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EMFit based Ultrasonic Phased Arrays with evolved Weights for Biomimetic Target Localization

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Abstract. Bats use the spatial filtering performed by their pinnae in localization tasks. We propose a similar localization scheme based on the spatial filtering of the received echoes by using a phased array. By evolving the weights of a linear phased array using a genetic algorithm, a very efficient spatial filter can be implemented. The localization performance of the evolved array in combination with the biomimetic localization algorithm is compared to a standard phased array localization scheme.

1 Introduction

Bats achieve target localization and identification performance levels far beyond what engineered in-air sonar can achieve [1]. A large group of bats, so-called fm-bats, emit broadband vocalizations (chirps). The outer ear and the head of the bat perform a frequency dependent spatial filtering (i.e. a Head Related Transfer Function, HRTF,[2, 3]) on the received echoes of this vocalizations. Experimental evidence indicates that the spectral cues introduced by this HRTF contribute significantly to the bats' localization capabilities. Inspired by bat biosonar, we propose the use of a sensor array combined with a biomimetic target localization method based on comparing a received echo spectrum to a set of learned templates. To compare the performance of the biomimetic sonar approach, the traditional Bartlett array sensor localization algorithm [4] has been implemented and tested on the developed prototype.

2 EMFit Transducer array

For the manufacture of the sensor array we use an electro mechanic film [5], called EMFit. The film is glued to a structured backplate using double sided adhesive tape to create an electret microphone (see fig. 1-IV). The voltage across every transducer element is measured to determine the received ultrasonic signal. The backplate is constructed by etching a structured electrode on a standard copper plated PCB. Using a structured backplate to create transducer arrays has been successfully applied to ultrasonic sensing before [6, 7]. This method of construction allows the production of planar 2D arrays with arbitrarily

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shaped transducer elements. The experiments in this work are all performed on a linear array consisting of 16 rectangular strips: width=1.5mm, height=70mm, spacing=0.5mm. To connect the EMFit foil to the copper electrode a strip of conductive tape is used. Figure 1-IV shows a schematic overview of array construction.

3 Biomimetic sonar systems

Certain types of bats (e.g. Phyllostomus *discolor*) use broadband, frequency modulated chirps as echolocation calls [3]. Our biomimetic sonar system aims to use the same type of call. We use a hyperbolic downward FM sweep from 120 kHz to 30 kHz in 3 msec. The pulse is also AM modulated with a Hamming window to eliminate transient effects from the Polaroid transducer, amplifier and EMFit transducers. Our biomimetic localization scheme (see [8, 7] for details) is based on a spectral template matching algorithm for the estimation of the direction of arrival. The received echo spectrum is compared with a set of learned spectra that, due to the spatial filtering performed by the transducer, are a function of the direction of arrival (DOA).

To construct the spectral template set, the array is mounted on a mechanized pan/tilt system, and an FM pulse is transmitted towards the array. The recorded signals (Fs = 500 kHz) are processed with the corresponding beamforming algorithm to create a spatial filter, and the spectrum is extracted with a functional model of the processing occurring in the bat's cochlea (see [8] for details). When a broadband FM chirp is used together with a beamforming process consisting of equal weight and time delay values (see figure 1-II), the resulting template set shows a main lobe that has a fixed position and sidelobes that scan through space due to the changing instantaneous frequency (see Fig 1-I a). This fixed main lobe results in an HRTF that shows less spatial variability than the one belonging to the bat. As the localization scheme is using spectral cues for discriminating between different DOA's, diverse spatial characteristics as a function of frequency are preferred.

4 Optimization of array parameters using a Genetic Algorithm

In order to improve the localization capabilities of the used transducer, i.e. to enhance the spatio-spectral filtering the transducer performs, the array parameters will be optimized using a Genetic Algorithm (GA). By using a performance measure derived from the distance matrix, one can optimize the array parameters for localization performance.

Each Delay-and-Sum beamformer is specified by two sets of parameters that configure the array. The first set consists of the gains of each array channel, $w_{i,i=1..16}$. The second set consists of the time delays for each channel, $\delta t_{i,i=1..16}$. These delays are an integer multiple of the sample period over which the original

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signals are delayed before they are summed. A graphic representation of the proposed beamforming algorithm can be seen in Fig. 1-II.

If one can come up with a single number that codes in a robust way for the localization performance of the array configuration, one can start to optimize the gains and delays to increase this localization performance. For the proposed 16 element array, there are 32 variables: $w_{i,i=1..16}$ and $\delta t_{i,i=1..16}$ to be optimized, resulting in a 32 dimensional space where an optimization algorithm has to find the solution.

We want to choose the set of parameters that optimizes the localization performance of the configuration under noisy conditions, i.e. minimize the probability that an echo received from angle θ_1 is confused with an echo received from θ_2. An exhaustive search is impossible because of the size of the search space and the complexity of the calculations for each point in the search space. A better way to do the optimization is using a meta-heuristic such as a genetic algorithm (GA), where the GA optimizes the weight and gain vectors. The GA used a population size of 50, performed a stochastic uniform selection function and ran for 100 generations. The population was initialized with random numbers in the range of $[-5, ..., 5]$.

To calculate the fitness of a particular array configuration the time-domain data is first passed through the beamformer with the current GA chromosomes as gains (w_i) and time delays (δt_i)

$$s_c(\theta, t) = \sum_{i=1}^{n_{chan}} (w_i.s_i^{in}(\theta, t + \delta t_i)) \tag{1}$$

where $s_c(\theta, t)$ is the output time signal of the array, s_i^{in} are the individual sensor signals, w_i is the channel gain and δt_i is the number of samples that the channel is delayed over.

Next, the spectral template set for this sensor configuration is calculated using noise free data. This has to be done for each member of the GA population as the template set depends on the array configuration (i.e. weights and delays). The $Template(s(t))$ operator extracts the template T from the time domain signal $s(t)$, as explained in [8]. The different templates for all the angles of arrival θ form the template set T_c

$$T_c(\theta, f) = Template(s_c(\theta, t)) \tag{2}$$

Next, additive uniform distributed white noise is added to the raw input signals. The noisy data is passed through the beamforming algorithm again and the template set is calculated. Several noise realizations η_i are used to obtain multiple noisy template sets

$$s_{n,i}(\theta, t) = \sum_{j=1}^{n_{chan}} w_j.(s_j^{in}(\theta, t + \delta t_j)) + \eta_i \tag{3}$$

$$T_i^n(\varphi, f) = Template(s_{n,i}(\varphi, t)) \tag{4}$$

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with i the index of the noise realization. Finally, the Euclidean distances between the noise free template set and all the noisy sets are calculated

$$d_i(\theta) = \sqrt{\sum_{f=1}^{n_f} \left(T_c(\theta, f) - T_i^n(\theta, f)\right)^2} \tag{5}$$

As multiple realizations of the T_i^n are calculated, multiple $d_i(\theta)$ can be calculated yielding a mean $\mu(d_i(\theta))$ and standard deviation $\sigma(d_i(\theta))$ of the distance for each azimuth position. These values are used to create a threshold curve that is a function of azimuth and is calculated by adding λ times the standard deviation to the mean value

$$Thresh(\theta) = \mu(d(\theta)) + \lambda.\sigma(d(\theta)), \lambda = 3 \tag{6}$$

All the entries in the distance matrix $D(T_c)$ associated with the templates set T_c that are below this angle dependent threshold increment the fitness value. Minimizing this fitness value will result in a minimization of the probability of an erroneous interpretation of the template due to noise added to the raw sensor signals

$$fitness = \sum (D(T_c) < Thresh(\theta)) \tag{7}$$

The template set created by the evolved configuration for the evolved Delay-and-Sum scheme is shown in Fig. 1-I(b). The set of templates is asymmetric, there are many sidelobes present and it looks rather chaotic. The performance of this template set can be inferred from the distance matrix. As the distance matrix of the standard transducer (fig. 1-I(c)) contains a strong secondary diagonal (which implies strong symmetry in the template set), the evolved set (fig. 1-I(d)) contains almost no such diagonal. Furthermore, the overall values of the distance matrix are higher for the evolved template set, indicating better localization performance.

The parameter λ acts as a scaling parameter for the threshold in the fitness criterion. The higher the value of λ, the better the localization performance of the array configuration will be. But if λ is chosen too high, all the points in the distance matrix (except the diagonal elements, which are 0 because of the way the distance matrix is calculated) will fall below the threshold for every individual in the population making optimization impossible. In our experiments we have chosen $\lambda = 3$ as this yielded the best results.

5 Experimental Results

The localization performance of the different beamforming schemes was evaluated. We only consider the Bartlett beamformer in the comparison with the biomimetic models. The different beamforming schemes are challenged to localize a single target in increasingly noisy conditions over a broad range of view (-70° to 70°), while this single target is moved over the complete azimuth range.

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For each azimuth position 50 localization trials are performed. The azimuth error is shown in figure 1-III, which shows the box plots of this error for the different schemes and different SNR's.

Under high SNR conditions (SNR=10dB), the three different systems perform equally well. SNR is defined as the ratio between the root-mean-squared (RMS) value of the beamformer output and the standard deviation of the noise distribution. As the SNR decreases however, the biomimetic model in combination with the standard transducer fails in localizing the target, with large angular errors as a consequence. This can be explained from the strong secondary diagonal in the distance matrix (see fig. 1-I(c)). Furthermore, the angular errors of the Bartlett start to increase. The biomimetic scheme in combination with the evolved transducer remains to produce good localization results under the noisy conditions, without any biasing effect.

6 Conclusions

We have shown that it is possible to perform spectral based localization using a phased array. By optimizing the weights of the phased array beamforming procedure using a genetic algorithm the localization performance of the system can be improved dramatically. It outperforms a Bartlett beamforming algorithm in noisy conditions over a wide field of view.

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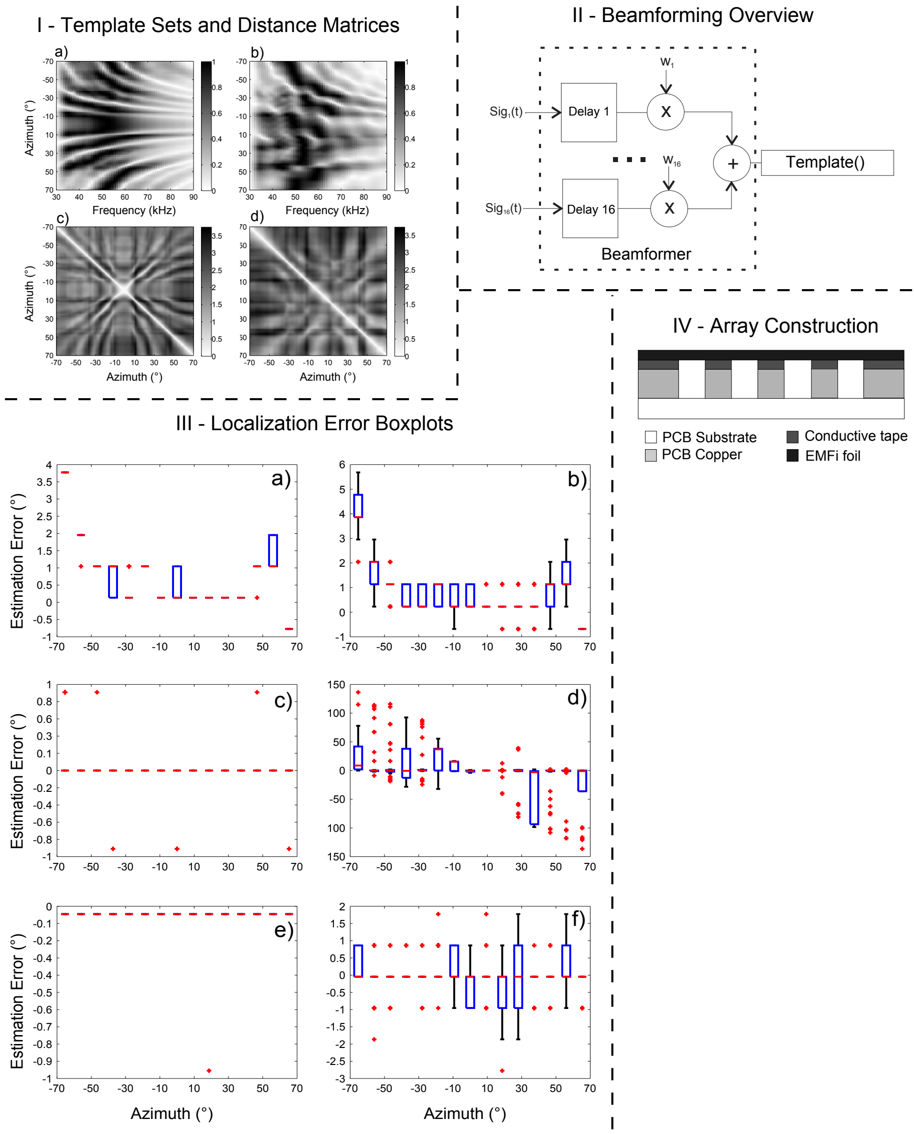

Fig. 1: I - Template sets for a) the standard array, b) the evolved array. The distance matrix for c) the standard array, d) the evolved array. II - Overview of the beamforming scheme for biomimetic target localization. III - Error box plots for a localization experiment of a single impinging sound wave using Bartlett beamforming a) SNR=10dB, b) SNR=-5dB. Biomimetic localization using standard array c) SNR=10dB, d) SNR=-5dB. Biomimetic localization using evolved array e) SNR=10dB, f) SNR=-5dB. IV - Schematic drawing of the constructed array.