

A new neutron energy spectrum unfolding code using a two steps genetic algorithm



H. Shahabinejad^{*}, S.A. Hosseini, M. Sohrabpour

Department of Energy Engineering, Sharif University of Technology, Tehran, Islamic Republic of Iran

ARTICLE INFO

Article history:

Received 12 August 2015

Received in revised form

28 November 2015

Accepted 14 December 2015

Available online 23 December 2015

Keywords:

Neutron spectrum unfolding

Genetic algorithm

TGASU

MCNPX-ESUT

LSQR

ABSTRACT

A new neutron spectrum unfolding code TGASU (Two-steps Genetic Algorithm Spectrum Unfolding) has been developed to unfold the neutron spectrum from a pulse height distribution which was calculated using the MCNPX-ESUT computational Monte Carlo code. To perform the unfolding process, the response matrices were generated using the MCNPX-ESUT computational code. Both one step (common GA) and two steps GAs have been implemented to unfold the neutron spectra. According to the obtained results, the new two steps GA code results has shown closer match in all energy regions and particularly in the high energy regions. The results of the TGASU code have been compared with those of the standard spectra, LSQR method and GAMCD code. The results of the TGASU code have been demonstrated to be more accurate than that of the existing computational codes for both under-determined and over-determined problems.

© 2015 Elsevier B.V. All rights reserved.

1. Introduction

The neutron detection systems and spectrometers such as proton recoil scintillators, Bonner sphere (BS) systems, and foil activation passive detectors deal with the inverse problem of unfolding when used to characterize neutron fields. The unfolding of neutron energy spectra is of importance in various problems of radiation protection or health physics [1].

In neutron unfolding process, the neutron energy spectrum $\varphi(E)$, which is to be unfolded from the measured detector response, the detector response matrix $R(H, E)$ and the count rate in the detector dN/dH are related through the Fredholm integral equation, as shown in Eq. (1).

$$\frac{dN}{dH} = \int_{E_{\min}}^{E_{\max}} R(H, E)\varphi(E)dE \quad (1)$$

here, $R(H, E) dH dE$ is the differential probability that a neutron of energy within dE about E leads to a pulse with amplitude within dH about H .

Due to the discrete distribution of the $R(H, E)$ and the dN/dH that is obtained with a multichannel analyzer, Eq. (1) may be solved in a discrete form as shown in Eq. (2).

$$N_i = \sum_j R_{ij}\varphi_j \quad (2)$$

here, N_i is the recorded count in the i th channel of multichannel analyzer, R_{ij} is the response matrix that couples the i th pulse height interval with the j th energy interval and φ_j is the radiation fluence in the j th energy interval [2].

Eq. (2) can be written in matrix notation as

$$N = R\varphi \quad (3)$$

here, $N = (N_1, N_2, \dots, N_n)^T$, $\varphi = (\varphi_1, \varphi_2, \dots, \varphi_m)^T$ and R is the response matrix with dimensions of $n \times m$.

If the number of channels (n) was more than the number of energy intervals (m), the problem is called over-determined. On the other hand, the problem is called under-determined if ($n < m$) [1].

Since there are no ideal natural or artificial monoenergetic neutron sources the experimental response matrix of scintillators will have some associated errors. Since there was no access to monoenergetic neutron sources in the laboratory, the pulse height distribution obtained from simulation may be an appropriate replacement of the experimental data.

1.1. MCNPX-ESUT code

MCNPX-ESUT (MCNPX-Energy engineering of Sharif University of Technology) is a computational code that has been developed based on MCNPX Monte Carlo code to simulate neutron/gamma pulse height distribution in a scintillation detector [3]. The simulated neutron pulse height distribution of this code has been benchmarked with the experimental data. The normalization of the energy and amplitude of the registered pulse is one of the built-in features of the MCNPX-ESUT computer code.

^{*} Corresponding author. Tel.: +989130414074.

E-mail addresses: shahabinejad1367@yahoo.com, shahabinejad@energy.sharif.ir (H. Shahabinejad).

The simulated neutron pulse height distribution using MCNPX-ESUT code consists of response matrix columns. Each column of response matrix represents the pulse height distribution due to each assumed mono-energetic neutron source.

The main advantage of MCNPX-ESUT code is that neutron/gamma pulse height distribution simulation may be performed without the use of any postprocessor. Also the developed MCNPX-ESUT code has the ability to perform pulse height simulation as well for both neutron and gamma sources. It thus has the ability to discriminate the neutron and gamma rays in the mixed fields.

1.2. Literature review

To unfold the neutron spectrum, conventional mathematical methods can be used, such as the Monte Carlo [4], the least squares [5] and the maximum entropy [6] methods. However, alternative methods have also been developed for the unfolding of information obtained by the BS system. These methods use techniques of Artificial Intelligence (AI), such as artificial neural networks [7] and Genetic Algorithms (GAs) [1,8–10].

Unfolding of neutron spectra using genetic algorithm was introduced by Mukherjee in 1999 [10]. He used a genetic algorithm code to unfold the neutron spectra of $^{241}\text{Am}/^9\text{Be}(\alpha,n)$ and $^{239}\text{Pu}/^9\text{Be}(\alpha,n)$ neutron sources obtained from 6 BSs in 24 energy intervals. In 2002, the same author applied the GA technique to unfold the neutron spectra of $^{241}\text{Am}/^9\text{Be}(\alpha,n)$ neutron source and 10 MW DIDO class research reactor obtained from 6 BSs in 80 energy intervals [8]. Characterization of the neutron spectrum of $^{241}\text{Am}/^9\text{Be}(\alpha,n)$ neutron source and a neutron spectrum inside a cyclotron accelerator obtained from TLDs embedded in 7 BSs and in 100 energy interval was performed by Santos et al. in 2012 [9]. Suman et al. developed a spectrum unfolding technique using the genetic algorithm method within the framework of Monte Carlo simulations in 2014 [1].

All these GA computational codes appear to encounter the same problem in some cases of the neutron unfolding process. They may not accurately adjust the φ elements (see Figs. 4 and 5) in a convenient stopping condition of the GA code and may need more iterations or a rigid stopping condition to obtain the desired results.

The objective of this work was to develop a new neutron spectrum unfolding code to unfold the neutron pulse height spectra from an NE-213 scintillator which was obtained by means of MCNPX-ESUT Monte Carlo code for both cases of over-determined and under-determined problems. The input of the MCNPX-ESUT code was the standard spectra of the ^{252}Cf and $^{241}\text{Am}-^9\text{Be}(\alpha,n)$ neutron sources and two spectra from the IAEA technical report series No. 403 [11]. The above mentioned neutron pulse height spectra were also unfolded using the LSQR method. To evaluate the performance of the present code, the unfolded spectra of the $^{241}\text{Am}-^9\text{Be}(\alpha,n)$ neutron source and a two merged Gaussians using this code was also compared with those of GAMCD code [1]. The average neutron channel and the integrated neutron fluence rate values and also a parameter to measure the similarity derived from the standard spectra and mentioned unfolding methods have been compared.

2. Material and methods

To obtain a spectrum that would reflect a nearly appropriate case of the true spectrum it is recommended to use several unfolding codes [10]. Genetic algorithm was the principal method used in this work.

2.1. Genetic algorithm

The genetic algorithm, as a branch of artificial intelligence (AI), is an optimization and search technique that mimics the process of natural selection. This heuristic process is routinely used to generate useful solutions to optimization and search problems. A GA allows a population composed of many individuals to evolve under specified selection rules to a state that minimizes the cost function (i.e., maximizes the “fitness”) [12]. The method was developed by John Holland [13] and was popularized by one of his students Goldberg [14].

Some advantages of the GA method may be summarized as [12]:

- Optimization with continuous or discrete variables.
- No requirement for derivative information.
- Simultaneous search from a large number of samples belonging to a cost function.
- Ability to deal with a large number of variables.
- Well suited for parallel processing.
- Variable optimization with extremely complex cost functions.
- Provision of a list of optimum variables (not just a single solution).
- Optimization may be done with the encoded variables.
- This method is equally applicable to numerically generated, experimental, or analytical results.

The principle of the common GA problem-solving technique shown as a flowchart in Fig. 1 can be explained as follows [12]:

(1) Selection of the variables and the cost function.

The first step of GA is to define the chromosome or a solution vector that must be optimized. If the solution vector has N_{var} variables given by $p_1, p_2, \dots, p_{Nvar}$, then the solution vector is written as an N_{var} element row vector as shown in Eq. (4).

$$\text{Solution vector} = [p_1, p_2, \dots, p_{Nvar}] \quad (4)$$

A cost function generates an output from a set of input variables (a solution vector). The cost function may be a mathematical function, an experiment, or a game. Each solution vector has a cost

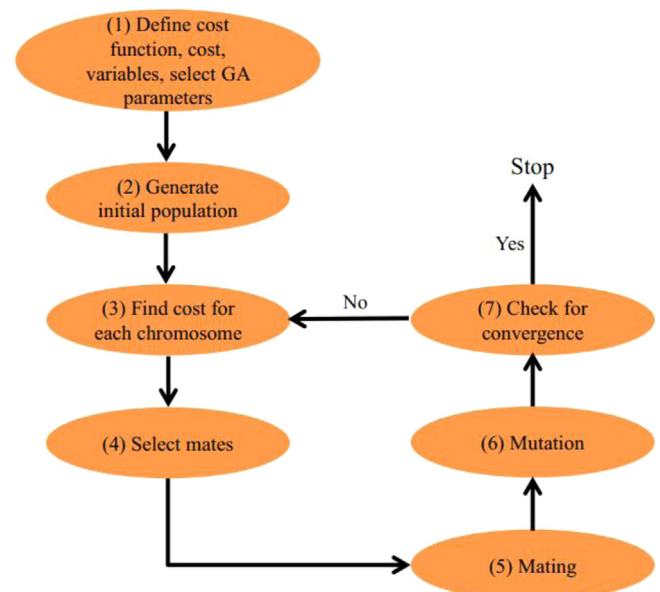


Fig. 1. Flowchart showing the principle of problem solving technique using a common genetic algorithm (GA).

Download English Version:

<https://daneshyari.com/en/article/1822228>

Download Persian Version:

<https://daneshyari.com/article/1822228>

[Daneshyari.com](https://daneshyari.com)