Investigating Traditional Machine Learning Models and the Utility of Audio Features for Lightweight Swarming Prediction in Beehives

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Abstract: Remote monitoring of the status of beehives is essential for efficient beekeeping, leading to less workload on the beekeeper and, because of not opening the hives too frequently, to less stress for the colonies. Sound analysis, utilizing machine learning models of various paradigms, is a common feature of so-called smart hives. Most of these models are aimed at the task of swarming prediction. Swarming of a colony, a fundamental phenomenon in the reproductive process of bees, can cause substantial losses in the production of the apiary and, thus, its prediction is of utmost importance. However, especially in case of nomadic beekeeping where the apiary is moved to the country without access to electricity and good internet connection, the used prediction models should run "on-site" with as low energy consumption as possible and using internet connection only to send alerts to the beekeeper. For such, lightweight models are required which can be achieved by using simpler prediction models and/or only the most important audio features. In this paper, the importance of audio features for swarming prediction is investigated by using a genetic algorithm. Various Machine Learning models are trained, using the selected features, and used for predicting swarming on real-world data collected in one Hungarian apiary. This experimental evaluation is the main contribution of this paper. While genetic algorithms are commonly used for feature selection, however, to the best of the authors' knowledge, they have not yet been used in the beekeeping domain.

Keywords: Precision Apiculture; Audio Feature Extraction; Feature Selection; Prediction; Machine learning; genetic algorithm based feature selection

1 Introduction

Beekeeping is one of the most ancient professions, almost as old as humanity. Although bees are not tamed, they are the most specialized pollinators and thus they are critical for keeping the overall environmental balance by pollinating different kinds of crops. The condition of bees is important not only for the beekeeper but on large scales for the whole world. Therefore, it is essential to observe and understand the basic phenomena in the life cycle of the bees, of which the most fundamental is swarming.

During swarming, many bees (sometimes even the half of the colony), including the queen, leave the hive in a very short time. The reasons for swarming might be various. Besides swarming belongs to the natural reproductive process of colonies, bees can swarm in case of shortage of space in the hive (i.e., too crowded colony), weakened or old queen (which leaves the hive with part of its population while the remaining bees raise a new queen), external factors, such as the presence of predators, or, due to some yet undiscovered reasons. It is often observed that 20,000-50,000 bees are lying on a nearby tree hanging in a cluster producing a loud buzzing sound.

If the swarming is not controlled or planned (for the reasons of extending the apiary) it can cause serious financial damage to the beekeeper. The best, and still the most common, practice for beekeepers is a manual inspection, by opening and checking the hive, to determine whether the colony is going to swarm or not. The biggest drawback of manual inspection, besides being manually laborious and time consuming, is that opening the hive causes an unnecessary stress for the colony and irregularities in the closed “ecosystem” of the hive.

As the importance of the Internet of Things (IoT) has grown in the last decades, more and more research has been addressed to examine the status of the hive without opening it. Additionally, remote monitoring allows the beekeeper to intervene only when it’s necessary, which results in more efficient production. Several sensors have been identified that can be used to obtain key information without opening the hive. Although the hive may contain 50,000 individuals, it turned out that the individuals behave similarly and follow clearly identifiable patterns of behavior. IoT based data collection and audio fingerprint analysis became one of the most effective ways to answer beehive related questions [1]. The aim of the paper is to investigate and present a new lightweight model to predict the natural swarming event at least one day before real event itself. For this purpose, a large-scale experimental was performed and as a result a novel prediction model of swarming in beehives is introduced. The algorithm uses the output of different feature extraction methods and includes a two-round Genetic Algorithm based feature selection step to train a reduced complexity Histogram-based Gradient Boosting prediction model, which, to the best of the authors’ knowledge has not yet been used for swarming prediction tasks.

This paper is organized as follows: After the Introduction, Related Work is discussed. Then, in Section 3, the complete workflow of the presented research and the experiments are introduced. Conclusions and Further Steps are presented in Sections 4 and 5, respectively.

2 Literature Review

Although beekeeping is essential for our environment [2; 3] and much research addressed to health status analysis of the colonies, recently the number of colonies have decreased significantly due to diseases [4]. The best practice to check the status of the beehive was, and still is in many cases, manual inspection, but since the spread of IoT, much research was addressed to non-invasive investigation of hive conditions, measuring such parameters like temperature [5], mass [6], and humidity [7]. Sound analysis turned out to be an effective method to answer questions regarding the status of the colony within a beehive, since the late 20th Century [8]. Recent studies are focusing on the two most meaningful indicator of the colony health, such as the presence of the queen [9] and detection of swarming [10; 11; 12; 13; 14; 15]. The sound of a hive in a “queenless” or in a not swarming state is easily separable even for a human ear from the state when the queen is present, or the hive is swarming [16; 17]. Therefore, it is not surprising that many ML techniques achieved good results on the mentioned tasks [9; 18]. Identifying the current health status [19] or the presence of external intruders [20] and pests [21], as well as monitoring bees’ daily activity [22] are just some of the challenging and relevant questions concerning hive status monitoring.

Most of the problems mentioned above are binary classification problems with audio analysis [23], while, in the recent years, some comparative audio analysis methods also arise [24; 25], focusing on finding the best audio features for hive status audio analysis. There are, however, only a few literature surveys [26; 27] on beehive sound analysis. On the other hand, various research is investigating the use of more complex ML models, such as Convolutional Neural Networks (CNN) [28], spectrogram [29] and time-series data analysis [30].

The first analysis was performed on the frequency range of 0-3 kHz [8], later it was extended to 0-4 kHz [31; 32] and, recently, to 0-8 kHz [25].

Despite their large number, related research on beehive audio analysis usually focuses on, and present, one approach, which is compared to one or a very few baselines’ approaches. However, comparing various ML models of different paradigms would provide better insight to the utility of these models for swarming prediction, which would be useful for development of lightweight approaches. Moreover, besides investigation of useful frequency ranges, there is no research on investigation of useful audio features which, if selected, would lead to much lighter models with comparative performance. This paper attempts to provide some answers to the above-mentioned issues.

3 The Proposed Swarming Prediction Workflow

During the analyses the following assumptions were made:

1) The sound patterns of swarming from different hives with the same species show similar audio patterns.
2) Although the recordings were made at least 500 m far from the city and any urban noises, some urban noise might have heard
3) Any urban noise, i.e., bells, vehicles, are denoted as noise.

The presented audio analytics workflow, illustrated in Figure 1, consists of the following four steps, introduced in the following subchapters: First, the collected data are converted from PCM to WAV format (subchapter 3.1). Then, audio features are extracted (subchapter 3.2) and their most descriptive subset is selected (subchapter 3.3). Finally, the chosen ML model is optimized, and predictions are made (subchapter 3.4).

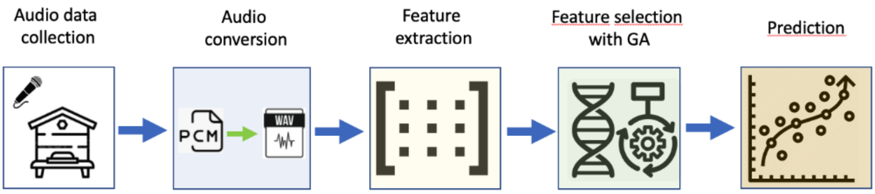


Figure 1
General analytics workflow

3.1 Data Collection and Conversion from PCM to WAV

The source of this research is the publicly available Naturami Dataset [33], collected by our external partner, the Naturami Mérnökiroda Kft. a Hungarian SME, developing IoT solutions for beekeepers [34]. The apiary consists of 200+ individual hives. All hives were separately sensored with an externally installed 1 channel microphone. Each audio recording was sampled at 8 kHz and consists of 65625 samples with a length of 8.2 seconds taken every 6-6.5 minutes. The differences between the recordings were sometimes higher due to the used technology. It took sometimes from 6 to15 minutes to save the recordings to a memory card, and thus the recordings were not fully regular. The format of the recordings is in Pulse Code Modulation (PCM) [35] format which were converted to WAV format [36] with the help of Python wave library with the parameters mentioned above. The series of recordings consists of audio data between May 2000 and June 2022. Two different dates for swarming for two different hives were provided by the beekeeper. In this work, all the recordings taken from these two hives from the 2 weeks period preceding the swarming, in a chronological order, are used.

Figure 2

Audio Data collection system and collector device [25]

3.2 Feature Extraction

Even though much research addressed to find the most effective features for honeybee audio analysis and further processing [25], due to the lack of scientific evidence for finding such features, an assumption that there is no such feature set yet was made. Thus, many basic as well as combined features have been used in this study, to avoid any bias a-priori. The input to the feature extraction phase is an audio file in the form of real-valued time series data of length N, where each x_t corresponds to the amplitude of the signal in time t defined as follows:

$$x(t) = \{x_t \mid 0 \leq t \leq N\} = \{x_0, x_1, \dots, x_{N-1}\} \tag{1}$$

In the following, the used features are summarized briefly.

3.2.1 Short Time Fourier Transformation (STFT)

$x(n)$ is broken up to windows $w(n\text{-}m)$ and STFT is expressed as Discrete Fourier Transform (DFT) [37] on $x(n)w(n\text{-}m)$ which transforms the real valued series $x(n)$ into a complex series y_k as

$$y_k = \sum_{n=0}^{N-1} x_n \left(\cos\frac{2\pi kn}{N} - \mathrm{i}\cdot\sin\frac{2\pi kn}{N}\right) \tag{2}$$

where m is the size of the window, N stands for the length of the signal, and i corresponds to the imaginary unit vector.

3.2.2 Mel Frequency Cepstrum Coefficients (MFCC)

MFCC feature extraction [38] consists of the following steps:

1) Extraction of DFT of *x(n)* to *y(n).*
2) Computation of Mel spectrum of the magnitude spectrum
3) Discrete Cosine Transformation is applied to the log Mel spectrum.

3.2.3 Chroma Features

Chroma feature extraction [39], a.k.a. extraction of tonal content of an audio signal includes the following six steps:

1) Extraction of STFT of $x(n)$
2) Filtering out frequencies outside of range 0 and 8 KHz
3) Detection of the local maximum values of the spectrum
4) Computation of reference frequency and estimation of the deviation with respect to 440 Hz, which is the frequency of the A4 chord,
5) Pitch mapping: weighting scheme with a cosine function with respect to the frequency calculated in step 4.
6) Normalizing the features frame by frame.

3.2.4 Spectral Centroid (SC)

SC [40] localises the "gravity centrum", a.k.a. the centre frequency of the *n*th frame is defined as:

$$SC(n) = \frac{\sum_{m=0}^{N-1} m \cdot |x[n,m]|^2}{\sum_{m=0}^{N-1} |x[n,m]|^2} \qquad (3)$$

3.2.5 Zero Crossing Rate (ZCR)

ZCR [41] measures the „noisiness" of the signal and is defined as

$$ZCR(n) = \frac{1}{2N} \sum_{m=1}^{N} |sgn(x[n+m]) - sgn(x[n+m-1])| \qquad (4)$$

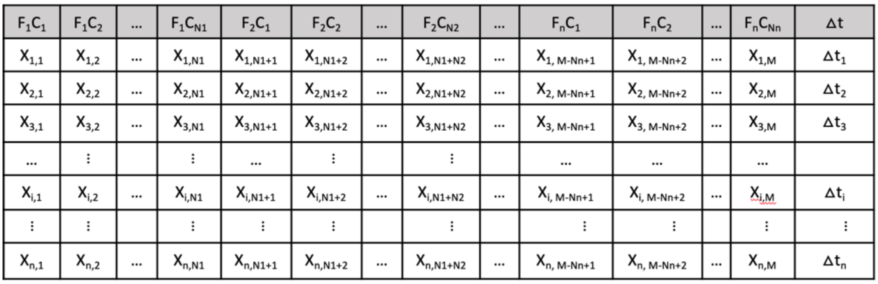
3.2.6 TimeDelta Column

An additional column was manually added to the set of features for each hive. An exact swarming time was provided by the beekeeper for all the hives, based on which an additional "feature", Δt, was created containing the time difference between the time of swarming and the current time of the feature within the spectrogram as follows

$$\Delta t_i = DT_0 - DT_k \frac{|R_k|}{N} i \tag{5}$$

where DT_0 is the given swarming time of hive, DT_k stands for the starting time of the kth recording, N denotes the number of frames the recording was divided into, and $|R_k|$ corresponds to the length of the kth recording in seconds.

As a result of the multiple feature extraction step, a huge feature matrix was created, shown by Figure 3, where F_iC_j denotes the jth component of the ith Feature type. The number of components of jth feature is N_j. The number of all components equals to M where $M=\sum N_i$.



F_1C_1	F_1C_2	…	F_1C_{N1}	F_2C_1	F_2C_2	…	F_2C_{N2}	…	F_nC_1	F_nC_2	…	F_nC_{Nn}	Δt
$X_{1,1}$	$X_{1,2}$	…	$X_{1,N1}$	$X_{1,N1+1}$	$X_{1,N1+2}$	…	$X_{1,N1+N2}$	…	$X_{1, M-Nn+1}$	$X_{1, M-Nn+2}$	…	$X_{1,M}$	Δt_1
$X_{2,1}$	$X_{2,2}$	…	$X_{2,N1}$	$X_{2,N1+1}$	$X_{2,N1+2}$	…	$X_{2,N1+N2}$	…	$X_{2, M-Nn+1}$	$X_{2, M-Nn+2}$	…	$X_{2,M}$	Δt_2
$X_{3,1}$	$X_{3,2}$	…	$X_{3,N1}$	$X_{3,N1+1}$	$X_{3,N1+2}$	…	$X_{3,N1+N2}$	…	$X_{3, M-Nn+1}$	$X_{3, M-Nn+2}$	…	$X_{3,M}$	Δt_3
…	⋮		⋮	…	⋮		⋮		…	…		…	
$X_{i,1}$	$X_{i,2}$	…	$X_{i,N1}$	$X_{i,N1+1}$	$X_{i,N1+2}$	…	$X_{i,N1+N2}$	…	$X_{i, M-Nn+1}$	$X_{i, M-Nn+2}$	…	$X_{i,M}$	Δt_i
⋮	⋮		⋮	⋮	⋮		⋮		⋮	⋮		⋮	⋮
$X_{n,1}$	$X_{n,2}$	…	$X_{n,N1}$	$X_{n,N1+1}$	$X_{n,N1+2}$	…	$X_{n,N1+N2}$	…	$X_{n, M-Nn+1}$	$X_{n, M-Nn+2}$	…	$X_{n,M}$	Δt_n

Figure 3
General structure of the generated feature matrix

3.3 Feature Selection with Genetic Algorithm

Genetic Algorithms have proven very effective in many areas [42;43] and one of the most usable filed is feature selection. Since, as mentioned earlier, there has not been a reported "best performing" audio feature extraction method in the literature, neither for general honeybee audio processing nor for swarming analysis, several basic feature types have been extracted, described in the previous chapter, resulting in a huge feature matrix, the processing of which is challenging due to its size. Moreover, the purpose of this paper, besides investigating the effectiveness of various ML models for swarming prediction at least one day before an event, is also to identify some "best performing" audio feature type for swarming analysis, or general honeybee audio analysis, if possible. Therefore, before creating the predictive model, a feature selection is performed using a simple, general Genetic Algorithm (GA) [44], shown in Figure 4. The expected outcome is a less complex predictive model, trained even in less time. GAs were used by many researchers before, and proved to be quite effective for feature selection [45; 46]. However, the use of GAs for audio feature selection for swarming prediction has not been reported yet.

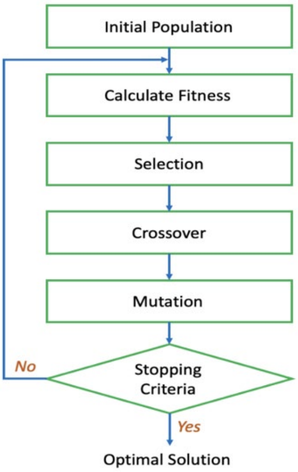


Figure 4
Working of Genetic Algorithm [47]

The population of the GA is represented by the feature matrix except the values in the time delta column. An individual (chromosome) is identified as the series of coefficients belonging to the same frequency component, a.k.a. all values in the same column, but all columns are different individuals. The genes are the values in the feature matrix. The fitness function (FF) is the main average error (MAE) between the predicted swarming times ($\widehat{\Delta t_k}$) and real swarming times (Δt_k) in seconds.

$$FIT\left(X_{,j}\right) = MAE(X_{,j}) = \frac{1}{n}\sum_{k=1}^{n}\left|\Delta t_k - \widehat{\Delta t_k}\right| \tag{6}$$

The selection method is the roulette wheel. The probability of crossover and mutation has multiple candidate values introduced in Subchapter 3.5. The elitism number, the number of preserved best individuals in the next generation, was set to 5. These values have been empirically determined.

3.4 Prediction and Validation

Since only 2 exact swarming times were specified and, thus, the number of different swarming patterns and the amount of relevant data is quite low, k-fold cross validation [48] was performed to get better models and to avoid overfitting. The result was obtained by taking the average of the MAE values of the sub models created within the k folds.

Such an experimental run is a computational heavy operation which may run for months or years, even with an optimized server. To comply with the principles of green computing, a preliminary run was made to choose the best performing and most effective regressor model, considering the runtime and the expected error. A small-scale run was performed on a small population of 50 individuals, with a small number (50) of genes and with a max number of iterations set to 5.

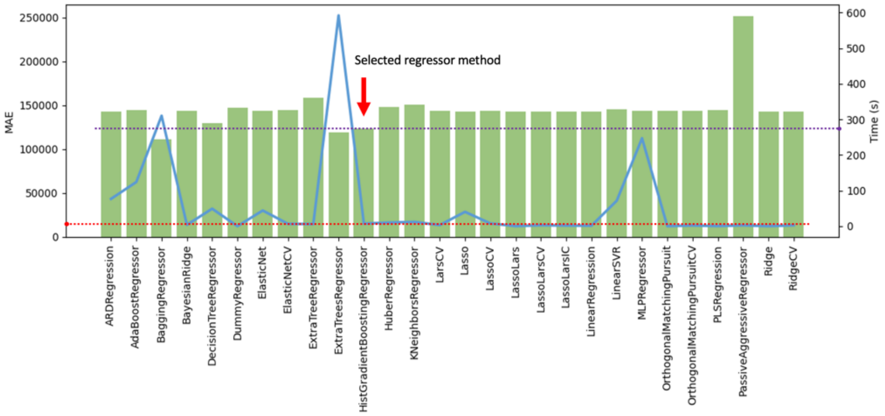


Figure 5

Comparison of regression models on runtime and achieved MAE on a small size test dataset

As Figure 5 shows, the optimal result on cost-benefit bases was produced by the Histogram-based Gradient Boosting Regressor, where the running time was not the best on its own but considering multiple aspects, the chosen regressor model was the most optimally performing on a small size dataset.

4 Experimental Run and Results

4.1 Phase 1 of Experimental Runs

The first phase of experimental runs was executed on all the different hives with all the possible hyper-parameter (HP) settings via a grid-search, looking for all the possible 270 combinations of the HP values described in Table 1.

Table 1

Hyperparameter value candidates

Hyperparameter name	Candidate values
Feature Extraction	
Number of frequency components	64
Hop length	64,100,128,256, 512
Cross Validation	

Number of folds (K)	5, 8
Genetic Algorithm	
Population size (S_{pop})	50, 70, 100
Number of Gene selected (N_g)	10
Probability of mutation (PR_m)	0.2, 0.3, 0.5
Probability of crossover (PR_{cr})	0.6, 0.75, 0.9
Number of elitism (N_e)	5

Despite several HP combinations being looked up for both hives, not even the best results meet the original expectations. The best 5 results for the different hives are summarized by Table 2.

Table 2

The 5 best result of two different hives' first round experiments

S_{pop}	N_g	PR_m	PR_{cr}	K	L_{HOP}	MAE(s)	Hive ID
50	10	0.2	0.9	8	256	99 559.3	Hive 1
50	10	0.2	0.9	8	256	99 568.8	Hive 1
50	10	0.3	0.75	8	256	99 737.9	Hive 1
50	10	0.2	0.9	5	256	99 764.8	Hive 1
75	10	0.2	0.9	8	256	99 844.5	Hive 1
50	10	0.2	0.6	5	100	116 846.8	Hive 2
50	10	0.3	0.9	5	100	117 122.1	Hive 2
50	10	0.2	0.6	5	64	119 230.4	Hive 2
50	10	0.3	0.9	5	64	119 178.5	Hive 2
75	10	0.2	0.6	5	128	121 523.9	Hive 2

The amount of data was twice as much in case of Hive 2 than in case of Hive 1. Results show that too much data causes divergence in many cases, but obviously leads to an inefficient regression model. If the model is more efficient on less amount of data, this means the data is too noisy and reducing the amount of input data may result in reduction of input noise. Among the top 20 results belonging to Hive 1, which produced the better results between the two hives, the value of 256 is the most common hop length value. But for other HPs, there is not clearly the best HP value.

On one hand the higher the hop length, the more the dimensionality of the feature matrix is. On the other hand, best results can be obtained with i) lower amount of data with higher hop length value or ii) higher amount of data with lower hop length value. Based on the first set of results, we set the hypothesis that the noise has the biggest impact on the quality of the model. The data is too noisy; thus, the amount of input noise should be reduced. Recognizing the need for further investigation, a second phase of experiments was planned.

4.2 Phase 2 of Experimental Runs on Hive 1

The second phase of experiments was built on a different approach. The amount of input data was reduced and only the files from the one-week period before the swarming until one day after swarming were selected. As a part of the filtering strategy, only one recording was kept from every 20 minutes. If two recordings are closer to each other than 20 minutes the second one was dropped. Some recordings were also useless due to heavy noise, resulting in only 160 audio files for the Hive 1. As a starting point of phase 2, the best performing HP values from Phase 1 were used (Hop length: 256, mutation probability: 0.2, crossover probability: 0.9, k-Fold CV with 8 folds, population size: 50, number of generations: 10). Keeping these values as constant, and varying only the time interval for filtering, the impact of time interval can be obtained. The results of the experiments, measured in terms of the mean average error (MAE) of the differences from the swarming time, are presented in Table 3.

Table 3

Impact of time frequency between two recordings on Hive 1

Minimal distance between recordings (min)	Number of recordings	MAE(s)
10	148	95 998.5
30	118	96 806.2
35	102	90 287.5
45	95	91 671.5
60	83	86 901.8

The next round of experiments kept the amount of data constant. We kept 1 recording every 60 minutes, resulting in 83 recordings. Hop length was kept to 256, Number of generations to 10 and the k value for k-Fold CV was kept to 8. Further fine-tuning was conducted on the mutation probability, crossover probability, and generation count. This iterative process involved exploring various hyper-parameter combinations to identify the optimal configuration. The five best results are summarized by Table 4.

Table 4

The 5 best results on Hive 1 in the second round of experiments

N_g	PR_m	PR_{cr}	MAE(s)
10	0.3	0.9	86 511.5
10	0.2	0.75	86 691.3
10	0.3	0.6	86 950.3
10	0.2	0.9	86 901.8
10	0.2	0.6	86 975.3

Last run of Phase 2 for Hive 1 was performed with the doubled number of generations (20). The result of the last run has finally met the originally set target and the average error rate fell below 86 400 as shown by Table 5.

Table 5

Result of experimental run on Hive 1 data with doublrd number of generations

N_g	PR_m	PR_{cr}	MAE(s)
20	0.3	0.9	86 393.6

4.3 Phase 2 of Experimental Runs on Hive 2

Similar filtering approach was applied to the Hive 2 as was applied for the Hive 1 in phase 2, with the difference that recordings were kept from only three days before and one day after the swarming. This is because significantly more recordings were found from the mentioned period for the Hive 2 than for the Hive 1. The filtering method resulted in 124 recordings. We used the HP values that were best performing from experiments from Hive 1. Hop length was set to 256, the value of k for k-Fold CV was set to 8 and the number of generations was set to 10. All the experimental runs with all possible HP value combinations for PRm and PR_{cr} were performed, described in Table 1. The best five results are summarized by Table 6.

Table 6

The 5 best results on Hive 2 in the second round of experiments

Ng	PRm	PRcr	MAE(s)
10	0.5	0.6	61 265.2
10	0.3	0.9	61 274.9
10	0.5	0.75	61 308.2
10	0.2	0.75	61 359.1
10	0.2	0.6	61 376.4

Conclusions

In this paper a lightweight approach for swarming prediction was investigated. Audio feature extraction methods (STFT, MFCC, Chroma, SC, ZCR) have been applied resulting in a high dimensional feature matrix as the input to the prediction model. To speed up the training process, and to gain a less complex model, feature selection was performed, using a simple genetic algorithm, before the training of the Histogram-based Gradient Boosting model. The first round of the experimental run showed that the input was so noisy, that the too much input data with low number of training iterations resulted in a poor-quality model. The second round of experimental runs with targeted HP tuning increased the quality of the model, so that the results met the original target to be able to predict swarming one day before it happens.

This work shows that the efficiency of feature selection optimization can lead to efficient and simple models, even after a small number of training iterations, which is a great advantage on the best performing but much more complex models (like, for example, deep neural networks).

Although the results met the original target, the presented research will be further expanded in several areas. The swarming prediction model will be integrated into a general beehive monitoring framework. To get a more general predictor, some extensions are needed in at least the following:

- Including DANi [25] into the list of extracted features and the base features should be combined with some smoothing/filtering method.
- Trying an audio-to-image transformation before further processing and then, using some image-based filtering and prediction models, e.g. Convolutional Neural Networks (CNN);
- Performing a more detailed and complex, but also more time-consuming, HP tuning with additional candidate values.

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