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Heuristic optimization of layered sound-absorbing structures using genetic algorithms

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ABSTRACT

This paper presents a heuristic structural optimization method using a genetic algorithm (GA) for the design of layered sound-absorbing structures with predefined frequency characteristics. The design model employs a symbolic knowledge representation in the form of a genome that encodes the number of layers, their materials, and thicknesses. This encoding enables the use of evolutionary mechanisms such as inheritance, mutation, and selection, typical of genetic algorithms. The evaluation of solution fitness was carried out through a semi-automated process integrating custom evolutionary software with the Norflag acoustic simulation tool. The proposed approach addresses an inverse design problem under constrained computational resources and limited simulation automation. The algorithm's effectiveness was confirmed experimentally – near-optimal structures matching the reference pattern were obtained within just 28 generations. This work contributes to the application of artificial intelligence in engineering design by demonstrating a logic-based, algorithmic reasoning process and highlighting the potential of heuristic methods in solving complex, multi-parameter optimization tasks.

Keywords: genetic algorithm, sound-absorbing layered structures, acoustic optimization, acoustic simulation, evolutionary computation.

INTRODUCTION

The design of sound-absorbing structures with predefined frequency characteristics poses a significant challenge in acoustic engineering, especially in industrial, environmental, and architectural applications. Traditional approaches, which rely on analytical models or experimental testing, tend to be time-consuming and become inefficient when dealing with complex multilayer topologies [5, 7, 10]. Recent developments in optimization theory and computational intelligence, including hybrid metaheuristics and multi-objective frameworks, have broadened the scope of heuristic search beyond acoustics. For instance, genetic algorithms have been effectively applied in structural engineering to optimize the layout of seismic isolators [11], while hybrid approaches combining ant colony optimization with grey wolf algorithms have been proposed to improve the exploitation–exploration balance in complex search spaces [12]. Comparative engineering studies have also highlighted the relevance of such algorithms for analyzing and optimizing material and structural configurations in other disciplines, such as concrete diagnostics [13]. These cross-domain advances further confirm the versatility of heuristic optimization techniques and motivate their application in challenging acoustic design problems.

In this work, the design task is reformulated as an inverse structural reasoning problem: a target acoustic performance (absorption coefficient spectrum) is predefined, and the aim is to identify the combination of materials and geometric configuration that yields such performance. Given the high dimensionality of the solution space and the lack of closed-form rules for optimality, especially in irregular and layered structures, classical techniques prove insufficient. Consequently, methods of artificial intelligence (AI), in particular evolutionary algorithms, offer a promising alternative [1, 6, 7, 9].

In the proposed approach, a genetic algorithm (GA) is used to model the de- sign process as a heuristic search over the solution space. Engineering knowledge is encoded symbolically as a genome describing the order of layers, selected materials, and thicknesses. This representation supports classical GA operators – inheritance, mutation, and selection – and enables logic-guided heuristic reasoning [4, 8].

Genetic algorithms have been successfully applied to the optimization of porous acoustic materials [7, 10], underwater anechoic coatings [3], active vibration control systems [4, 9], and noise barriers with optimized reactive geometries [1]. They are also effective in topology-based design and predictive modeling using hybrid AI techniques [5, 8].

The aim of this study is to develop and experimentally verify a GA-based de- sign method for layered sound-absorbing structures, achieving target frequency characteristics via a semi-automated evaluation loop. The proposed approach frames the design process as a decision-making system operating under partial information and limited resources, aligning with current AI logic paradigms ap- plied in optimization and automated reasoning.

Problem identification

In recent years, there has been growing interest in the application of optimization algorithms in the design of sound-absorbing materials and structures. Among these, genetic algorithms have proven effective in solving high-dimensional, non-differentiable optimization problems, especially in contexts where analytical models are not available or impractical to use.

GA-based techniques have been successfully applied in various acoustic domains: the optimization of porous materials with high absorption efficiency [7, 10], the design of gradient-index acoustic lenses (GRIN lenses) [6], T-shaped noise barriers with reactive surfaces [1], and systems for active noise and vibration reduction [4, 9]. Further studies addressed the optimization of underwater anechoic coatings [3], lightweight damping materials [2], and hybrid intelligent models for predicting acoustic material behavior [8].

Despite these advances, the specific problem of designing multilayer soundabsorbing structures with predefined frequency characteristics remains insufficiently explored. Prior research typically focuses on homogeneous materials or simple geometries, often neglecting the combinatorial complexity of multilayer systems where both material type and thickness vary.

Another important limitation is the lack of batch processing capabilities in most available simulation tools, such as Norflag or ZORBA. This limits the degree of automation, making the optimization process highly manual and inefficient, especially when many candidate designs need to be evaluated in sequence. Consequently, even with GA, the evolutionary loop is often constrained by human interaction, reducing scalability and robustness [3, 4].

This problem can be formalized as an inverse design task: given a desired frequency-dependent absorption profile, the objective is to identify a materiallayer configuration that best reproduces it. However, in the absence of an analytical model that would allow the application of classical techniques (e.g., gradientbased methods) [5], heuristic search strategies must be employed. Among them, genetic algorithms offer a natural framework for symbolic reasoning in solution space.

Each valid design must also satisfy a set of physical and acoustic constraints, including material properties, manufacturing feasibility, and performance requirements. The solution space is thus non-convex and multimodal, requiring strategies that maintain population diversity and avoid premature convergence [1, 9].

In this context, the genetic algorithm serves not only as an optimizer but also as a symbolic reasoning framework for structural hypothesis generation and evaluation. The genome encodes a discrete representation of a structural configuration, while the evolutionary process acts as a logic-guided search mechanism. This approach fits within the broader paradigm of AI-based decision-making systems operating under limited information and constrained automation.

Research objectives and hypothesis

The main objective of this study is to develop and experimentally validate a design method for multilayer sound-absorbing structures with specified frequency characteristics, using a genetic algorithm as a heuristic optimization tool. The proposed approach relies on a symbolic representation of structural knowledge in the form of a genome that encodes the number of layers, the choice of materials, and their respective thicknesses. This encoding enables the use of genetic operators such as inheritance, mutation, and selection for systematically searching for configurations that match a predefined acoustic pattern.

The specific goals of the study are as follows:
- to verify whether an appropriately designed genome representation combined with a GA is capable of producing structures that approximate a target absorption curve, even under conditions of limited population size and number of generations;
- to evaluate the effectiveness of the selected selection and mutation strategies in terms of convergence quality and optimization efficiency;
- to analyze the impact of manual control over the simulation process and to identify opportunities for further automation.

Based on these goals, the following research hypothesis is formulated:

Hypothesis: A genetic algorithm, combined with a well-designed genome encoding, can effectively generate multilayer sound-absorbing structures that approximate a desired acoustic response, even under resource-constrained and semi-automated simulation conditions.

It is expected that, despite the limitations related to computational resources and the absence of full automation, the algorithm will be capable of achieving a high level of accuracy within a relatively small number of evolutionary iterations. This would confirm the suitability of heuristic methods for engineering applications and support further development toward fully automated design workflows.

MATERIAL AND METHODS

Genetic algorithms, which belong to the class of evolutionary algorithms, are inspired by the principles of natural selection and biological evolution. Their core components include selection, crossover, and mutation. GA operate by iteratively exploring a solution space where each potential design is encoded as an individual genome.

In this study, a GA was applied to search for a multilayer configuration with specified acoustic absorption properties. Each individual in the population represents a candidate structure defined by the number of layers, the materials used, and their respective thicknesses. The genome was designed to enable inheritance of traits, mutation operations, and the selection of the fittest individuals – those whose frequency-dependent absorption characteristics best approximate a predefined target curve.

Due to limited computational resources and the absence of full automation in the simulation process, several constraints were introduced, including a small population size and a simplified fitness evaluation. An elitist strategy was also implemented to reduce the risk of losing the best-performing individuals across generations.

Genome

The acoustic structure considered in this study is modeled as an acoustic metamaterial composed of several layers with different sound-absorbing properties. Each layer is described by two parameters: the type of material and its thickness. To represent such a structure, a symbolic genetic encoding was employed, consisting of two chromosomes: M and D.

The significantly limited range of acceptable values for material thickness and their number is a result of constraints imposed by the experimental design. The inability to run the algorithm for calculating sound absorption characteristics in a batch process and the need to perform a significant portion of the operations manually forced a reduction in the search space for solutions (the space of cases). This approach enabled the algorithm to converge within a reasonable time (in this case, approximately 30 generations). For the same reasons, a small population was used.

The maximum genome length was limited due to the fact that layers located deeper in the structure have a smaller impact on the characteristics the deeper they are located. Increasing the genome length would rather increase the size of the search space for a solution, without significantly improving its acoustic parameters.

The M chromosome contains a sequence of symbols corresponding to the materials used in successive layers, while the D chromosome encodes their thicknesses. The genome length varies between individuals and corresponds to the number of layers in a given structure. A schematic of the genome representation is shown in Figure 1.

The material set includes eight predefined types, labeled from a to h, comprising porous media (e.g., mineral wool), foams, metals, and air as a reference medium. Each material is characterized by a set of physical and acoustic properties, including density, Young's modulus, porosity, flow resistivity, Poisson's ratio, and loss factor. Layer thickness is encoded as an integer value, interpreted differently depending on the material type. For materials b–e, the encoded value corresponds directly to the thickness in millimeters. For materials a, f–h, the thickness is scaled (e.g., code 1 represents 10 mm, code 9 = 90 mm). Table 1. summarizes the material definitions and their associated properties. The acoustic and mechanical material parameters listed in Table 1 are taken from the material specifications available in the NorFlag software and its documentation. These are the parameters NorFlag takes into account when estimating the acoustic parameters of a layered structure. This genome structure enables the use of crossover and mutation operations while preserving a clear mapping to the physical design of the structure. At the same time, it allows for effective exploration of a broad design space during the optimization process.

Reproduction

The reproduction process in the implemented genetic algorithm involves generating a new individual from the genomes of two parents. The offspring is produced in four steps:

1. Shift – the genome of Parent_2 is shifted by a random number of positions relative to Parent_1.
2. M-chromosome cutting – the cutting point for the M chromosome is selected within the overlapping region of the two parents.
3. D-chromosome cutting – similarly, the cutting point is selected for the D chromosome.
4. Fusion – the offspring is created by joining the segment of Parent_1 before the cut with the segment of Parent_2 after the cut.

The M and D chromosomes are split independently. The resulting genome length depends on the parent genomes, the shift size, and the cutting points. If the offspring's genome exceeds the predefined maximum length, it is truncated by randomly removing excess genes from either the beginning or the end. The replication process is illustrated in Figure 2.

Parent selection is performed using the roulette wheel method, where each individual's probability of being selected is proportional to its fitness value. This approach favors better-adapted individuals while still preserving weaker ones, which helps maintain population diversity and prevents premature convergence to local optima.

Additionally, due to the small population size, an elitist strategy was employed: the two best-performing individuals in each generation are carried over unchanged to the next generation.

M-chromosome	m_1	m_2	$\dots$	m_{N-1}	m_N
D-chromosome	d_1	d_2	$\dots$	d_{N-1}	d_N

Figure 1. Structure of an individual's genome. The M and D chromosomes represent material type and layer thickness, respectively

Table 1. List of materials used in the experiment

Symbol	Type	Thickness	Att. coef.	Density	E-modulus	Poissons number	Loss factor	Resistance	Resistivity	Porosity
		[mm]	[1/km]	[kg/m³]	[Gpa]	[--]	[--]	[Pa·s/m]	[kPa·s/m]	[%]
a	Air	10–90	0							
b	Gum/elastic	1–9		1100				8000		
c	Wooden chipboard	1–9		650	3.8	0.2	15			
d	Steel	1–9		7800	200	0.3	0.1			
e	Aluminium	1–9		2700	70	0.34	0.1			
f	RockWool lowdensity	10–90							40	95
g	RockWool highdensity	10–90							194	95
h	Expanded Polystyrene	10–90		15	0.0015	0.12	10			

Parent 1:

m_1	m_2	m_3	m_4	m_5
d_1	d_2	d_3	d_4	d_5

Parent 2:

M_1	M_2	M_3	M_4
D_1	D_2	D_3	D_4

M-chromosome:

m_1	m_2	m_3	m_4	m_5	
		M_1	M_2	M_3	M_4

D-chromosome:

d_1	d_2	d_3	d_4	d_5	
		D_1	D_2	D_3	D_4

Descendant:

m_1	m_2	m_3	M_2	M_3	M_4
d_1	d_2	d_3	d_4	d_5	D_4

Figure 2. Diagram of the replication process

This mechanism protects the most promising solutions from being lost during evolution.

Mutations

Mutations are applied with a fixed probability of 0.01 after the reproduction phase. Their purpose is to introduce diversity into the population by randomly modifying genomes, which helps prevent the algorithm from getting stuck in local optima and enhances solution space exploration.

The algorithm defines three types of mutation, which may occur at a randomly selected position in both the M chromosome (material) and the D chromosome (thickness).

Figure 3 shows an example genome prior to mutation. The mutation at a given position (e.g., index 4) can take one of the following forms:
- replacing the existing gene (material and/or thickness) with a new randomly selected value (Figure 4a);
- inserting a new gene (layer) between existing ones, increasing the genome length by one (Figure 4b), in this case the length of the genome is extended by 1, which entails the need for a possible correction of the length in if the maximum length is exceeded (see section Reproduction);

m_1	m_2	m_3	m_4	m_5
d_1	d_2	d_3	d_4	d_5

Figure 3. Example genome before mutation

- removing a single gene pair (material + thickness) from the genome (Figure 4c).

The selection of mutation type is random and uniformly distributed. This mechanism enables the algorithm to introduce new traits into the population while maintaining optimization stability due to the low overall mutation rate.

The mutation rate was determined experimentally in the initial phase of the experiment during the first attempts to run the test procedure. At a lower value, the rate of change in the objective function value in subsequent generations was very slow. At a higher value, the effect of destroying potentially promising individuals was observed. In both cases, the algorithm's convergence rate was not satisfactory.

Objective function

The objective function (fitness function) is used to evaluate the quality of each individual in the population. In the context of designing sound-absorbing structures, its role is to determine how closely the frequency-dependent absorption characteristics of a candidate structure match a predefined reference curve.

Evaluation is based on the mean squared error (MSE) between the absorption coefficient values for the tested structure and those of the reference model, computed across one-third octave frequency bands. The frequency range considered is from 50 Hz to 2000 Hz, which includes the most relevant bands for practical acoustic applications. This range consists of 17 one-third octave bands.

a)

m_1	m_2	m_3	M_x	m_5
d_1	d_2	d_3	D_x	d_5

b)

m_1	m_2	m_3	m_4	M_x	m_5
d_1	d_2	d_3	d_4	D_x	d_5

c)

m_1	m_2	m_3	m_5
d_1	d_2	d_3	d_5

Figure 4. Examples of mutation operations applied to the genome: (a) gene replacement with a new material and thickness, (b) insertion of a new gene at a random position, (c) removal of a gene from the genome

The objective function is defined as:

$$O_f = \frac{1}{T}\sum_{t=1}^{T}(f_{Ot} - f_{it})^2 \qquad (1)$$

where: $T = 17$ is the number of evaluated frequency bands, f_{Ot} is the absorption coefficient for the reference curve at band t, f_{it} is the corresponding coefficient for the tested structure.

The objective value O_f decreases as the individual's curve more closely approximates the reference. The square root is deliberately omitted (i.e., MSE is used instead of RMSE) to more strongly penalize poorly matched individuals and to emphasize high-fidelity solutions. This formulation enables precise control over the evolutionary direction of the population and plays a central role in the selection mechanism of the genetic algorithm.

The experiment

To verify the effectiveness of the algorithm, numerical experiments were conducted to find a multilayered acoustic metamaterial structure whose absorption characteristics closely matched a predefined reference curve.

The Norflag software was used to numerically estimate the acoustic properties of each tested structure. Although Norflag provides a graphical user interface (GUI) to define and analyze layered configurations, it lacks support for batch processing. As a result, every simulation step must be executed manually, which hinders repetitive processing and limits automation. Fortunately, Norflag reads input and writes output in text format, which enables partial automation.

To manage this limitation, a custom software application was developed in C++. It handled the generation of the population, creation of Norflag input files, and parsing of output results for further evaluation. The general flow of the experiment is illustrated in Figure 5.

To guarantee the convergence of the algorithm, a reference structure with genome {M=eacgah, D=191554} was selected. This structure was chosen based on the non-trivial shape of its absorption characteristic α(f). It exhibits a high absorption coefficient in the frequency range up to 200 Hz, with a maximum between 100 Hz and 125 Hz.

To enhance the selection pressure in the evolutionary process, the reference curve was slightly modified by increasing the target absorption level in the 100–125~Hz range. Figure 6 presents both the original and the modified curves used for evaluating evolving individuals.

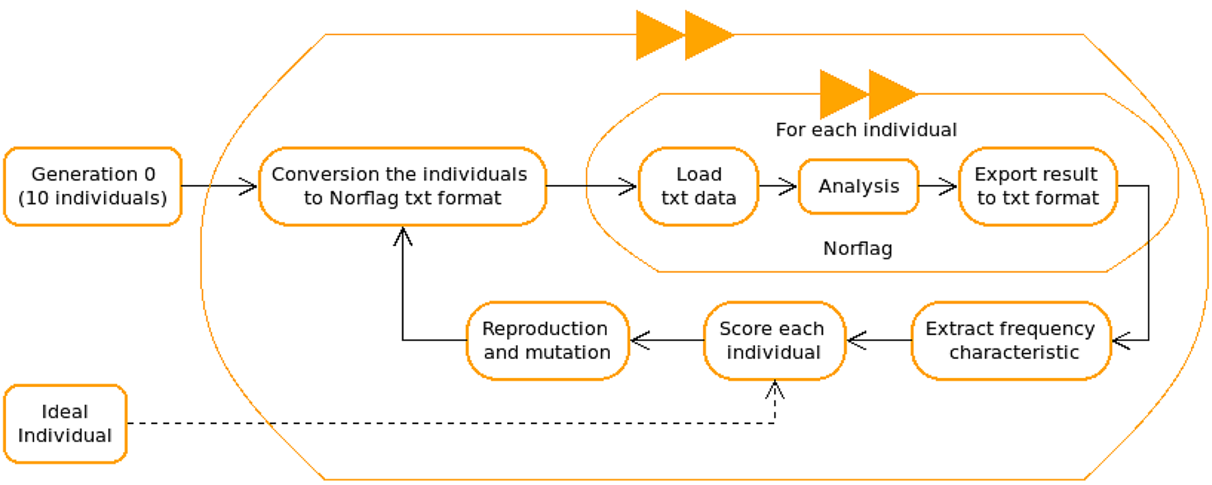

Figure 5. Flowchart of the experiment

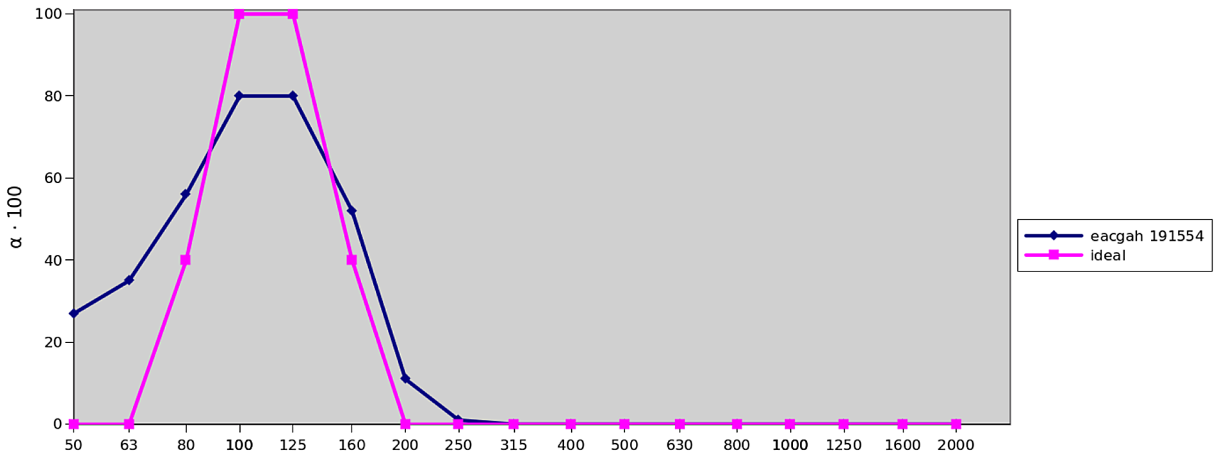

Figure 6. Absorption characteristics of the reference system (ideal) and its modified version used in the evaluation process

Next, an initial population was generated and each individual's genome was converted into a set of text files in Norflag format, describing the type, thickness, and order of layers. Each configuration file was manually loaded into Norflag, a simulation was performed, and the results were saved.

The output files were then transferred to the C++ genetic algorithm engine, which assessed each solution by comparing it with the modified reference curve. Based on the evaluation, crossover and mutation operations were carried out to form the next generation. The process was repeated in a loop until satisfactory results were obtained.

RESULTS

The genomes of individuals from the initial, randomly generated population are listed in Table 2. These structures differ significantly in the number of layers, types of materials used, and their thicknesses. Likewise, the objective function values span a wide range from 927 to 281. Despite substantial differences in objective function values, none of the individuals in the initial population demonstrated characteristics that closely matched the target. Only two cases; {M=hgfhb, D=23378} with O_f = 634, and {M=cg, D=26} with O_f = 462, showed frequency responses somewhat similar in shape, but their peak absorption occurred at 630 Hz and 315 Hz respectively, which are outside the desired range.

The frequency characteristics of individuals in the initial population, along with the reference and ideal curves, are shown in Figure 8. In subsequent iterations of the genetic algorithm, individuals with a wide range of genome structures and acoustic properties were obtained. Every few generations, there was a noticeable drop in the objective function value of the best-adapted individual. This behavior is the result of implementing elitism in the reproduction process. Table 3 lists the best-performing individuals identified during the evolutionary process, along with their fitness values and the generation in which they appeared. Figure 7 shows the course of changes in the minimum, maximum and average values of the objective function in subsequent generations.

The corresponding frequency response curves for these individuals are shown in Figure 2. The lowest objective function value, O_f = 127, was achieved in generation 28 by the individual {M=eafdh, D=15791}. However, the

Table 2. Initial population

Chromosome		fit
M	D	
fedb	8888	925
bb	56	285
bdbb	1247	281
gbe	921	674
hgfhb	23378	634
gegdd	86386	672
fec	888	922
cg	26	462
fe	94	927
be	47	284

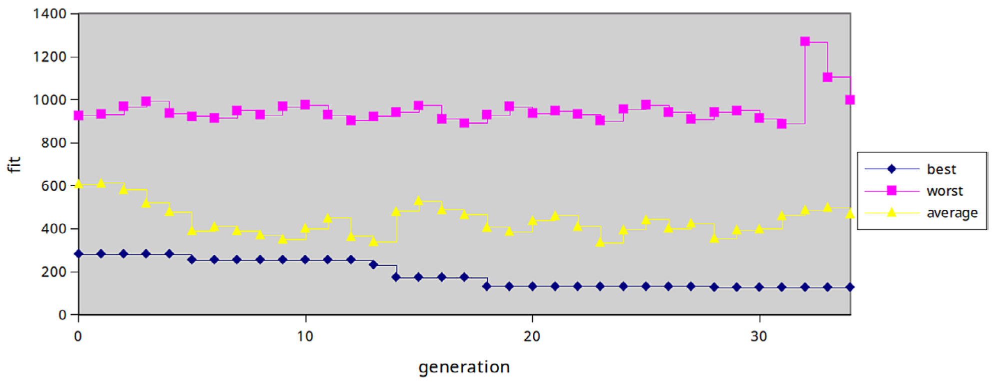

Figure 7. Convergence graph across generations

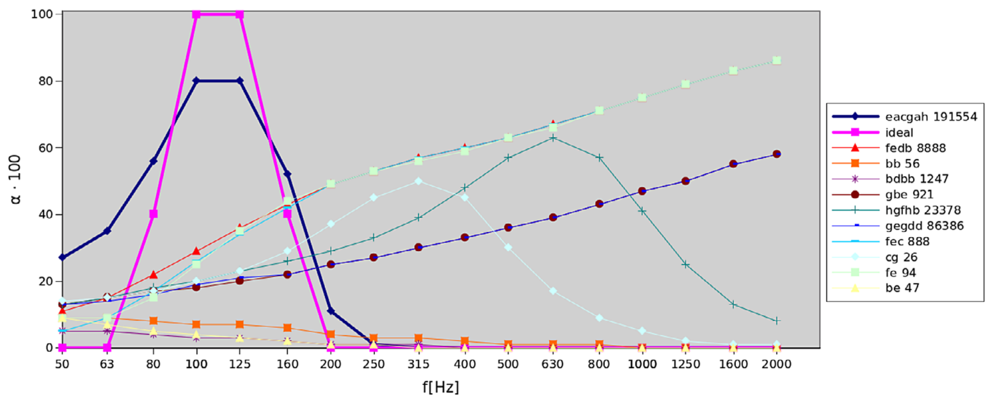

Figure 8. Absorption coefficient as a function of frequency for the initial population compared to the reference and ideal characteristics

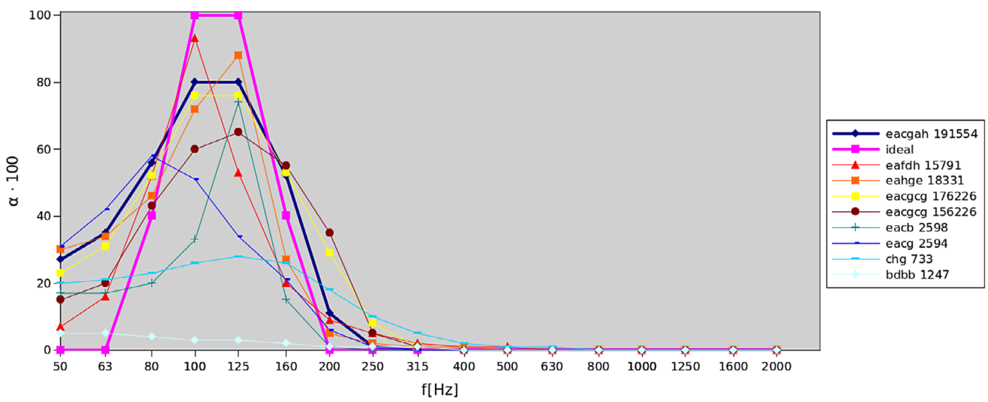

Figure 9. Frequency characteristics of the best individuals in the course of evolution

Table 3. A list of the best individuals in the course of evolution

Generation	Chromosome		fit
x	M	D	
0	bdbb	1247	281
5	chg	733	255
13	eacg	2594	232
14	eacb	2598	173
18	eahge	18331	132
28	eafdh	15791	127

experiment continued through generation 34. In generation 33, the algorithm produced an individual {M=eacgcg, D=156226} with $O_f = 169$), followed by {M=eacgcg, D=176226} in generation 34, also with $O_f = 169$.

Although their fitness values were higher, the shape of their frequency response curves appeared better aligned with the target profile, indicating the potential existence of multiple locally optimal solutions with comparable effectiveness.

CONCLUSIONS

Despite significant progress in the application of genetic algorithms to the design of acoustic structures, the design of complex, multi-layer systems with specified frequency characteristics remains a challenge due to the large number of design variables and high computational requirements. An additional difficulty lies in the limited automation of available simulation tools, which complicates integration with optimization algorithms. The aim of this study was to address this gap by developing an optimization procedure adapted to conditions of limited computational resources and the absence of full automation. The conducted experiments confirmed the high effectiveness of using genetic algorithms in designing layered sound-absorbing structures with desired frequency characteristics. A significant match with the reference curve was achieved as early as the 28th generation. In subsequent iterations, structures were obtained whose characteristics were very close in shape to the assumed ideal. These results show that even with a small population size and manual control of simulation steps, it is possible to carry out the optimization process effectively. The proposed method proved viable despite limitations related to the lack of full simulation automation, thanks to appropriately designed genome encoding, selection, and mutation strategies. However, further development of the methodology requires access to tools that support automated data processing, such as open simulation software with API access or batch processing capabilities. Due to the lack of commercially available solutions offering such features, future research should focus on developing dedicated, open platforms for acoustic analysis. These platforms would allow full integration with optimization algorithms, improving the efficiency of the design process, reducing optimization time, and expanding the range of analyzed structures. The experiment is a prelude to broader research and was designed to allow for the evaluation of each of its components. It was intended to demonstrate the feasibility of developing a proprietary engine for calculating the acoustic parameters of layered structures. The experiment was successful, so in the longer term, we intend to implement an algorithm for calculating acoustic characteristics that allows batch processing. At that point, we will investigate other, more sophisticated methods for calculating the objective function, with an expanded list of materials and more varied layer thicknesses.

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