Variational Autoencoders for Anomaly Detection in Respiratory Sounds

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Abstract. This paper proposes a weakly-supervised machine learning-based approach aiming at a tool to alert patients about possible respiratory diseases. Various types of pathologies may affect the respiratory system, potentially leading to severe diseases and, in certain cases, death. In general, effective prevention practices are considered as major actors towards the improvement of the patient's health condition. The proposed method strives to realize an easily accessible tool for the automatic diagnosis of respiratory diseases. Specifically, the method leverages Variational Autoencoder architectures permitting the usage of training pipelines of limited complexity and relatively small-sized datasets. Importantly, it offers an accuracy of 57%, which is in line with the existing strongly-supervised approaches.

1 Introduction

The human respiratory system may be affected by pathological conditions which typically alter the patterns of the emitted sound events [31]. Recently, due to the COVID-19 pandemic, such kind of diseases became of primary importance for the public health, being a novel cause of death for large part of the population [24]. Interestingly, medical acoustics, i.e. the scientific field using audio signal processing and pattern recognition methods for health diagnosis [1], can play a fundamental role in the development of user-friendly tools to prevent and limit the spread of respiratory diseases [17]. The ability to create automatic methods to detect anomalies is useful for both patients and physicians. If the first ones can take advantage from automatic diagnosis methods, physicians can save time and minimize potential errors in the performed diagnoses, improving the treatment path for the patients. Importantly, such solutions may also reduce the overall pressure on public health systems.

Respiratory/breathing cycle is the result of the combined operation of the diaphragm and rib muscles enabling inhalation and exhalation, i.e. breathing in and out. Breathing cycles are evaluated by physicians with the aid of a stethoscope to spot abnormalities that can represent the onset of a disease. Unfortunately, stethoscopes can suffer from external noises, sounds emitted by a variety of organs, etc.

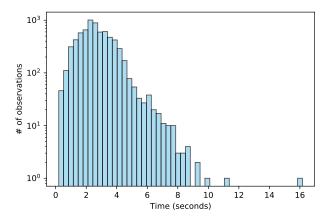


Fig. 1. Breathing cycle length versus number of observations. The lengths vary from a minimum of 0.2 seconds to a maximum of 16 seconds.

A respiratory cycle can be classified as normal or abnormal. Abnormal breathing cycles can mainly contain two types of abnormal sounds: crackles and wheezes. Crackles are mostly found in the inhalation phase, although in some cases, they appear in the exhalation phase [4]. They are characterized by a short duration and they are explosive. Wheezes are longer than crackles, around 80-100 milliseconds, and the frequency can be below 100 Hz. They are usually between 100 Hz and 1000 Hz and rarely exceed 1000 Hz [4].

The literature includes various works focusing on the creation of automatic systems that can detect abnormalities in respiratory cycles. Usually, feature extraction is performed to capture significant properties of the signals (audio features) in order to train machine learning models, such as Hidden Markov Model [11], Support Vector Machine [27] or boosted decision tree [6]. Recently, deep learning has been introduced in the audio signal processing community, bringing advances to medical acoustics as well. In this case, typical features are matrix-like representations of the signal in a frequency-time space. Usually, FFT-based representations are extracted and used as an input for training deep learning networks, such as MLP [9], CNN [8,9,20], RNN [21], and other neural architectures [22, 23]. In some works, multiple type of features are used with exceptional results [9, 29].

Most of the existing works dealing with the classification of respiratory cycles assume availability of data representing every potential class, thus modeling the specific task as a multi-class classification problem. In this paper, instead, we propose an anomaly detection approach. The underlying idea is that abnormalities in respiratory cycles are difficult to record and can vary between different patients, due to different ages and/or sexes. To account for such variability, a sophisticated modeling would be required, which is a hard requirement given the little amount of available data. Therefore, we decided to opt for an anomaly

detection task that requires fewer data for training. Interestingly, Variational Autoencoders have been successfully employed for anomaly/change/novelty detection tasks, such as bird species [18], ultrasounds [15], time series [13], computer networks [10], etc.

The main contribution of this article is to investigate how Variational Autoencoders (VAE) can be effectively employed for detecting anomalies existing in respiratory sounds. The proposed method achieves state-of-art results, while only requiring recordings of normal cycles for training, and as such improving considerably the model's generalization abilities. To distinguish the abnormalities, a threshold must be set, which can be optimally computed from a set of abnormalities. The following sections describe the a) employed dataset of respiratory sounds, b) audio signal preprocessing, c) VAE's architecture and training procedure, d) experimental set-up and results, as well as e) our conclusions.

2 The Dataset of Respiratory Sounds

We used the Respiratory Sound database provided by the 2017 International Conference on Biomedical and Health Informatics (ICBHI) [25]. The database consists of 5.5 hours of audio: 6898 breathing cycles from 920 audio recordings of 126 patients. Audio recordings last from 10 to 90 seconds and the audios include different types of noises typical of real-world conditions. Moreover, the audio samples were acquired using various equipments, sampling rates and detection methods. Each respiratory cycle is categorized into four classes: crackles, wheezes, crackles and wheezes, and normal.

The creators of the challenge predefined train and test subsets of data which permits the reliable comparison between different approaches. Such division is performed at the level of recordings – i.e. the 920 records from which the respiratory cycles are extracted. In this way, a patient's observations can be either in the train set or in the test set, but not in both of them. As such, any patient-specific bias is eliminated. The direct consequence is that using the predefined division, the generalization abilities of the models are better assessed.

The predefined division is shown in the Table 1. Overall, the train set accounts for the 60% of the whole dataset, while the test part consists of the remaining 40%. In addition to the predefined division, several works in literature used random splits defined at the breathing cycle levels. To compare the proposed method to existing works, we tested our method in this setting as well. Namely, we used 80% of the cycles for training and the remaining 20% for testing – see Table 2.

Table 1. ICBHI Dataset 60%/40% splitting (statistics at the cycle level). Note that in the train set abnormal cycles are excluded.

		Crackles	Wheezes	Both	Normal	Total
Tr	aining	962	401	281	1669	3313
Val	idation	253	100	89	394	829
$T\epsilon$	esting	649	385	143	1579	2756
Γ	'otal	1864	886	506	3642	6898

Table 2. ICBHI Dataset 80%/20% splitting. Note that in the train set, abnormal classes are excluded.

	Crackles	Wheezes	Both	Normal	Total
Training	1192	572	325	2325	4414
Validation	290	144	93	577	1104
Testing	382	170	88	740	1380
Total	1864	886	506	3642	6898

Finally, since the proposed method performs anomaly detection, we grouped all the anomalies in one class $(anomalies = \{crackles, wheezes, both\})$ and the normal observations in another class $(normal = \{normal\})$. Moreover, for the sake of evaluating the generalization abilities of the proposed model, we used a validation set randomly drawn from the train set. Since the proposed method is weakly supervised, in the training set we disregarded the abnormal respiratory cycles and only employed the normal ones. We still used the abnormal cycles in the validation and test sets following both of the above-mentioned divisions.

3 Preprocessing of Respiratory Sounds

All recordings were resampled at 4 KHz since, according to the literature [11,27], most of the relevant information is below 2 KHz. As such, according to the Nyquist Theorem, 4 KHz is the minimum-sample rate that allows to reconstruct the important information content. Subsequently, we extracted each breathing cycle from each audio file using the annotations available in the dataset; in the example shown in Table 3, we extracted 9 audio excerpts, disregarding the remaining non-useful portions of audio. The available audio excerpts varied in duration, with the average being 2.7 seconds. Fig. 1 shows the distribution of the obtained audio duration.

To ease the processing of the audio excerpts, and similarly to previous works, we used a fixed-length for each excerpt [26]. Specifically, respiratory cycles lasting less than 3 seconds were wrap-padded while those that lasted more 3 seconds were truncated. To represent the audio characteristics of each excerpt and their evolution in time, we extracted Mel-Frequency Cepstral Coefficients (MFCCs) on moving windows. MFCCs are widely used in audio signal processing, includ-

Table 3. Example of breathing cycles recorded in one audio file. 0 means "absence", 1 means "presence".

ID	Start	End	Crackles	Wheezes
1	2.3806	5.3323	1	0
1	5.3323		0	0
3	8.2548		1	1
4	11.081	14.226	1	1
5	14.226	17.415	1	1
6	17.415	20.565	1	1
7	20.565	23.681	0	1
8	23.681	26.874	0	1
9	26.874	30	0	1

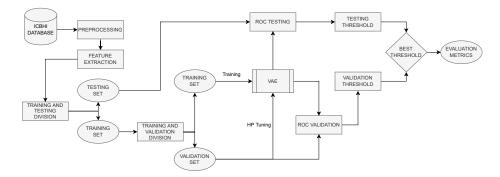


Fig. 2. Block diagram of the proposed anomaly detection approach. Starting from the database, a pre-processing phase is performed which is followed by a feature extraction step. The model is then trained with samples belonging to the normal class learning how to reconstruct the input, the optimal hyper-parameters are determined and tested. Finally, the optimal thresholds for the validation and test sets are determined.

ing speech emotion recognition [12], acoustic scene analysis [19], music analysis [28], and medical acoustics [16]. First, the audio signal was converted in a log-amplitude spectrogram using windows lasting 40ms and overlapping by 50%; Hamming windowing function was applied before of computing the FFT-based log-amplitude spectrum. Then, the Mel filter banks are applied to each spectrogram column in order to extract perceptually relevant audio characteristics. Finally, the Discrete Cosine Transform (DCT) is used to compress the extracted information; the first component, which is proven to be highly correlated with the energy of the signal [32], was removed to prevent the model of learning information strongly correlated to the recording conditions. As such, 12 MFCCs were considered.

4 Anomaly Detection Model

Variational Autoencoders (VAE) are neural networks that unify variational inference approaches with autoencoders. Autoencoders are neural networks composed by two parts: the first part, named encoder, learns a mapping from the input sample x to a latent representation z; the second part, instead, is named decoder and learns to map a point from z to x.

In variational inference, instead, a distribution is inferred via point-estimation methods to approximate Bayesian inference when the number of parameters or the size of datasets makes the problem intractable with Monte Carlo methods [3].

In the case of VAEs, the latent representation z must satisfy two important properties, i.e. it must be a) a continuous distribution, and b) easily samplable. Usually, z is modeled as a Gaussian distribution. In this case, for each sample, the encoder predicts a mean and a variance, defining the corresponding latent Gaussian distribution. Then, a single point from the predicted distribution is sampled and passed to the decoder. Figure 3 depicts a VAE with Gaussian latent distribution.

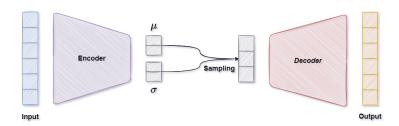


Fig. 3. Structure of the proposed VAE consisting of 4 convolutional layers.

Compared to basic autoencoders, VAEs allow to draw random samples at inference time, making them suitable for generation tasks, such as creativity in music applications [30]. Moreover, they allow to mimic Bayesian models, which by construction predict distributions. Indeed, when multiple samples are drawn from z, one can analyze a set of outputs that constitute a distribution by themselves, allowing to analyze the epistemic certainty measure of the model regarding its own prediction. In other words, VAEs can be used to help the final user with an estimation of the certainty of the prediction; for instance, a medical expert could decide if the probability score predicted by the model should be trusted or not.

As regards to the loss function, we used the sum of Mean Squared Error between the reconstructed matrix and the input, and the Kullback-Leibler Divergence between the unit Gaussian and the latent distribution. We defined each layer as the sequence of a convolutional layer, a batch-normalization layer, a ReLU function, and a dropout layer while training. The encoder is then built from a sequence of such layers, while the decoder is composed by the corresponding layers with transposed convolutions instead of simple convolutions. The latent means and standard deviations are computed with pure convolutional layers. Figure 4 illustrates the whole anomaly detection pipeline.

4.1 VAE Training

Table 4. Hyper-parameters and the optimal value found for each of them. BH indicates the best hyperparameters while HS indicates the hyperparameter space that has been considered.

	BH	HS
Loss function	$MSE + D_{KL}$	{MAE,MAPE,MSE, MSLE}
Optimizer	Adam	{SGD, RMSprop, Adam, Adadelta}
Learning rate	1×10^{-4}	$\{1 \times 10^{-5}, 1 \times 10^{-4}, 1 \times 10^{-3}\}$
Epochs	1000	-
Patience	10 epochs	{5,10,15}
Batch size	32	{32,64,128}
Activation Functions hidden layer	ReLU	{LeakyReLU, ReLU, sigmoid, tanh}
Activation Functions output layer	Linear	{linear, sigmoid}
Dropout rate	0.3	{0.1,0.2,0.3,0.4,0.5}

0.61

0.60

0.58

Validation threshold ACC TPR TNR Validation 0.33 0.80 0.57 60%/40% split threshold Test 0.440.70 0.57threshold Validation 0.48 0.71 0.60

threshold Test

threshold

Table 5. Results obtained on the testing set using two different thresholds, one computed on the validation and one computed on the testing set.

During training, we first searched for the optimal hyper-parameters using Bayesian Optimization method [5] with a Gaussian Process as surrogate model, 2.6 as exploration-exploitation factor k, and Lower Confidence Bound (LCB) as acquisition function. The hyper-parameters and their optimal values are shown in Table 4. We then trained the model using the Adam optimization algorithm with a learning rate equal to 1×10^{-4} .

Training is performed in a weakly-supervised fashion by using the anomaly labels of the validation set only. Specifically, the model is trained to reconstruct samples from the normal class, thus when the input is an excerpt from the abnormal class, we expect that the model will not be able to efficiently reconstruct the input. Since the network is trained to minimize the Mean Squared Error (MSE) between the input and the output, we expect a small MSE for normal respiratory cycles and larger MSEs for abnormal ones. Consequently, the MSE computed on the training set observations can be used as a threshold to spot anomalies.

Since the dataset is not fully balanced, the threshold is chosen so that it maximizes the balanced accuracy on the validation set. Balanced accuracy, compared to Matthews Correlation Coefficient [14], allows for an easy interpretation, being the average between true-positive-rate (TPR) and true-negative-rate (TNR). In our case, TPR is the rate of correctly identified anomalies, while TNR is the rate of correctly identified normal observations [2,7].

5 Experimental Set-Up and Results

80%/20% split

In the context of the ICBHI challenge, the multi-class accuracy is computed as the average of TPR for each class. Having combined all the anomalous classes into one, we calculated TPR for two classes (anomalies and normals) and from there, the ICBHI score, which corresponds to the balanced accuracy. Moreover, we assessed the performance of the model using ROC curves and AUC values which are well-established figures of merit in the related literature.

We first observed the distribution of the MSE values in the validation set – see Fig. 4 – finding that MSE allowed to partially separate excerpts coming from the two classes. We also observed the ROC and AUC while training, discovering that an optimal threshold could successfully separate the two classes. Fig. 5 shows the performance of the trained model on the validation set.

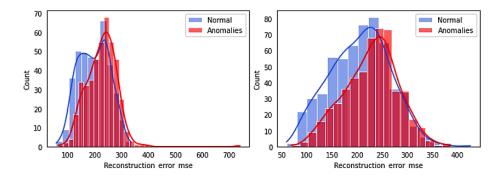


Fig. 4. Distributions of normal and anomalous samples existing in the validation set. The figure on the left is related to the division in 60%/40%, while the one on the right in 80%/20%.

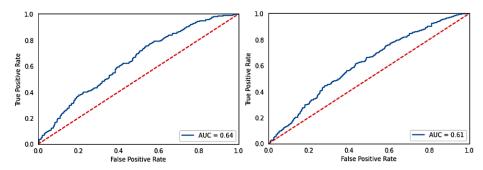


Fig. 5. ROC and AUC computed on the validation set. The left image is related to the 60%/40% division, while the one on the right to the 80%/20% one.

We performed the same evaluation on the testing set to assess the generalization abilities of the model – see Fig. 6 and 7. It is particularly interesting comparing the optimal threshold computed on the validation set and the corresponding one computed on the testing set. Using the 80%/20% division, the proposed method identified a slightly smaller threshold than using the 60%/40% division.

However, by comparing the results obtained using the two thresholds – see Table 5 – we observe that the validation threshold is an effective approximation of the testing one, proving the generalization abilities of the model.

A fundamental aspect that must be considered when comparing different works is the data division into training and testing sets. As explained in Section 2, the creators of the database offer a subdivision (60%/40%) at the level of audio recordings, so that observations associated with a given patient can be either in train or test set. The division into 80%/20% used by some authors is instead extracted randomly at the level of the excerpts in which each audio recording is segmented (respiratory cycles). Unfortunately, such a division may be biased due

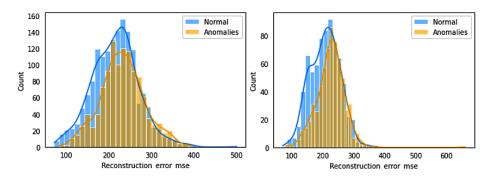


Fig. 6. Distributions of normal and anomalous respiratory sounds as regards to the testing set. The left image is related to the division in 60%/40%, while the one on the right to the 80%/20% one.

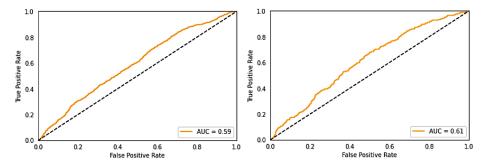


Fig. 7. ROC and AUC computed on the testing set. The left image is related to the division in 60%/40%, while the one on the right in the 80%/20% one.

to patient dependency. Using such a division, the performance measure increases essentially for two reasons:

- there is a greater amount of data in the training phase, and
- observations of the same patient can be both in training and in testing. Moreover, the usage of random seeds can generate dataset division that are particularly successful, thus hiding a pre-bias i.e. searching good random splits to boost the final scores.

Overall, the proposed approach offers performance which is in line with the state of the art even though it employs respiratory sounds representing only healthy conditions. Interestingly, such a line of thought addresses the problem in a more realistic way since it is unreasonable to assume availability of abnormal respiratory sounds representing the entire gamut of such diseases.

6 Conclusions

In this work we presented a framework modeling the MFCCs extracted from healthy respiratory sounds using a fully convolutional Variational Autoencoder.

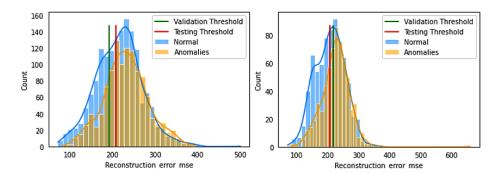


Fig. 8. MSE thresholds when processing the testing set. The left image is related to the division in 60%/40%, while the one on the right in the 80%/20% one.

Table 6. ICBHI Challenge results on the detection of crackles and wheezes (fourclass anomaly detection-driven prediction) with the proposed method. TPR is the true-positive-rate, TNR is the true-negative-rate and ACC is the balanced accuracy (corresponding to the ICBHI score).

Method	TPR	TNR	ACC	Split	Task
HMM [11]	0.38	0.41	0.39		
STFT+Wavelet [27]	0.78	0.20	0.49		
Boosted Tree [6]	0.78	0.21	0.49	60/10	4 classes
Ensemble DL [23]	0.86	0.30	0.57	00/40	
Proposed Method	0.33	0.80	0.57*		2 classes
LSTM [21]	0.85	0.62	0.74		
CNN-MoE & C-RNN [22]	0.86	0.73	0.80		4 classes
LSTM [21]	-	-	0.81		
CNN-MoE & C-RNN [22]	0.86	0.85	0.86	80/20	0 1
Proposed Method	0.58	0.61	0.60*		2 classes

To the best of our knowledge, this is the first time that the detection of respiratory diseases is faced from an anomaly detection perspective. Interestingly, the proposed model achieved state of the art results in a patient-independent experimental protocol even though it is only weakly-supervised.

The small size of the available dataset poses the problem of overfitting and model generalization abilities. To this end, we employed Variational Inference, which allows the model to estimate its own epistemic confidence, in addition to the estimation of the anomaly probability.

In order to improve the performance of the presented anomaly detection system, data augmentation could be a fundamental addition, as it will provide additional training samples. Moreover, different architectures could be tested including networks able to take into account time dependencies, such as attention-based nets and Recurrent Neural Networks. Finally, multiple features could be used to improve the reconstruction abilities [9, 29].

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