



Uncertainty analysis of delayed neutron fissile material assay using a genetic algorithm



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ABSTRACT

An uncertainty analysis of non-destructive assay of spent fuel using a delayed neutron method was conducted to explicitly define the accuracy with which plutonium content in an uncharacterized sample can be assessed. Perturbing various parameters allowed for an investigation of the sensitivity of this method to various nuclear data, and it was determined that the relative delayed neutron group abundances had the largest effect on the genetic algorithm. Specifically, for a sample containing ^{235}U , ^{238}U , and ^{239}Pu , irradiations in the thermal spectrum were shown to be more sensitive to ^{235}U and ^{239}U data, while irradiations in a fast spectrum were shown to be more sensitive to the ^{238}U data. The overall uncertainties of the mass estimates were 15%, 5%, and 30% for ^{235}U , ^{238}U , and ^{239}Pu , respectively. Finally, reducing the first delayed neutron group abundances by a factor of three as suggested by recent research reduced the overall uncertainties to 10%, 3%, and 20%.

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1. Introduction

Non-destructive assay (NDA) of spent nuclear fuel is an important research area due to the need in international safeguards for a direct and independent method of determining plutonium (Pu) mass in spent fuel. Currently, a wide range of methods is being investigated. These are generally divided into passive and active interrogation methods. The passive methods detect radiation coming off the sample and are grouped according to the radiation being detected. The active methods are divided according to the interrogating source (neutrons or gammas) and the detected radiation (gammas, prompt neutrons, and delayed neutrons). An overview of ongoing research can be found elsewhere (Runkle et al., 2012).

The National Nuclear Security Administration (NNSA) of the United States Department of Energy (DOE) launched the Next Generation Safeguards Initiative (NGSI) to address the challenges of the nuclear nonproliferation regime. One of the technical goals is to combine several different NDA techniques in order to reduce the large uncertainties on Pu assay obtained by individual measurement types (Tobin, 2012). None of today's techniques are capable of delivering an accurate estimate of Pu content in a spent fuel element of unknown composition, initial enrichment, and burnup.

Active neutron interrogation focusses on the prompt fission neutron signal as well as the die-away thereof (Jordan and

Gozani, 2007). It is used in detection of special nuclear material (SNM) rather than characterization of materials. A major weakness of prompt fission neutron techniques is that the fission signal is difficult to discriminate from interrogation neutrons when the source is turned on. Valuable information is therefore lost. One way to overcome this is by using low energy interrogation neutrons, which can be distinguished from the higher energy neutrons produced from fission events (Kerr, 2007; Lewis et al., 2014). Another method, however, is to look at the delayed neutron signal, which can be done using off-the-shelf neutron generators. It has been shown that larger quantities (kilograms) of SNM can be quickly detected in this manner (Moss et al., 2005).

The delayed neutron signal itself contains isotope specific information. Normally, the delayed neutrons are arranged in 6 or 8 groups according to the respective half-lives of their precursors (ranging from 0.2 s to 55.6 s). The division of these groups is a numerical exercise in order to facilitate the mathematical treatment of the many precursors and their subsequent decay. Since the delayed neutron group yields vary for different isotopes, the overall delayed neutron signal (as a function of time) varies as well. The delayed neutron signatures from the three most important isotopes in spent fuel are shown in Fig. 1. The delayed neutron data used to calculate these signatures were measured by Keepin et al. (1957). The delayed neutron response also depends on the energy of the interrogating neutrons, which offers the possibility of using different interrogation energies to further separate the isotopic contributions to the overall delayed neutron signal.

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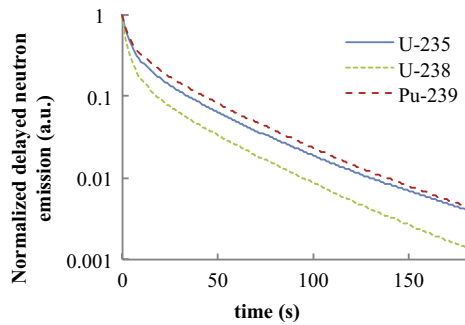


Fig. 1. Delayed neutron signatures of the three most important fissioning isotopes.

Even though more recent data sets exist, the Keepin data is the set that agrees best with integral experiments and is therefore still widely used (Spriggs and Campbell, 2002). However, uncertainties of these parameters are still large (up to 39% of the first delayed neutron group of ^{239}Pu). Table 1 summarizes the relative delayed neutron group abundances for ^{235}U , ^{238}U , and ^{239}Pu , and the associated uncertainties. Reducing these uncertainties will allow for better isotopic determination.

This paper attempts to assess the usefulness of the delayed neutron signal for the problem of quantifying isotopic masses of fissile material in a sample. The delayed neutron emission from the sample and its detection are simulated. A genetic algorithm (Holland, 1973) is used to find the combination of fissile masses that best fits the simulated measurement. This idea has been proposed before (Aumeier and Forsmann, 1998). It was concluded that the application of a genetic algorithm is a potentially powerful approach to delayed neutron NDA data analysis. However, the uncertainties associated with this technique have never been published. The current study focusses on the sensitivity of the algorithm to various nuclear data needed to estimate the isotopic masses. The most important of which are the relative delayed neutron group abundances (which define the percentage of delayed neutrons that will be emitted in each group).

Section 2 describes the modeling used for this analysis and gives an overview of the genetic algorithm. The results of the sensitivity studies and the overall uncertainty analysis are given in Section 3. Conclusions and applications are drawn in Section 4.

2. Modeling

2.1. Genetic algorithm

Fitting a number of parameters, in this case the isotopic weights, to experimentally measured data can be done in a number of ways. For this study, a genetic algorithm was chosen, which gets its name from evolutionary processes. A brief overview of the main

principles involved in a genetic algorithm follows. A comprehensive description of genetic algorithms can be found in Davis (1991) and Goldberg (1989).

Genetic algorithms have proven very capable of finding optimal solutions in a variety of difficult optimization problems (Gallagher and Sambridge, 1994; Yao and Sethares, 1994). They have been found particularly useful in situations with many local maxima/minima, in which other algorithms tend to get stuck. Genetic algorithms mimic the processes that are involved in evolution: selection (survival of the fittest), reproduction, and mutation.

To begin the optimization problem, an initial population of possible solutions is created that spreads across a predefined range of the parameters. In this case, the individual isotopic weights were limited to be greater than zero (since a negative mass is impossible) and less than or equal to the total sample mass (since the mass of any individual isotope cannot exceed the total mass of the sample). These individual sets represent the first generation, where each individual is a separate guess of the j isotopic masses in the sample. For this study, $j = 3$ due to the 3 isotopes being investigated. The centerpiece of the algorithm is the fitness function by which the individual solutions are rated. The higher the score of the fitness function for a certain individual, the more likely this individual survives the selection and the more likely it is to be considered as a reproducing parent. The entire population of the current generation is rated and ordered according to their individual fitnesses.

The selection principle dictates that fitter individuals are more likely to reproduce than the individuals of lesser fitness. Two individuals are chosen as parents for a certain number of children. These children are a genetic combination of their parents. In the current parameter space this means that their isotopic weights lay between the boundaries of the parental isotopic weights. An addition to the selection process is the elite count, which defines a number of individuals (the fittest in each generation) that survive unaltered to the next generation. This mechanism ensures that the best individuals of a given generation are at least as fit as the best individuals of the previous generation, and thus the algorithm does not regress.

The mechanism that makes this algorithm different from other optimization strategies is mutation, where a certain characteristic of a given individual is randomly changed. For the given parameter space, this means that a certain isotopic weight is randomly altered. This enables the algorithm to search the entire parameter space. It also helps to get the algorithm out of a local minimum in which it might be stuck.

There are a number of possibilities to terminate the algorithm. They can all be changed by the user and include the total number of generations, total run time, and minimal change in the average fitness between generations. Since genetic algorithms are based on the randomness of evolution, running the same optimization problem twice will yield two different results. The extent to which

Table 1

Delayed neutron group abundances and their associated relative uncertainties. There is no data for ^{238}U in the thermal irradiation spectrum since this process is kinetically forbidden. Data taken from the proposed selection of Spriggs and Campbell (2002).

Group	Thermal irradiation spectrum		Fast irradiation spectrum		
	^{235}U	^{239}Pu	^{235}U	^{238}U	^{239}Pu
1	0.033 ± 13%	0.032 ± 38%	0.034 ± 2%	0.008 ± 16%	0.029 ± 7%
2	0.154 ± 4%	0.237 ± 14%	0.150 ± 2%	0.104 ± 2%	0.225 ± 2%
3	0.091 ± 10%	0.083 ± 2%	0.099 ± 3%	0.038 ± 2%	0.095 ± 10%
4	0.197 ± 12%	0.182 ± 29%	0.200 ± 2%	0.137 ± 15%	0.149 ± 29%
5	0.331 ± 2%	0.294 ± 10%	0.312 ± 2%	0.294 ± 4%	0.351 ± 2%
6	0.090 ± 5%	0.082 ± 2%	0.093 ± 4%	0.198 ± 1%	0.037 ± 51%
7	0.081 ± 2%	0.072 ± 43%	0.087 ± 5%	0.128 ± 10%	0.097 ± 94%
8	0.023 ± 41%	0.018 ± 2%	0.025 ± 4%	0.093 ± 4%	0.017 ± 229%

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