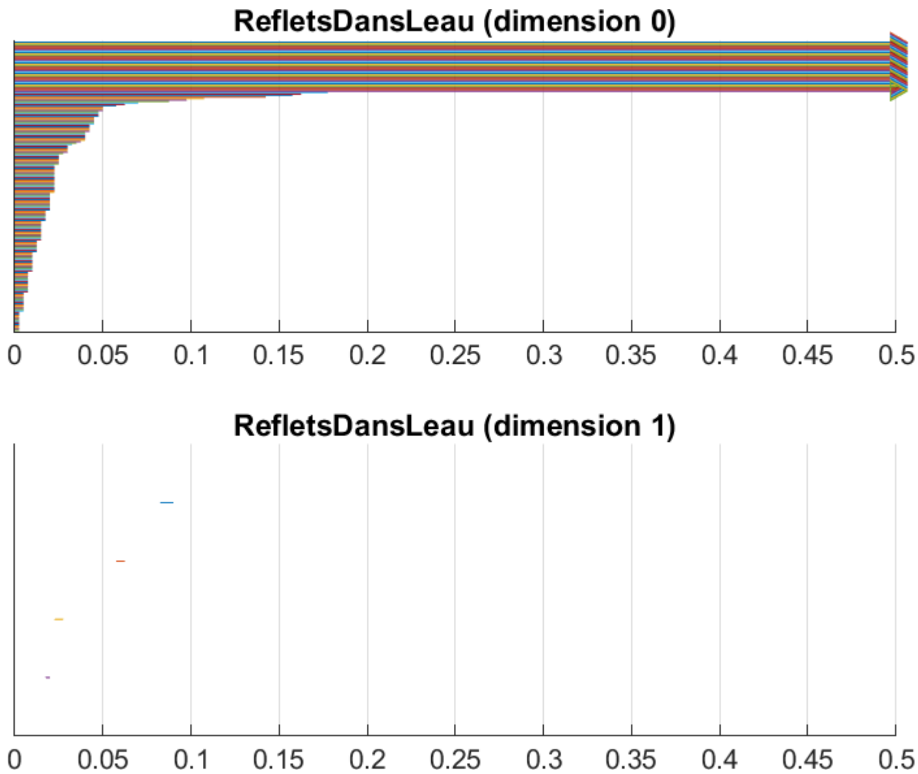
Figure 3
Persistent homology barcode of Reflets dans l'eau.



Note. This barcode represents the piece's pitch structure, highlighting tonal connectivity and brief harmonic ambiguities.

A comparison between Clair de Lune (Figure 2) and Reflets dans l'eau (Figure 3), both composed by Debussy, reveals notable similarities in their persistent homology barcodes. In both cases, dimension-0 features merge rapidly, indicating strong harmonic connectivity and tonal coherence. This suggests that despite Debussy's impressionistic techniques, his music maintains an underlying structural unity (Pasler, 2012).

In dimension-1, both pieces exhibit a few short-lived loops, reflecting brief harmonic ambiguities. These align with Debussy's fluid harmonic language, where harmonies blend rather than strictly adhere to functional progressions. Despite the differences in compositional style— Clair de Lune being more lyrical and Reflets dans l'eau more textural—both pieces rely on a fundamentally tonal or modal framework (Robert, 2011).

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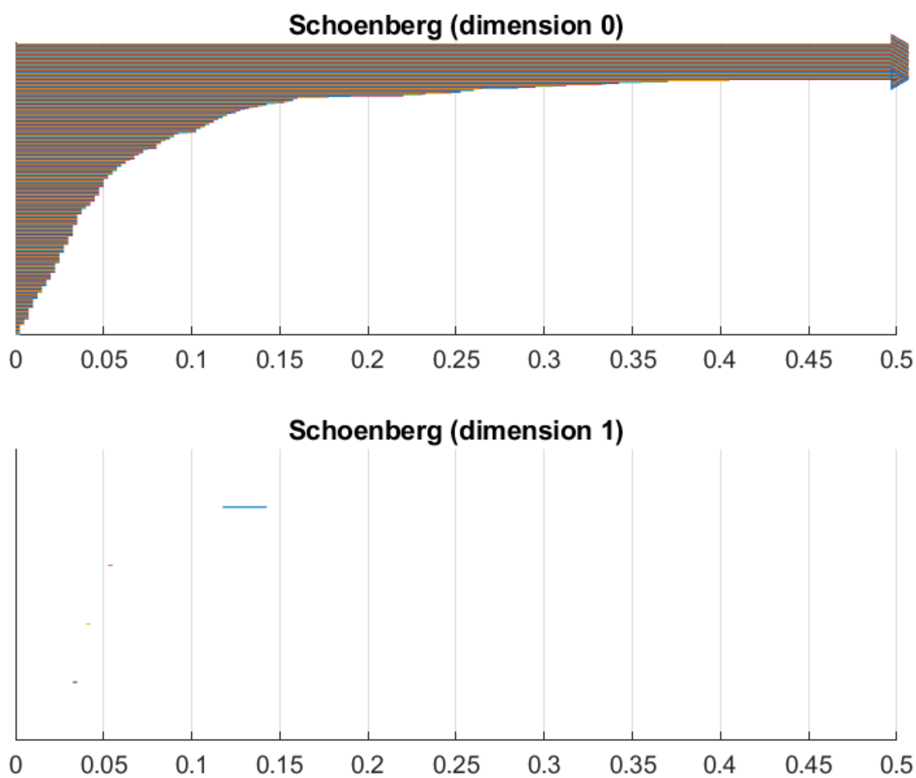
Figure 4
Persistent homology barcode of Schoenberg's Op. 11, No. 1



Note. This barcode highlights a fragmented pitch structure and the absence of a strong tonal center, characteristic of atonal music.

In contrast, the barcode of Schoenberg's Op. 11, No. 1 (Figure 4) exhibits significant structural differences. The dimension-0 barcode shows a slower merging of components compared to Clair de Lune, reflecting the absence of a strong tonal center and a more fragmented pitch organization (Morgan, 1991). This aligns with Schoenberg's atonal approach, where pitches are treated independently rather than being organized around functional harmony (Boss, 2009).

In dimension-1, the barcode reveals fewer but more persistent loops. This reflects the chro- maticism in Schoenberg's work, where pitch relationships are shaped by intervallic structures rather than traditional harmonic functions (Straus, 1990).

These differences illustrate a contrast between Debussy's and Schoenberg's compositional languages. Debussy's music retains tonal, modal, or whole-tone influences, while Schoenberg uses an atonal language.

CONCLUSION

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This study applies topological data analysis, specifically persistent homology using Javaplex (Tausz et al., 2011), to multiple pieces. Exploring the structural relationships in Debussy's Clair de Lune and comparing it with Reflets dans l'eau also by Debussy and Schoenberg's Op. 11, No. 1 demonstrates the uniqueness of Debussy's composing style. For Clair de Lune, the data portrays Debussy's use of harmonic ambiguity, consistent with his impressionistic style. A com- parison with Reflets dans l'eau, another piece by Debussy, shows similarities in the harmonic connectivity. By contrasting these two Debussy pieces with Schoenberg's Op. 11, No. 1, the data reflects Schoenberg's atonal approach, where pitch relationships are more fragmented and independent, without the cohesion seen in Debussy's work. The barcode analysis thus effectively highlights the fundamental differences between Debussy's tonal/modal framework and Schoenberg's atonal language. The study reveals that topological analysis provides a novel way to quantify musical structures, offering a deeper understanding of compositional techniques and stylistic differences in music from the early 20th century.

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