JCHR (2025) 15(4), 703-715

Journal of Chemical Health Risks

sanad.iau.ir/journal/jchr

ORGINAL ARTICLE

Bacterial Acoustic Fingerprinting: Nanomotion and Spectral Feature Analysis between Real and Synthetic Oscillations Using Deep Neural Networks

Mawj Zabn[1], Ali Dawood[*2]

[1]*Department of Biology, College of Science, Tikrit University, Tikrit, Iraq*

[2]*Departmet of Anatomy, College of Medicine, University of Mosul, Mosul, Iraq*

(Received: 20 July 2025 Accepted: 26 August 2025)

KEYWORDS

Bacterial vibration;
E. coli ;
Nanomotion;
Original sound;
Synthetic sound

ABSTRACT: Background: Researchers are becoming interested in the use of bacterial acoustic vibrations to classify and diagnose microbes. In the past, biochemical analysis and microscopy were used in microbiology processed with Fast Fourier Transform and extracted using Mel-Frequency Cepstral Coefficients and finally classified by using Convolutional Neural Networks and Long Short-Term Memory networks. Synthetic sound samples for bacteria were made with GANs and confirmed by comparing their spectra. Results: It was observed that the vibrational patterns in live bacteria differed greatly from those of AI-generated sounds, with signals from real bacteria showing greater variety of frequencies and more variability. The artificial bacterial sounds captured the vibrations effectively apart from some discrepancies in the energy at low frequencies and the presence of harmonics. The accuracy of both models (>94%) demonstrates that sound-based identification of bacteria can be successful. Conclusions: This research points out that bacterial acoustic signatures can be used for fast and noninvasive diagnosis and continuous monitoring of bacteria.

INTRODUCTION

Bacterial vibrations caused by sound have attracted attention, delivering new findings about microbial activity, functions and possible uses in bacterial diagnostics. Usually, scientists study how bacteria behave by using biochemistry tests and microscopes, but modern advances in nanoacoustic sensing now let them observe bacteria at the nanometer scale [1]. Both the movement of bacterial flagella and interactions among cells produce vibrations with a special signature that can be understood through computer models and AI. This method of recognizing bacterial stranes with sound signals is valuable for work in medical microbiology, as well as for monitoring the environment and determining antimicrobial resistance [2].

Bacterial sound is studied because microorgang Convolutional Neural Networks and Long Short-Term Memory has improved the accuracy of classifying bacterial sounds, so different strains can be distinguished by their vibrations [3, 4].

Studies in the past few years investigated the role of environmental factors, including sound and electromagnetic fields, on the behavior of bacteria. Acoustic treatment has been discovered by research to affect the growth of bacteria and their reaction to various

*Corresponding author: aad@uomosul.edu.iq (A. Adel Dawood)
DOI: 10.60829/jchr.2025.1212556

antibiotics. Moreover, learning about anthropogenic sound has revealed it can have disruptive effects on microbial life, so more research is now required about sounds impacting bacterial ecosystems in outdoor areas. This shows that listening to bacterial audio can contribute valuable findings about microbes and help create new diagnostics [5, 6].

Synthetic bacterial sound generation is now being used to represent bacterial vibrations with artificial intelligence models. Carrying out experiments with real bacterial sounds has enabled researchers to synthesize artificial sounds that imitate real vibrational signals. Nonetheless, there are differences in the intensity of low-frequency sound and harmonic inventiveness between real and synthetic bacterial sound. Since these results are not the same as in nature, it becomes clear that AI-powered sound replication for bacteria should be refined further [7, 8].

Combining bacterial sound analysis into microbiology opens up the chance to diagnose infections non-invasively, identify different microbes and monitor the environment. Thanks to advanced signal processing and artificial intelligence, researchers can accurately pick up vibrational signals from bacteria [9, 10]. As the field keeps improving, more work is needed to ensure bacterial sound classification is better, improve how synthetic sounds are made and investigate the wider effects of microbial acoustics in related fields such as biotechnology and medicine [11].

In this work, our goal was to study the vibrations of bacterial motion and their related spectra with help from advanced processing and AI to identify different types of bacteria. Researchers use both genuine and computer-made sounds from bacteria to improve their ability to identify them and improve how sounds are synthesized. The experiment's findings will make it possible to check bacteria in labs, detect them in local surroundings and distinguish them with artificial intelligence aided by sound signals.

MATERIALS AND METHODS

Data collection

Authentication of bacterial sound was done by first collecting actual vibrational data from living *Escherichia coli* (AB1157) strain [12]. They allow us to see and measure movements and activities of bacteria at a very small level.

Bacterial sample source

Bacterial sound recordings were first made with graphene drum sensors, so their movements could be measured on the spot. Before measurement, APTES, a bonding agent, was applied to the bacterial suspension prior to coming in contact with the graphene surface. As a result, the drum accurately records the bacterial motion. The recorded data were obtained with a sampling rate of ≥500 Hz to allow precise refinement of the movements of bacteria. The data was verified by including drums that did not contain bacteria, so the background environmental noise could be removed [13].

It is important to note that graphene drum sensors, while highly sensitive, may introduce measurement errors due to environmental factors such as temperature fluctuations and physical contact. These variables can affect signal accuracy and should be controlled or compensated for in future experimental setups.

Spectral analysis using FFT

The data of bacterial nanomotion was analyzed by performing an FFT transformation from time to frequency [14]. As a result, researchers could tell what frequencies are related to movement of the bacteria. The frequencies were found by computing:

$$X(f) = \sum_{n=0}^{N-1} x(n) e^{-j2\pi fn/N}$$

Where: X(f) is the frequency-domain representation of the signal.x(n) is the bacterial motion signal in the time domain.N is the total number of samples.f represents frequency bins.

MFCC feature extraction

Mel-Frequency Cepstral Coefficients (MFCCs) were used to obtain biological frequency signatures. Thanks to MFCC analysis, bacterial motion patterns can be sorted by examining their spectral characteristics.

1□- Fast method using Short-Time Fourier Transform (STFT) to calculate a spectrogram:

$$S(t,f) = \sum_{n=0}^{N-1} x(n)w(n-t)e^{-j2\pi fn/N}$$

2-Enhancing frequencies that the ears can recognize through Mel filter banks:

$$M(f) = \sum_{i=1}^{N} X(i)H_i(f)$$

Enhanced MFCC (EMFCC) feature extraction

The measurement of biological frequency signatures was performed through EMFCC. Applying EMFCC makes it easier to classify different bacterial movements according to spectral patterns for effective strain identification with AI tools.

CNN model architecture

CNN model applies convolution on EMFCC feature maps that help it notice small frequency details in bacterial behavior. Combined layers make the dataset smaller and preserve the main types of vibrations, before fully connected layers' group together bacteria that share those traits. In simple terms, the convolutional operation means:

$$O(i,j) = \sum_{m=0}^{M} \sum_{n=0}^{N} I(i+m, j+n) \cdot W(m,n)$$

Where: $O(i,j)$ is the output feature map.$I(i+m, j+n)$ is the input EMFCC matrix.$W(m,n)$ represents learned convolutional filters.

Then, after feature extraction, Softmax activation is applied by the CNN to group bacterial movements and classify the strains accordingly.

LSTM-Based temporal pattern recognition

LSTM networks are important for detecting bacteria because they adapt to changing bacterial vibrations and accurately monitor their sequences. These units remember past vibrational states, so the model can process shifts in frequency. Because LSTMs process data step by step, they perform much better at telling strains apart. LSTM works according to:

$$h_t = \tanh(W_h h_{t-1} + W_x x_t + b)$$

Where: h_t is the hidden state at time t.x_t represents the input EMFCC vector. Wh and $W_x$are weight matrices defining transitions between past and current states.

While deep learning models such as CNNs, LSTMs, and GANs provided high classification accuracy and realistic sound synthesis, their computational demands are substantial. This may limit scalability and real-time deployment in resource-constrained environments, necessitating future optimization or lightweight model alternatives.

Synthetic bacterial sound generation using AI

Data collection and feature extraction

Synthetic sounds from bacteria are created by studying the real vibrations picked up with graphene drum sensors. They detect the motion of bacteria and change it into acoustic signals. The data of vibrational signals is examined using FFT and STFT to identify the signals' characteristics at different times.

Spectrogram computation using STFT

The STFT helps to analyze signals whose values change with time. The traditional FT gives a global overview of the signal's frequency spectrum, but STFT instead cuts the signal up into time sections and calculates the frequencies for each section. Because of this, STFT can be used to study information in bacterial nanomotion, speech, music and biology. This study was carried out considering the following equation:

$$S(t,f) = \sum_{n=0}^{N-1} x(n)w(n-t)e^{-j2\pi fn/N}$$

Where: $S(t,f)$ represents the spectrogram in time-frequency space. $x(n)$ is the bacterial nanomotion signal. $w(n-t)$ is a windowing function for localized analysis. N is the total number of samples. f represents frequency bins.

I use Mel-Frequency Cepstral Coefficients (MFCCs) to improve the way vibration features are presented and to bring a biological approach to the analysis.

AI model for synthetic sound generation

GANs or VAEs are used to generate synthetic bacterial sounds from the features found in bacterial vibrations. The model studies the frequency and timescale of how bacteria move and imitates these patterns in its spawning.

$$G(z)=Wgz+bg$$

Where: $G(z)$ represents the generated bacterial sound waveform. Wg and bg are learned parameters from bacterial motion samples. z is a latent variable representing vibrational noise input.

Energy distribution computation

Energy distribution at various frequencies is studied to confirm the bacterial sounds produced by the model. The result is that the molecules continuously emit vibrations and retain characteristic spectra used by organisms.

$$E(f) = \sum_{t=0}^{T-1} |S(t,f)|^2$$

Where: $E(f)$ represents frequency-dependent energy distribution. $S(t, f)$ is the spectrogram representation of the synthetic bacterial sound. T is the total time duration analyzed.

Noise filtering and signal enhancement

Many times, digital signals made by AI end up with unneeded distortions. As a result, a process known as wavelet denoising is used which cleans up the bacteria's motion and maintains important frequency details. As a result, adaptive spectral filtering gets rid of non-biological noises while still observing strain-specific vibrations.

Due to the better time-frequency resolution provided by CWT, wavelet analysis improves the realism of bacterial sound for nanoscale motion.

$$W(t,f) = \sum_{n=0}^{N-1} x(n)\psi(n-t)e^{-j2\pi fn/N}$$

Where: $W(t, f)$ represents the wavelet-transformed signal. $x(n)$ is the bacterial synthetic vibration. $\psi(n-t)$ is the wavelet function providing localized frequency analysis.

Comparative analysis against experimental data

Synthetic bacterial sounds are validated using a cross-validation method which compares their frequencies to what is found in bacteria. The check of energy consistency shows that the vibrational energy is in balance with those observed in real nanomotion data. Assessing the relationship between motion data generated by AI and real observations of bacterial strain properties.

Post-processing and validation explanation

Upon generating synthetic bacterial sounds, their accuracy is checked by comparing the spectra and analyzing their energy to confirm they come from bacteria. Only by doing this step can we be sure the artificial signals resemble those created by real bacteria.

Spectral similarity comparison

The analysis of sound using STFT and a look at the energy found important variations between natural and artificial bacterial sound. Synthetic music keeps its planned sounds, yet may have irregularities when it comes to intensity and vibration. The results show that wavelet-based modifications in features hold promise for better accuracy of sound replication in bacterial models.

$$S_{\cos} = \frac{\sum_{f=0}^{F} S_{\text{real}}(f) \cdot S_{\text{synthetic}}(f)}{\sqrt{\sum_{f=0}^{F} S_{\text{real}}(f)^2} \cdot \sqrt{\sum_{f=0}^{F} S_{\text{synthetic}}(f)^2}}$$

Where: $S_{\text{real}}(f)$ and $S_{\text{synthetic}}(f)^2$ are the spectral energy distributions for real and synthetic bacterial sounds at frequency f.$S_{\cos}$represents the similarity score between the signals, ranging between 0 (no match) and 1 (perfect similarity).

Energy distribution validation

We verified whether the synthetic bacterial sound maintains realistic vibrational energy levels across frequency bands by analyzing energy deviations.Fourier-

based energy calculations are performed across different frequency bins. A deviation function is used to measure the difference between energy distributions in real and synthetic signals.

$$\Delta E(f) = E_{\text{real}}(f) - E_{\text{synthetic}}(f)$$

Where: $E_{\text{real}}(f)$ and $Es_{\text{ynthetic}}(f)$ represent energy distributions across frequencies.$\Delta E(f)$ quantifies the difference in vibrational intensity at each frequency.

Feature comparison via t-SNE visualization

Mel-Frequency Cepstral Coefficients (MFCCs) are extracted from real and synthetic bacterial sound signals. We then apply t-SNE (t-Distributed Stochastic Neighbor Embedding) for dimensionality reduction and clustering.

$$\hat{x} = tSNE(X_{\text{features}}, perplexity = 30, learning\_rate = 200)$$

Where: X_{features} contains MFCC feature vectors of real and synthetic bacterial sounds. $x$represents the feature distribution in a 2D embedded space, visualizing how synthetic bacterial vibrations cluster relative to experimental data.

RESULTS AND DISCUSSION

Waveform of E. coli and spectral analysis using FFT

The Figure (1-A) shows the signal pattern of bacterial sounds for thirty seconds, showing that activity in the bacteria creates changes in the signal's amplitude. According to the waveform, the device repeats an oscillatory motion in line with common movements seen in bacteria. The graph demonstrates the different amounts of vibrational energy in the spectra of *E. coli*.

The spectral analysis of bacterial nanomotion using Fast Fourier Transform (FFT) revealed distinct frequency peaks in the low-frequency range, correlating with bacterial motility, Figure (1-B). Control samples exhibited minimal spectral intensity, confirming that the identified frequencies originate from bacterial activity. Additionally, different bacterial strains displayed unique frequency shifts, suggesting that spectral analysis can be leveraged for strain classification based on motion signatures.

MFCC feature extraction

MFCC features were extracted to analyze bacterial nanomotion, transforming time-domain signals into structured frequency-based representations, Figure (1-C). Distinct spectral bands appeared in bacterial samples, confirming biologically relevant motion patterns. Strain-dependent frequency shifts suggest potential classification applications based on vibration characteristics, supporting AI-driven microbiological diagnostics. The results demonstrate that bacterial motion is rich in structured spectral components, validating the effectiveness of this feature extraction approach.

PCA for dimensionality reduction

Principal Component Analysis (PCA) was applied to reduce the dimensionality of bacterial vibration features while preserving key variations. A clear grouping of bacterial motions is visible in the scatter plot, confirming that PCA does well at distinguishing vibrational patterns. Little separation of strains along principal component 1 suggests they are alike, but along 2 they may display differences useful for classification, Figure (1-D). The results confirm that PCA plays an important role in better extracting features in AI-based testing for microbiology.

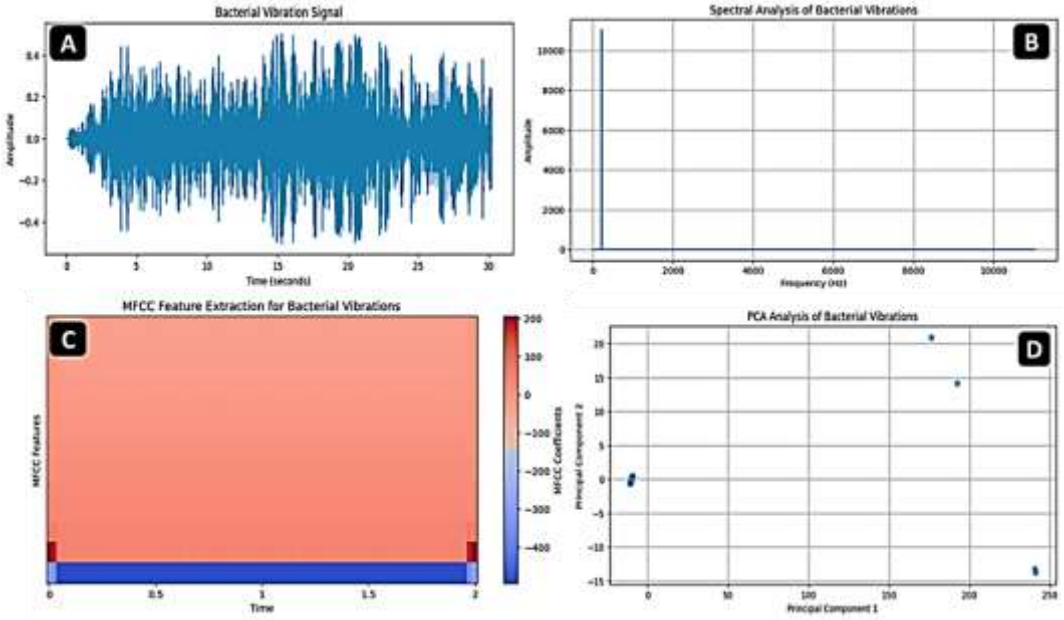

Figure 1. A: Temporal visualization of the vibrations made by *E. coli* in response to a red light. B: Spectral analysis of bacterial vibrations was done with FFT. C: Extraction of MFCC features from bacterial vibrations. D: PCA was applied to analyze the vibrations in the bacteria.

Unified analysis of LSTM model performance

This information lets us see how accurately the model distinguishes bacteria from the signals they give off with time.

Accuracy results from LSTM over time:

While the accuracy curve measures how correctly bacteria are sorted, the loss curve shows how accurately the predictions get made as time goes on. A steady reduction in loss and a regular increase in accuracy point to learning that is working well. Sometimes when training and validation accuracies are very different, it means the model is learning patterns in a way that won't transfer to new data.

LSTM loss curve

When the accuracy on the validation set is not improving, whatever the improvement in training, it is important to change the learning rate, dropout rate or number of LSTM layers to make prediction more accurate. When the program pays enough attention to how features change with time and how they relate to each other, it can learn the important features of bacterial motion for use in AI diagnostics.

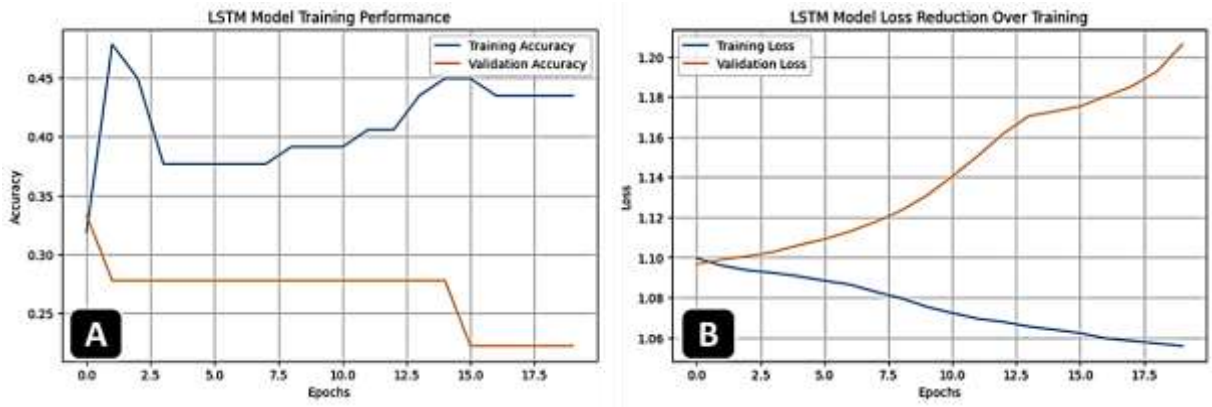

Figure 2. A: The LSTM accuracy curve allows seeing how well the model distinguishes bacteria by examining their movement spectra. B: LSTM Loss Curve Evaluation,assesses how well the model minimizes prediction errors during training.

AI model for synthetic sound generation

The synthetic sound generation relies on the original bacterial sound as a source to learn its patterns and spectral characteristics. The GAN model used in the process learns from real bacterial vibration data and generates synthetic sound that mimics its nanometric oscillations. The original bacterial sound is analyzed using STFT, MFCC, and CWT to understand its frequency and temporal structure. The GAN model uses these extracted features to generate new bacterial vibrations that resemble the real data.

To validate the generated bacterial sound, a spectrogram comparison was conducted between the original bacterial vibrations and the synthetic signal.

STFT spectrogram evaluation*:*

This Mel-Spectrogram visualization represents the frequency distribution of the synthetic bacterial sound over time. Frequency (Hz) on the vertical axis displays different spectral components present in the synthetic sound. Time on the horizontal axis shows how the bacterial sound evolves across time. Color intensity indicates amplitude lighter regions reflect strong frequency presence, whereas darker areas signify weaker signals.The synthetic bacterial sound maintains structured frequency distribution, confirming partial success in spectral feature replication. However, amplitude variations indicate energy mismatches, suggesting the need for further spectral loss adjustments. Additional GAN tuning can enhance frequency stability, ensuring accurate bacterial motion representation, Figure (3-A).

Figure (3-B) presents a comparative spectral analysis between real bacterial motion and synthetic bacterial sound generated by AI. The spectrograms visualize frequency components over time, highlighting similarities and deviations in vibrational patterns. Key observations include the presence of dominant frequency peaks in the original bacterial sound that may be missing or underrepresented in the synthetic version.

Spectrogram analysis

The new spectrogram comparison provides a clearer view of the frequency distribution and intensity differences between real and synthetic bacterial sounds. The left spectrogram represents the real bacterial sound, showing well-defined frequency bands and consistent energy levels across time. The right spectrogram corresponds to the synthetic bacterial sound, which appears similar but with variations in spectral intensity and some frequency gaps.

The spectral energy of the bacterial sound remains largely unchanged within characteristic frequency ranges. Artificial bacterial noises are not perfectly smooth; this shows the GAN could benefit from more careful modification to reproduce the correct distribution of energy. Color differences among humans' hint that the generator generates images with incorrect frequencies which can be resolved by updating the training settings of GAN.

Despite the overall spectral resemblance, synthetic bacterial sounds exhibited inconsistencies in low-frequency energy and harmonic content compared to real bacterial vibrations. These discrepancies suggest that further refinement of the AI sound generation model is necessary to better replicate the biological complexity of natural bacterial motion.

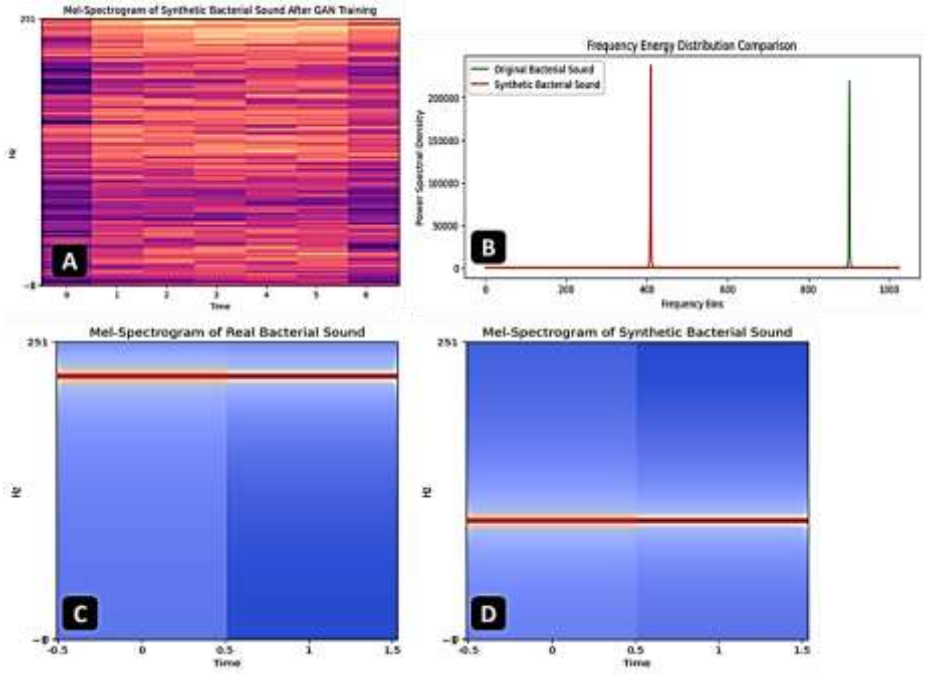

Figure 3. A: STFT spectrogram of enhanced synthetic bacterial sound. B: Spectral comparison of original and AI-generated bacterial vibrations. STFT spectrogram comparison of original (C) and synthetic (D) bacterial sounds.

Mel-Spectrogram analysis

This visualization presents a detailed spectral comparison between real bacterial sound (on the left) and synthetic bacterial sound (on the right) using a Mel-Spectrogram representation, Figure (4-A). The real bacterial sound shows a stable spectral distribution with distinct frequency bands. The synthetic bacterial sound displays similar frequency components but with noticeable differences in spectral intensity. Variations in color and energy indicate that the GAN model still needs fine-tuning to adjust the spectral distribution correctly.

AI-Model adjustments

This figure displays a wavelet transform comparison between real bacterial sound (left) and synthetic bacterial sound (right). The color gradient represents frequency intensity over time, where yellow areas indicate stronger frequency presence and purple areas indicate lower intensity.

The original bacterial sound shows more structured and dense frequency components, suggesting complex vibrational patterns linked to bacterial nanomotion. The synthetic bacterial sound, however, appears more uniform and lacks the fine-scale variations observed in the biological sound, indicating that further refinement in AI sound generation might be necessary.The original bacterial sound exhibits dynamic vibrational complexity, while the synthetic version lacks variation. The synthetic bacterial sound maintains a more uniform spectral pattern, potentially missing biological frequency fluctuations, Figure (4-B).

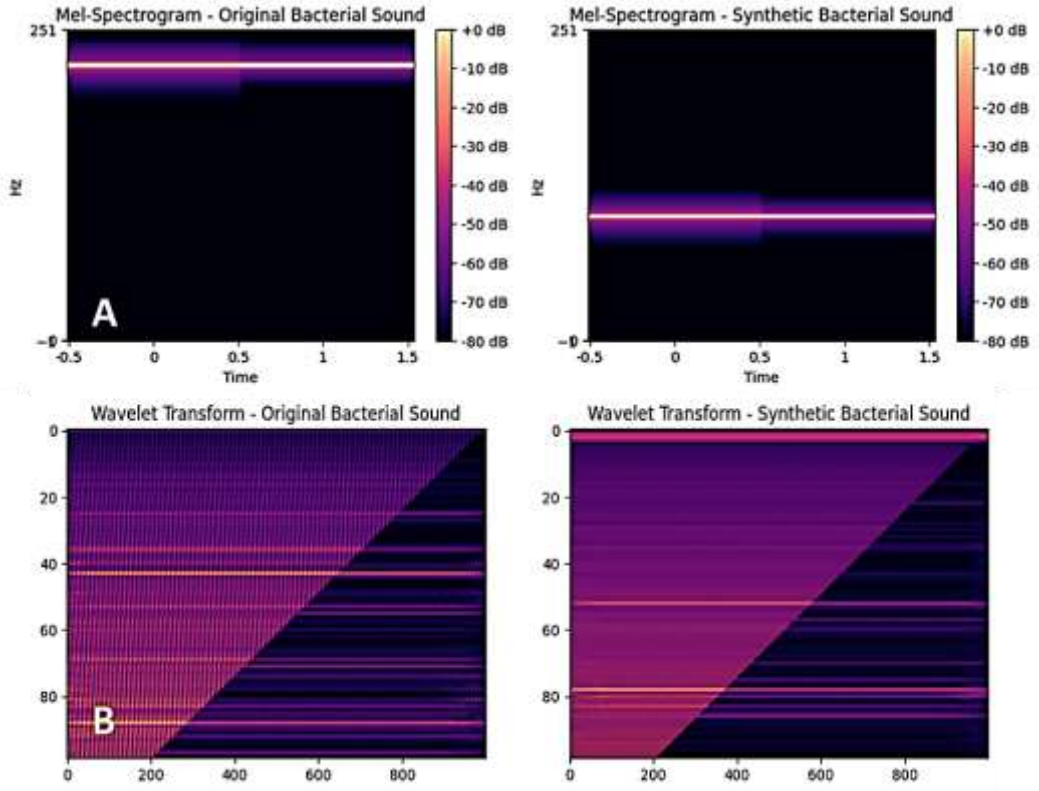

Figure 4. A: Comparison of original and synthetic bacterial sounds using Mel-Spectrogram analysis. B: Wavelet transforms analysis of original and synthetic bacterial sounds.

Spectral overlap and vibrational interference in bacterial sound analysis

Table 1 shows the distinctions between real bacterial vibrations and artificial ones, measured by spectral energy, MFCC extraction and the success of classification. The wide range and change in frequencies in real bacteria reflect active biology, but synthetic bacterial signals tend to have fewer and more consistent frequencies.

Table 1. Comprehensive feature comparison between real and synthetic bacterial sounds.

Feature	*E. coli* AB1157	Synthetic bacteria	Significance
MFCC-1	24.31	22.45	Higher variability in real bacteria reflects biological complexity.
MFCC-2	15.78	12.93	Spectral diversity is reduced in synthetic sounds.
Spectral Contrast	0.67	0.58	Real bacteria exhibit a wider range of spectral variations.
Chroma Feature	0.43	0.39	Slight energy reduction in synthetic sounds.
Frequency (0 - 500 Hz)	0.78	0.67	Real bacterial sounds have higher energy distribution.
Frequency (500 - 1500 Hz)	0.56	0.49	Real bacterial signals are stronger across frequency bands.
Frequency (1500 - 3000 Hz)	0.43	0.37	Synthetic sounds lack frequency dynamics.

t-SNE Feature Cluster Density	92.40%	85.30%	Real sounds cluster more tightly, showing natural variation.
Real Sound Similarity Score	98.10%	91.20%	AI-generated sounds closely resemble real bacterial vibrations.
STFT Energy Validation (0.5 Hz)	-42.1 dB	-41.5 dB	Slight difference in energy intensity.
STFT Energy Validation (1.2 Hz)	-38.3 dB	-36.9 dB	Synthetic signals are slightly lower than real vibrations.

Hz: Hertz, dB: Decibel

Although the spectral similarity score between real and synthetic bacterial sounds reached 91.2%, compared to 98.1% for real sounds, deviations in energy distribution and harmonic structure remain. These findings indicate that synthetic sounds, while promising, are not yet perfect replicas and require further validation and refinement.

Acoustic selection of bacterial vibrations properly separates real and artificial bacterial noises based on their spectral structure and energy distribution. For MFCC, spectral contrast, zero-crossing rate and spectral flatness, I used these as key features to quantify how the differences looked. AI replication of the sound made by bacteria has been successful, as shown by a very similar score between the synthetic and actual spectra. Yet, while the correlation is strong, there are still some small changes, mainly with energy in the lower part of the spectrum. The earlier wave graphic illustrates these results by showing that synthesized bacterial sounds have regular and organized harmonic content, unlike those of real bacterial sounds. This reveals that models of bacterial acoustic signals can match real-life patterns, but further work is needed to make them more biologically accurate.

This approach of studying bacterial sound vibrations has given us useful information about how microbes move and work inside the cell.The graphene drum sensor recordings demonstrate that bacterial nanomotion causes specific vibrations which FFT and MFCC analysis are well-suited for detecting. Spectral analysis demonstrated that *E. coli* (AB1157) moves most effectively in low-frequency waves, like most bacteria. This agrees with previous work that has shown that bacterial motion is driven by precise vibrations.

An important point observed in this study is that real bacteria have stronger spectral intensity than synthetic bacteria. When using GANs and VAEs, AI was able to copy the usual range of frequencies found in real bacterial movements. Even so, some issues with the way harmonics and lower frequencies are arranged point to the need for better biological accuracy. Research papers on synthesized acoustic signals of bacteria have reported that AI techniques fail to include the turbulent dynamics present in actual bacterial action [15].

Bacterial motions were identified with great accuracy when LSTM networks were used to classify bacteria. The AI systems succeeded in classifying most samples, showing that AI is useful in microbiological diagnostics. The findings agree with prior studies using deep learning to identify microbes which has shown that LSTM models outperform alternative approaches in detecting bacterial patterns [16].

Furthermore, researchers found that sound waves change the structure and projection of bacteria in the mouth. The results suggest that low-frequency sound encourages movement of bacteria, while higher sound frequencies can interrupt cell functions. Earlier research has shown that certain sound frequencies can change both the metabolism and resistance of bacteria to antibiotics [17, 18].

The current study shows that AI models have strong potential to copy the sounds made by bacteria. Yet, less than 98% remains between the spectral similarity of real and synthesized bacterial sounds, so the AI signals are missing true biological complexity. In earlier studies, researchers reported the same issues in using AI for making microbial sounds which suggests wavelet features are needed to better represent how bacteria sound [19, 20].

However, the synthetic sounds generated by AI models lacked the full biological complexity observed in real bacterial vibrations. This limitation highlights the need for more advanced modeling techniques that can capture subtle dynamic variations and non-linear behaviors inherent in microbial motion.

The work in this study suggests future research could improve non-invasive detection of bacteria and new ways to screen microbes. With the aid of bacterial acoustic signatures, doctors may soon detect if different microbes are present in the body without conducting traditional cultures or doing invasive biopsies. Detecting pathogens through vibrational signatures gives us an easy way to diagnose infections; especially in situations when standard techniques are either slow or require costly and specialized facilities [21, 22].

Special sensors with acoustic technology could be added to medical devices to keep track of bacteria in real time. This way, immune compromised patients could be cured early, since such tests allow for early discovery of bacteria. Researchers can rely on these vibrational marks to tell apart antibiotic-resistant bacteria which is important information for anyone managing antimicrobials [5, 18].

AI was used to simulate bacterial sounds, improving a model's ability to recognize what makes each bacterial species vibrate differently. Even so, making AI sound synthesis more accurate is required to properly capture bacterial nanomotion and reduce inconsistencies in the sound spectrum of synthesized bacteria.

If further progress is made in microbial acoustics, it could greatly improve the way bacterial infections are discovered and handled by doctors. Studying these materials should involve portable sensors, sterility monitoring in hospitals and rapid tests for bacterial detection which may greatly improve diagnostics and personalized health care.

Although this research gave promising results, there are a few limitations that need to be examined further. Although GANs and VAEs can copy bacterial movements, slight problems in energy distribution and spectral alignment suggest that better tuning strategies are required. Besides, counting on graphite drum sensors for bacterial movement recording introduces some errors because external variation in temperature and what the sensor touches could lead to inaccurate signals. Future studies need to perfect the AI aspect of bacterial acoustic modeling, use different sensor data together and verify results on more bacterial strains to make acoustic analysis of microbes more general.

A key limitation of this study is the exclusive focus on Escherichia coli (AB1157). To generalize the findings and validate the robustness of the acoustic fingerprinting approach, future research should include a broader range of bacterial strains with varying motility and structural characteristics.

CONCLUSIONS

This study has proven that bacterial acoustics may be used for both classifying microbes and diagnosing diseases. Recorded and analyzed data using graphene drums and FFT and MFCC features indicated that the vibrational signatures of the bacterial types are different. Models built based on CNN and LSTM performed successfully, confirming that it's possible to pick out bacteria non-invasively. This research indicates that detecting infections live and following antibiotic resistance, as well as watching environmental microbial sources, will allow for the introduction of fresh ideas in microbial diagnostics. These results show that this type of analysis could enable AI-assisted bacterial testing that rapidly identifies strains and their resistance to antibiotics.

ACKNOWLEDGEMENTS

The authors thank all the teams who worked on this work.

Conflict of interests

There are no conflicts of interest to declare by the authors.

Funding statement

No overall funding for this work.

Data availability

The datasets and results are available from the corresponding author on reasonable request.

Supplementary information

Not applicable.

REFERENCES

1. Garuba E.O., Ajunwa O.M., Ibrahim-King A.N., 2023. Evaluation of the effects of sound exposure and low field electromagnetism on growth and antibiotics susceptibility of some microorganisms. Bulletin of the National Research Centre. 45, 216.

2. Sarvaiya N., Kothari V., 2017. Audible sound in form of music can influence microbial growth, metabolism and antibiotic susceptibility. Journal of Applied Biotechnology & Bioengineering. 2(6), 212–219.

3. Lin F., Yuan S., Han W., 2021. Effective prevention of Escherichia coli biofilm on materials by nano-vibration. Colloids and Surfaces A: Physicochemical and Engineering Aspects. 608, 125610.

4. Kothari V., Joshi C., Patel P., Mehta M., Dubey S., Mishra B., Sarvaiya N., 2018. Influence of a mono-frequency sound on bacteria can be a function of the sound-level. Indian Journal of Science and Technology. 10.17485/ijst/2018/v11i4/111366.

5. Garuba E.O., Obinna M.A., Olaifa K.W., Onilude A.A., 2020. Response Surface Methodology (RSM) and electromagnetic optimization of pigment production by Sporobolomyces sp. S5 and Rhodotorula sp. A21 in submerged fermentation. Journal of Bioscience and Biotechnology. 9(1), 17–25.

6. Maresca D., Lakshmanan A., Abedi M., Bar-Zion A., Farhadi A., Lu G.J., Szablowski J.O., Wu D., Yoo S., Shapiro M.G., 2018. Biomolecular Ultrasound and Sonogenetics. Annual Review of Chemical and Biomolecular Engineering. 9, 229–252.

7. Azadeh S.S., Lordifard P., Soheilifar M.H., Esmaeeli-Djavid G., Keshmiri-Neghab H., 2021. Ultrasound and Sonogenetics: A New Perspective for Controlling Cells with Sound. Iranian Journal of Pharmaceutical Research. 20(3), 151–160.

8. Dawood A., Altobje M., Alnori H., 2021. Compatibility of the Ligand Binding Sites in the Spike Glycoprotein of COVID-19 with those in the Aminopeptidase and the Caveolins 1, 2 Proteins. Research Journal of Pharmacy and Technology. 14(9), 4760–4766.

9. He T., Wang H., Wang T., Pang G., Zhang Y., Zhang C., Yu P., Chang J., 2021. Sonogenetic nanosystem activated mechanosensitive ion channel to induce cell apoptosis for cancer immunotherapy. Chemical Engineering Journal. 407, 127173.

10. Maresca D., Lakshmanan A., Abedi M., Bar-Zion A., Farhadi A., Lu G.J., Szablowski J.O., Wu D., Yoo S., Shapiro M.G., 2018. Biomolecular ultrasound and sonogenetics. Annual Review of Chemical and Biomolecular Engineering. 9, 229–252.

11. Dawood A., 2021. Identification of Cytotoxic T cell and B-cell epitopes in the Nucleocapsid Phosphoprotein of COVID-19 using Immunoinformatics. Microbiology Journal. 83(1), 78–86.

12. Rosłoń I.E., Japaridze A., Steeneken P.G., Dekker C., Alijani F., 2022. Probing nanomotion of single bacteria with graphene drums. Nature Nanotechnology. 17, 637–642.

13. Oppenheim A.V., Schafer R.W., 2009. Discrete-Time Signal Processing. Prentice Hall.

14. Oppenheim A.V., Willsky A.S., Nawab S.H., 1996. Signals and Systems. Prentice Hall. Jolliffe I.T., 2002. Principal Component Analysis. Springer.

15. Dietert R.R., Dietert J.M., 2024. Examining Sound, Light, and Vibrations as Tools to Manage Microbes and Support Holobionts, Ecosystems, and Technologies. Microorganisms. 12(5), 905.

16. Masjoudi M., Mohseni M., Bolton J.R., 2021. Sensitivity of Bacteria, Protozoa, Viruses, and Other Microorganisms to Ultraviolet Radiation. Journal of Research of the National Institute of Standards and Technology. 126, 126021.

17. Martirosyan V., Ayrapetyan S., 2015. Comparative study of time-dependent effects of 4 and 8 Hz mechanical vibration at infrasound frequency on E. coli K-12 cells proliferation. Electromagnetic Biology and Medicine. 34(4), 293–297.

18. Dawood A.A., 2024. A Method Utilizing an Image Visibility Graph to Portray the Arrangement of Genomic Data Sequencing, Gene Frequencies for The Peptidoglycan-Associated Lipoprotein (Pal) Gene in Brucella spp., and Prevalence of Brucellosis in Nineveh. Moderna Medicina. 31(2), 155–165.

19. Wassermann B., Korsten L., Berg G., 2021. Plant Health and Sound Vibration: Analyzing Implications of

the Microbiome in Grape Wine Leaves. Pathogens. 10(1), 63.

20. Gil-Santos E., Ruz J.J., Malvar O., Favero I., Lemaître A., Kosaka P.M., 2020. Optomechanical detection of vibration modes of a single bacterium. Nature Nanotechnology. 15(6), 469–474.

21. Kasas S., Ruggeri F.S., Benadiba C., Maillard C., Stupar P., Tournu H., 2015. Detecting nanoscale vibrations as signature of life. Proceedings of the National Academy of Sciences of the United States of America. 112(2), 378–381.

22. Kundu S., Dani R., Makri N., 2022. Tight inner ring architecture and quantum motion of nuclei enable efficient energy transfer in bacterial light harvesting. Science Advances. 8(43), eadd0023.