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A method for deconvolution of gamma spectrum by genetic algorithm

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ABSTRACT

In this study, the application of a genetic algorithm for unfolding an experimentally obtained gamma spectrum is presented. Genetic algorithm (GA) and Richardson-Lucy deconvolution method is used to obtain detector response function. The proposed method was tested with a Co-60 and Cs-137 spectra obtained with NaI(Tl) detector. Experimental results show that the proposed method is effective in unfolding measured spectra. The detector response function obtained with the genetic algorithm is comparable to the response function calculated from experimental data.

1. Introduction

A γ-spectrum gives information that is distorted by the detector system and the environment and it does not provide complete information about the original data [1]. Different disturbances and instrumental conditions obscure the true spectrum shape. Such factors become especially important in systems with low resolution [2]. The main purpose of analyzing the γ-spectrum is to identify the radioisotopes contributing to it. In an environment containing more than one radioisotope, the identification of radionuclides becomes more difficult due to multiplets seriously overlapping. Spectral unfolding is a process applied to eliminate the effects of the measurement system and environmental effects and to identify energy peaks and distinguish overlapping ones.

The spectrum measured by spectrometer can be expressed as follows:

$$\boldsymbol{y} = \boldsymbol{H}\boldsymbol{x} + \boldsymbol{e} \quad (1)$$

where $\boldsymbol{y}$ represents the measured spectrum, $\boldsymbol{x}$ denotes the real spectrum, and $\boldsymbol{H}$ stands for the response function of the spectrometer. Data measured by a spectrometer is actually the convolution of real data by instrument response function. It is the main cause of degradation. Therefore, accurate estimation of the instrument response function is very important for deconvolution algorithm [3].

Deconvolution has been the subject of numerous studies in optics, spectroscopy, analytical chemistry, and chemometrics [4]. Many different methods (direct inversion, least-squares, Monte Carlo, iterative, AI, neural network, GA) have been proposed to solve Eq. (1) for $\boldsymbol{x}$ [2], [4-5]. For deconvolution of the gamma-ray spectrum there are many techniques proposed in the literature, such as the least square method [2], Maximum Likelihood Expectation Maximization (ML-EM) [6], Maximum Entropy Method (MEM) [7], Gold algorithm [8, 9], Richardson-Lucy method (RL) [10-12].

In order to find the full energy peaks of a γ-spectrum, the measurement vector ($\boldsymbol{y}$) and detector response matrix (DRM), $\boldsymbol{H}$, have to be known. This matrix includes both the response of the detector to incoming photons and the effect of environmental conditions on the measurement. In principle, the detector response function is defined as the probability distribution of a photon source emitted with energy $\boldsymbol{E}_i$ being recorded at energy $\boldsymbol{E}$ [1]. Generally, experimental [13], semi-empirical [14, 15] and Monte Carlo simulation [16, 17] methods are used to determine $\boldsymbol{H}$ [18].

2. Method

a. Genetic algorithm

The basis for GA which is proven to provide robust search in complex spaces was also studied as a powerful alternative to other techniques [19]. This technique has been used for spectral deconvolution [20] and for unfolding of neutron spectra [21]. It is proposed as an optimization technique to calculate energy calibration parameters and the gamma response function of plastic scintillator detectors [22].

GA as an optimization method is based entirely on natural selection processes [20]. GA method does not require knowledge about the structure of the problem. GA mimics genetic crossover in biological processes and results in individuals as the next generation. Individuals with better properties will be kept for next

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generation while weak ones are eliminated according to selection criteria (fitness function). Basically, GA consists of genome, chromosome, population, selection criteria (fitness), mutation and crossover elements. In this work, elements of DRM are genomes, columns are chromosomes and every DRM is an individual. GA is suitable for parallel processing, has better global optimization and capable of automatic optimization of search space [3, 19, 23].

Considering the basis of deconvolution technique is to find the solution vector ***x*** satisfying,

$$\hat{x} = arg_x min||y - Hx||^2 \quad (2)$$

GA algorithm as an optimization process can be used. GA is simple to implement, efficient and effective in search and free of convergence problems [19]. It is well suited for parallel processing [21]. Implementation of algorithm starts with the construction of initial population (x) created randomly [19-22]. This population is expected to converge to an individual representing real spectrum regardless of initial guess. Then each member of the population is assigned a value which measures how close they are to the measurement vector (y). This evaluation requires solving Eq. (1) for every individual [6, 12].

b. Blind deconvolution

Deconvolution methods requires knowledge for ***H*** [14-17]. If ***H*** is not available then Blind Deconvolution (BD) is applied [24-25]. BD was first used in the restoration of old sound recordings, and was subsequently developed in subjects such as seismic data analysis and finding the rate of change in Doppler shift in radar echoes [24]. For blind deconvolution, the general algorithm is shown in Figure 1 [25]. This general approach requires 2 consecutive deconvolution process for each iteration.

c. Proposed method

In this study unfolding of a spectrum is stated as a blind deconvolution problem. We propose an algorithm

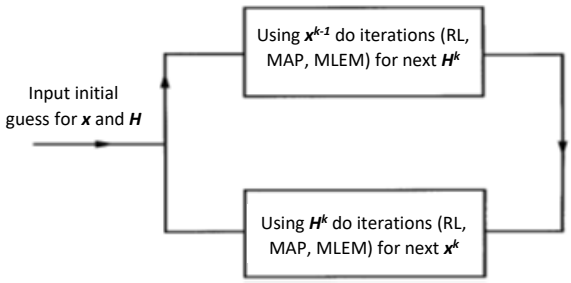

Figure 1. General approach for blind deconvolution in γ-spectrum [25]

to solve Eq. (1) when we only have a measurement vector ***y***. The detail of the proposed method is as follows:

1. Randomly define non-zero elements of ***h*** vector (***psf***), then construct DRM (H). Repeat to obtain DRM population $(H_1^0, H_2^0 \ldots\ldots H_{n-1}^0, H_n^0)$ as the first generation.
2. Solve for x^{k+1} for each DRM (individual
3. Calculate fitness value ($f=||y-Hx||^2$) for each solution ***x*** $(x_1^1, x_2^1 \ldots\ldots x_{n-1}^1, x_n^1))$
4. Apply GA
   a. Select strong individuals $(H_1^{k+1}, H_2^{k+1} \ldots\ldots H_{n-1}^{k+1}, H_n^{k+1})$
   b. Apply crossover and/or mutation
   c. Add new individuals and
   d. Construct the next generation

Flowchart of the proposed algorithm is given in Figure 2. Instead of searching for convergence of ***x***, this study proposes to search for detector response matrix (***H***). Once ***H*** is obtained then ***x*** is solved with any deconvolution method.

d. Construction of H

In the spectrum, an ideal peak has Gaussian distribution and the number of channels in which it is distributed is not actually very large. Therefore, the elements of the ***H*** contributing to detector response function have non-zero values only in this range [26]. It

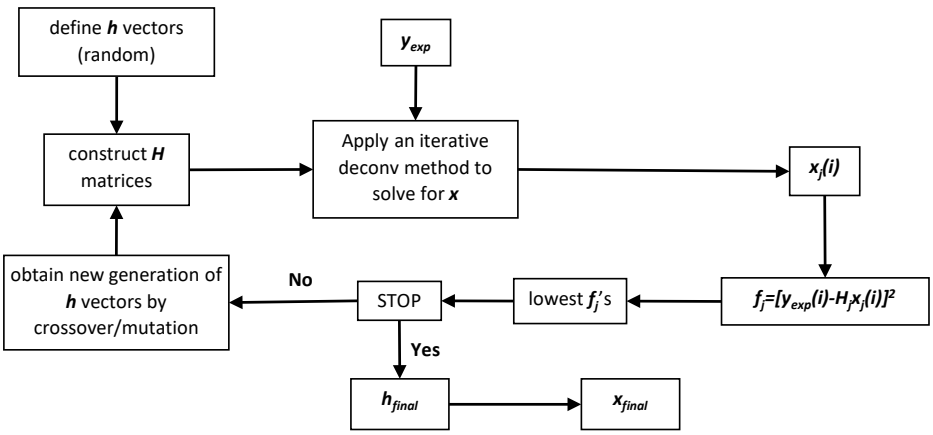

Figure 2. Flowchart of calculations

is recommended that the peak points of the Gaussian distribution width be considered as half of the base widths [18]. The columns of ***H*** are represented by vectors ***h*** cyclically shifted by one position [26]. For example, if the base width of a peak is ***2m+1*** channel then the non-zero elements of ***h*** vector can be taken as *m*. ***h*** vector represents point spread function (***psf***) of convolution. Once *m* number is generated randomly then we obtain the detector response matrix.

e. Experiment

The experimental data (y_{exp}) used in the study were obtained with a 1.5"x1.5" NaI(Tl) detector. The source is 3.0 cm away from the detector surface in order to get higher count rates as the source strength was low. There is no directional dependence in measurement as the sources are isotropic. The detector is in a 1.0 mm thick Al coating on the surface and 3.0 mm on the sides. Experimental Co-60 and Cs-137 spectrums were converted into net counts by background elimination (Figure 3).

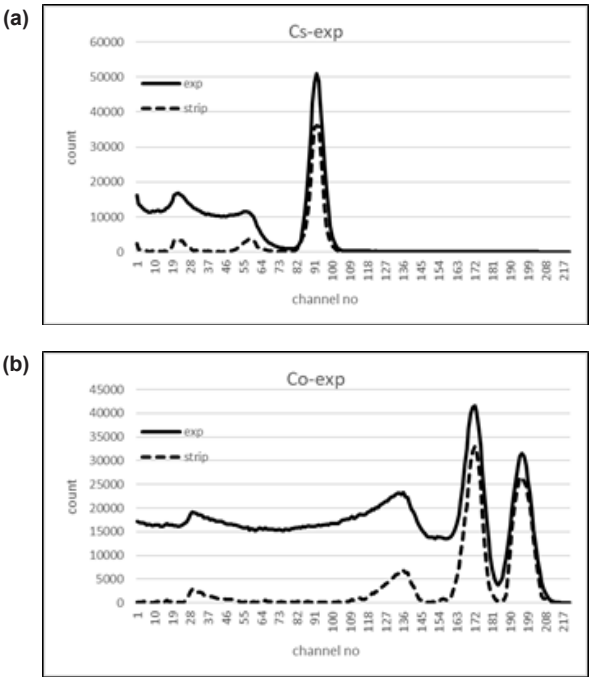

Figure 3. Experimental measurements (exp) and background eliminated net counts (strip) of Cs-137 (a) Co-60 (b)

3. Results

The Richardson-Lucy algorithm (RL) ([10, 11]) was selected as iterative deconvolution part of problem. It's based on Bayesian maximum likelihood and is stable in the presence of high noise levels [25]. Gold [8], maximum a posterior (MAP) and other methods [27] can also be used, but this is not the objective of this study and the reader may choose among any of deconvolution method. While implementing RL algorithm, optimization of matrix operations [26], boosting [12] and Tikhonov regularization [12, 28] is applied.

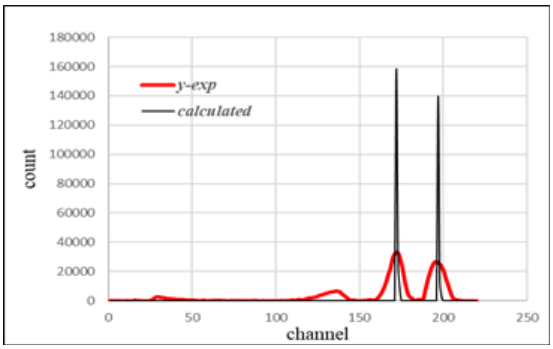

Figure 4. Deconvolution of Co-60 spectrum.

For GA part of the problem, the population in every generation is set to 100. Larger population increases calculation run-time but large population also means higher probability to obtain best generation earlier. While some studies report 8000 individuals [20] in every generation, some use 100 individuals [22]. The size of the population is generally recommended to be 20-50 [3].

Crossover and mutation ratios are other parameters that can be optimized. Small crossover ratio causes slow approach to the best generation. The genetic algorithm acts like a random search if it is too high. The crossover ratio is recommended to be between 0.4-0.9 and mutation should be far less than that of crossover [3]. In this study, the crossover ratio is taken as 80% and that of mutation is 20 % during construction of the next generation.

Like population size, the iteration number is also a parameter that affect calculation time. Convergence is fast at the beginning and slows down. Increasing the iteration number does not practically change the results. Additionally, it increases computational time.

Results of blind deconvolution of experimental Co-60 spectrum using GA and RL deconvolution (1000 iteration) is given in Figure 4. Calculation is stopped when fitness function reaches a value or number of generation exceeds maximum number. In this paper stopping rule is set to $\Delta f < 10^{-4}$ for ten consecutive generations. It is clear that unfolding is accomplished without prior knowledge of ***H***. Calculated spectrum is average of 10 runs. Each run is a solution obtained independently by proposed method. The number of generation is maximum 27 (Figure 5).

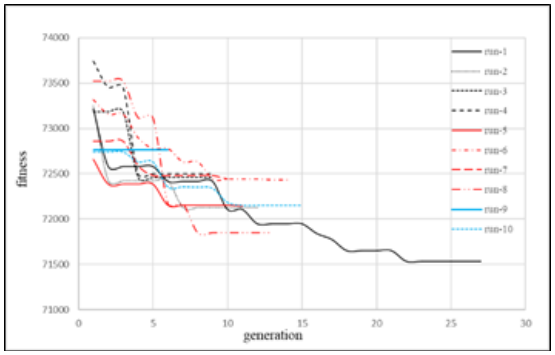

Figure 5. Evolution of fitness function

Computational time for each generation is 7.5 s. Each RL iteration takes 5.22×10^{-5} s. All calculations were performed with desktop equipped with 3.2 GHz Intel Core i5-3470 cpu and 8 GB RAM.

In Figure 6 we present combined experimental Cs and Co spectrums (a) and spectrum after the RL deconvolution (b). It is obvious that the DRM calculated with proposed algorithm is successful in a wide energy range.

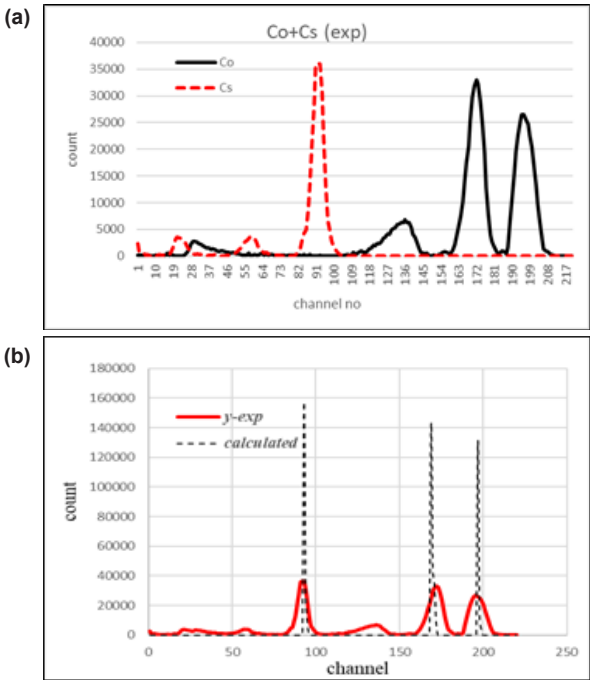

Figure 6. Combined net counts of Cs-137 and Co-60 (a) and deconvolution with proposed algorithm

To see the effectiveness of the method in case of overlapping peaks, the 2nd peak of Co was placed next to 1st peak and combined with Cs spectrum to form an overlapping peak (Figure 7 (a)). The proposed algorithm unfolded overlapping peaks completely (Figure 7 (b)).

The point spread function (***psf***, non-zero elements of the ***h*** vector) obtained with the proposed method is given in Figure 8. As can be seen from the graph, the proposed algorithm gives approximate results to the experimental values.

4. Conclusion

The study presents blind deconvolution method combined with GA in γ spectroscopy to unfold measurement data. Instead of consecutive iteration cycles for solution vector x and detector response matrix ***H***, the proposed method focuses on calculating ***psf***. This method also ensures representative DRM since it enables environmental effects during measurement to be included in DRM. This method does not require prior knowledge of ***psf*** and benefits from global optimization of GA. Therefore, it would be greatly effective in a real time scenario.

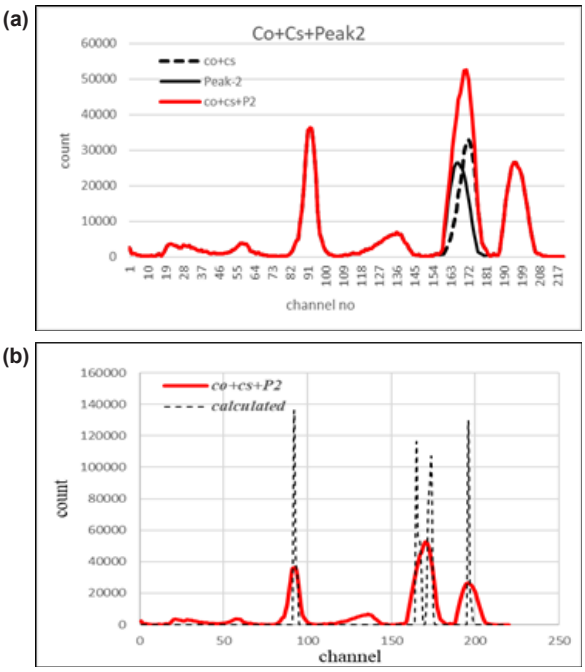

Figure 7. 2nd peak of Co-60 was placed under 1st peak and combined with Cs-137 (net counts) (a) and deconvolution with proposed algorithm (b)

Computational time can be significantly reduced by faster hardware options and parallel processing option for GA. The population size and number of iterations are parameters that can be studied further.

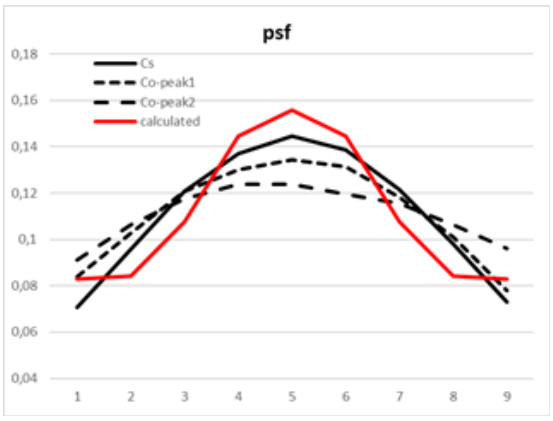

Figure 8. Calculated and experimental point spread function

5. Conflict of interest

There is no conflict of interest.

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