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Visualization of Radioisotope Detectability Over Time

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Background

A radioactive isotope is an atom that has an unstable nucleus. The isotope can undergo radioactive decay, the process in which excessive nuclear energy is emitted from the nucleus in many different forms, such as gamma radiation, alpha particles, or beta particles. The important thing to note is that these emissions act as a signature for the isotope. Each radioisotope has a particular emission spectrum, emitting radiation at different energies and at different rates.

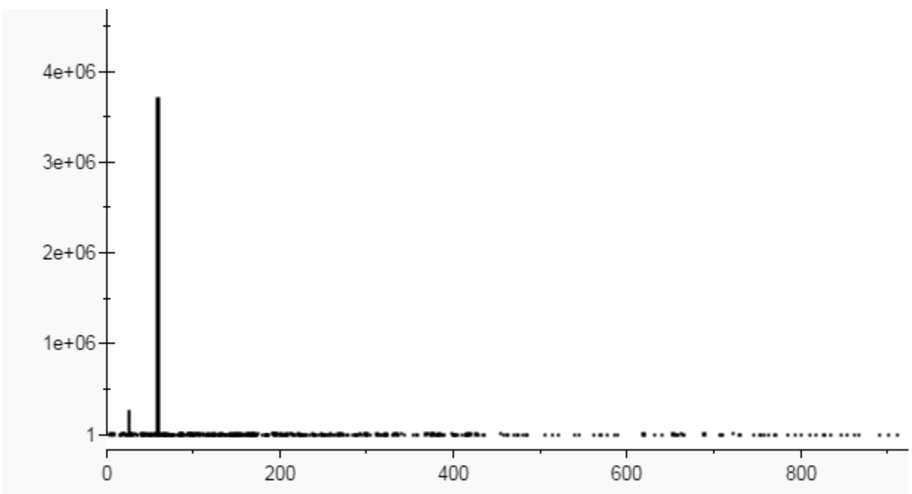


Figure 1 This is the emission spectrum for the decay of Americium 241. The x-axis shows the energies, measured in keV. Notice there is a photo peak at 59.54 keV. If we were to observe this spectrum in a detector, we would be able to narrow down and identify the source of these emissions as Am-241.

After a decay, the isotope ends up in a more stable state (e.g. Americium 241 decays into the more stable Neptunium 237). This means that the amount of a radioisotope in a source will decrease over time. The rate of radioactive decay is proportional to the amount of radioisotope N present:

$$\frac{dN}{dT} = -\lambda N$$

Where λ is the decay factor. This means that the amount of radioisotope follows an exponential decay over time:

$$N(t) = N_0 e^{-\lambda t}$$

This also implies that the activity of the radioisotope, or the amount of emitted radiation, follows the same type of relationship.

Radioisotopes are commonly used for medical purposes, especially for diagnostics. When a person ingests a medical radioisotope drug, the physical decay continues as normal. However, the properties of the drug affect how the body will distribute and ultimately excrete it, such that the radioisotope is no longer a source of radiation in the body. The complex path from the points of ingestion to excretion is abstracted into a biological decay factor, assuming the rate of excretion is also an exponential decay (although we know that it is discrete). So our formula becomes:

$$N(t) = N_0 e^{-(\lambda_{physical} + \lambda_{biological})t}$$

Most resources will talk about the decay factor in terms of a half-life, which is the amount of time it takes for N_0 to be halved. This means that the total decay factor is:

$$\lambda_{physical} + \lambda_{biological} = \frac{ln2}{\tau_{physical\ half\ life}} + \frac{ln2}{\tau_{biological\ half\ life}}$$

Radiation detection is really a counting experiment; the detector simply counts the number of particles it sees and organizes them by energy. For example, if I were to put an Americium 241 source in front of a detector and allow it to detect for a period of time, I would expect to observe a spectrum with a bunch of counts in the 59.54 keV energy bin. However, the probabilistic nature of decay means that repeated experiments over the same time interval would yield a different number of counts. The mean, or expected number of counts, is just the decay time multiplied by the time interval, but there can be deviation from this value. We want to be able to analyze what is a reasonable deviation in counts.

The above derivation for decay discusses an ensemble of particles, but a decaying particle does not really care about the particles around it. A single particle actually decays as a Poisson process, and the whole ensemble decay is just the sum of all the particle decays. Thus, we can use Poisson statistics to analyze our counts. In particular, the only thing we care about is the standard deviation of a Poisson distribution, which is calculated simply by the square root of the expected number of counts.

The above discussion is important because we are looking for a minimum detectable activity, which is basically a statistically significant count. In reality, when we use a detector in the field, it cannot just isolate radiation from a particular source. There is a background radiation spectrum that comes from sources all around and it is just always there to interfere with our counting. So a statistically significant measurement is one that deviates far from the expected background spectrum. We will consider it significant if the detected spectrum is three standard deviations different from the expected background spectrum. The formula we will use for the minimum detectable activity is derived by:

$$3 = \frac{detected\ counts - background\ counts}{\sqrt{background\ counts}}$$

Now we have a mathematical model to follow.

Objective

The purpose of this visualization is to aid US ports of entry where radioisotope detectors are in use. It is very reasonable for a person entering from a port of entry to have been administered medical radioisotope drugs, and these people would trigger the detector. We want to give a resource to help determine whether a medical patient would reasonably set off a detector, so that a worker would know whether or not to proceed with suspicion.

How it works

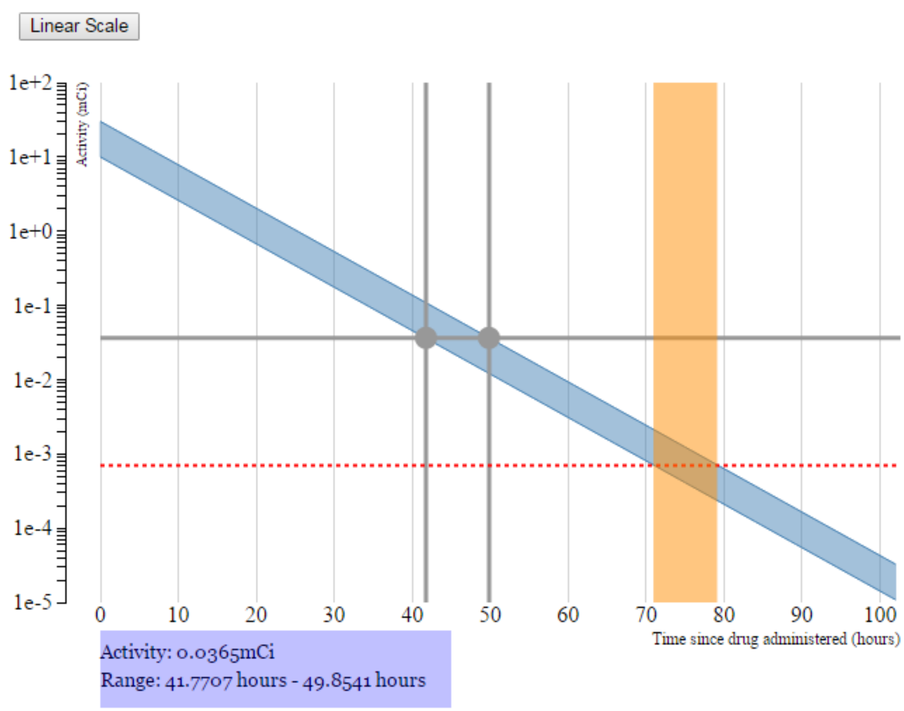


Figure 2 Screenshot of the visualization

This visualization was created in JavaScript. The light blue region shows the exponential decay over time of the radioisotope, which includes both the physical and biological decay factors. The important part of the visualization is the red dotted line, which represents the minimum detectable activity (MDA). This value depends on the detector that is being used. We estimate this value in the following section.

Finding Minimum Detectable Activity

The minimum detectable activity (MDA) is the amount of activity, in the same counting time, which gives a count which is different from the background by three times the standard deviation of the background counting rate. We will be simulating these counting events in GADRAS. GADRAS is a powerful piece of software that can do a lot of things that I am unfamiliar with. But, I do know that we can use it to generate emission spectra of radioisotopes, given a piece of shielding. In our case, we will be shielding with a human body.

Generating Emission Spectra

First, we have to select a detector. Upon initializing GADRAS, the very first tab is the detector tab. On this interface, you will see many variables that can be changed, but we won't worry about that. Just click file, and change detector to see a list of detectors already saved that you can choose from. In this case, we will be using the handheld Detective-EX100.

Next, we have to input into the program a reasonably accurate model of a person. Click into the 1DModel tab and create a new model. I was informed that GADRAS does not model most shapes very well. It takes the model that you create and collapses it into a single point at the origin, and the relevant information is extrapolated by this single point. So, it is the most accurate to just use a sphere to model our human being. Go to the shell material drop down menu on the rightmost column. Under the materials tab, you can right click and add nuclides. Here is where we build the human flesh.

Add the following elements in these amounts:

Element	Symbol	Percentage
Oxygen	O	65
Carbon	C	18.5
Hydrogen	H	9.5
Nitrogen	N	3.2
Calcium	Ca	1.5
Phosphorus	P	1.0
Potassium	K	0.4
Sulfur	S	0.3
Chlorine	Cl	0.2
Magnesium	Mg	0.1

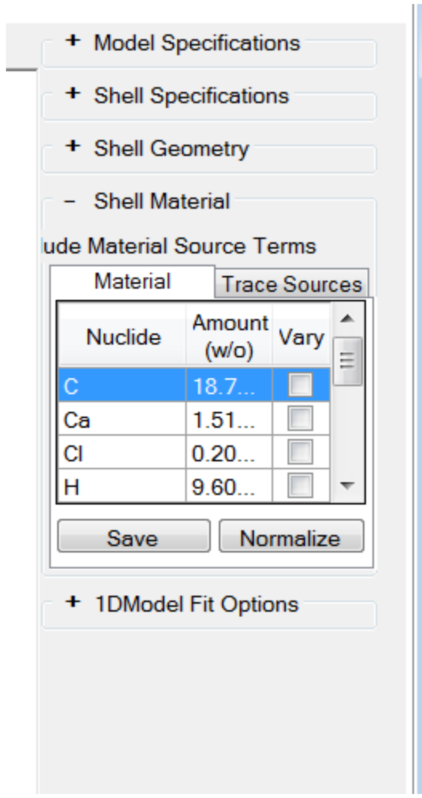


Figure 3 What the tabs on the right hand column look like. The Shell Material tab is expanded.

Click the save button. Now this "human flesh" material will be selectable for future models.

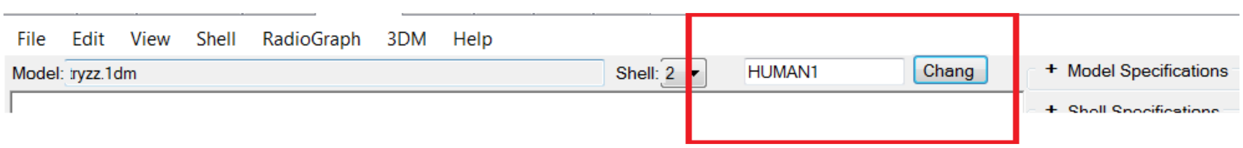
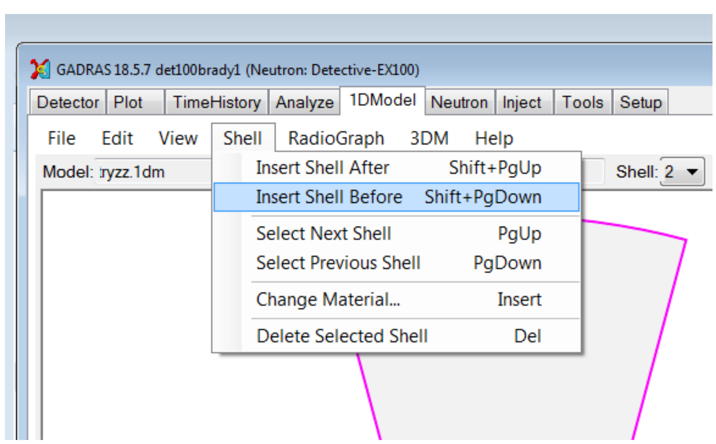


Figure 4 The type of material can be selected here.

Next, we want to add the radiation source. Click on the shell drop down menu and click Insert Shell Before.



Select this new shell and look on the right to find the Trace tab under the Shell Material section. Right click and add a trace isotope. Here, you select the isotope that you are currently investigating. The activity should be the dosage of the medical radioisotope drug, but I recommend that you set it to 1mCi because there is a section later that allows you to adjust the activity of the source.

The parameters for the shell specifications are given in the table below:

Outer Shell	Density (g/cc)	1.6
	Age (years)	20
	AD(g/cm2)	16
	Thickness (cm)	10
	Outer Rad. (cm)	15
	Mass (kg)	21.78
Inner Shell	Density (g/cc)	0
	Age (years)	20
	AD(g/cm2)	0
	Thickness (cm)	5
	Outer Rad. (cm)	5
	Mass (kg)	0

Now, you save the model. Preferably title it so that it tells you the specific isotope and the activity. This saves as a .1dm file, but also creates a .gam file that will be used.

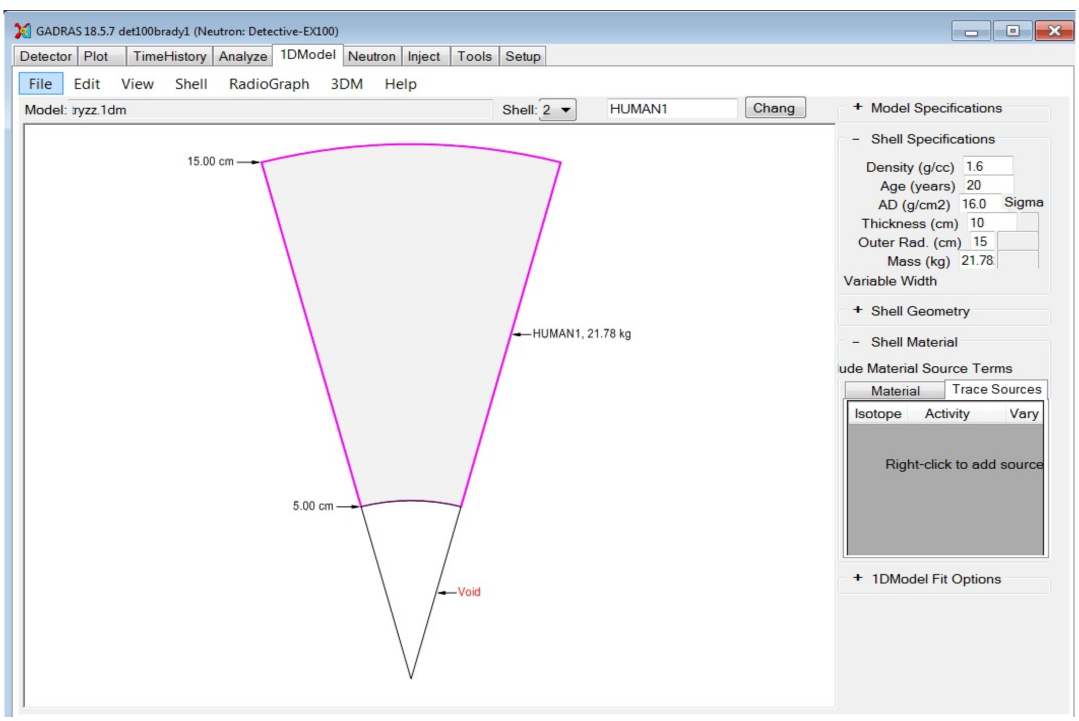


Figure 5 What it looks like all put together.

Next, we want to create the inject files that we display our emission spectra from. Go to the Inject tab located at the top toolbar. Select the correct Date/Time. The Output File field will be where the data will be output to and it contains all the information. If this is the first spectra generated for this isotope, you have to fill in this field with a title and as a .pcf file type.

You can have multiple spectra in the same inject file, and they are distinguished by their Record number that you can fill out to the right of the Output File field. For Record 1, you should be creating the Background spectrum, so title it Background and keep the Source field empty. For the other Records, select your model generated in the Source field. GADRAS will auto-fill the field with the title of the model, as well as something that says 1C. This 1C is the proportion of activity the source will have, so if it is set as 1C, the activity of the isotope will be whatever you set it as in the model .gam file. This makes it easy to adjust the activity of the source by simply changing it from 1C to 0.5C if you want the activity to be cut in half and so on.

Set the Distance to 100, Height to 100, and Time to 300 with the Real time bubble and the Apply Poisson Statistics box checked.

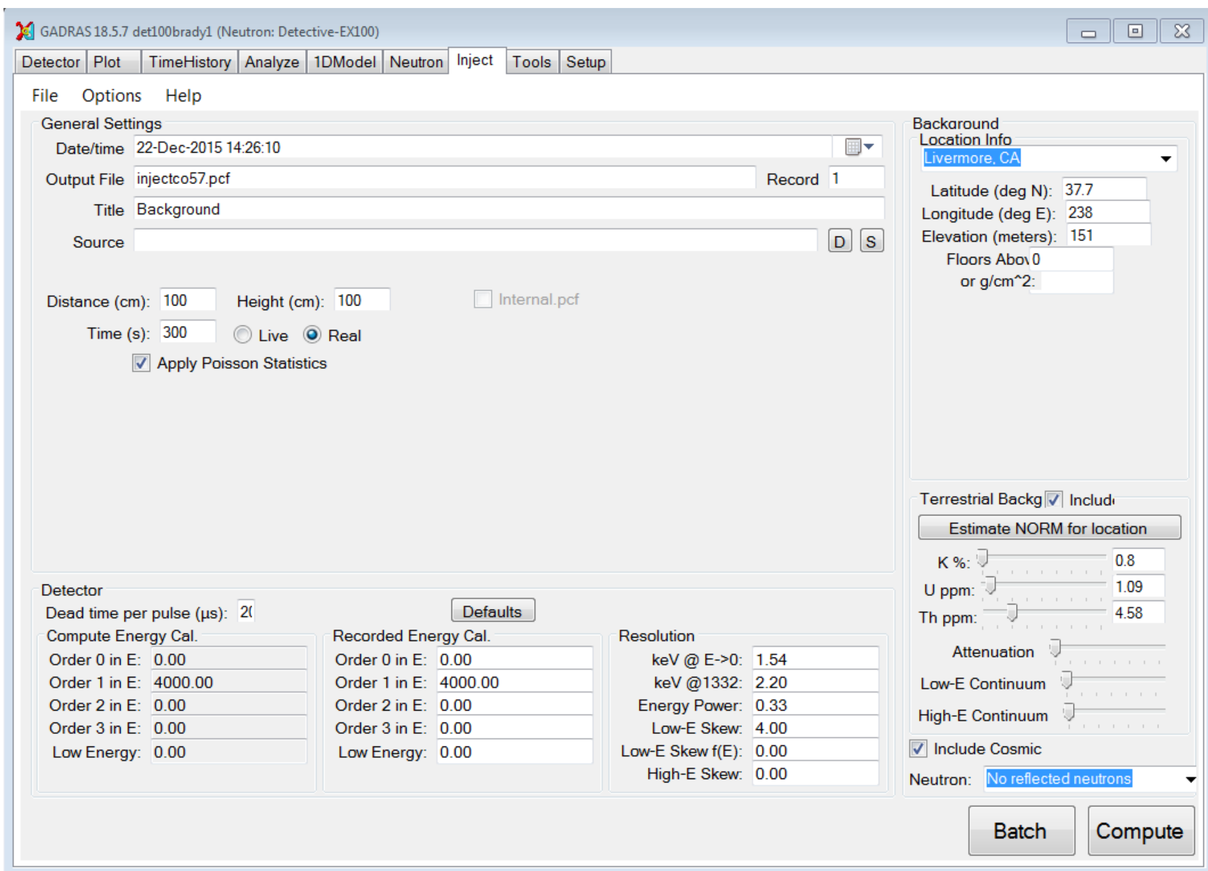


Figure 6

On the right you will see the Location Info section. Click the drop down menu and select the location of interest. This is important because different locations will have different background spectra. I tended to only analyze two locations: Livermore and Los Alamos, though it is probably important to generate spectra for even more locations. After the location is selected, click the Estimate NORM for Location button below. Once everything is set, click Compute. The inject file is now completed, and GADRAS will plot it for you, though it is preferable to use Interspec to view spectra.

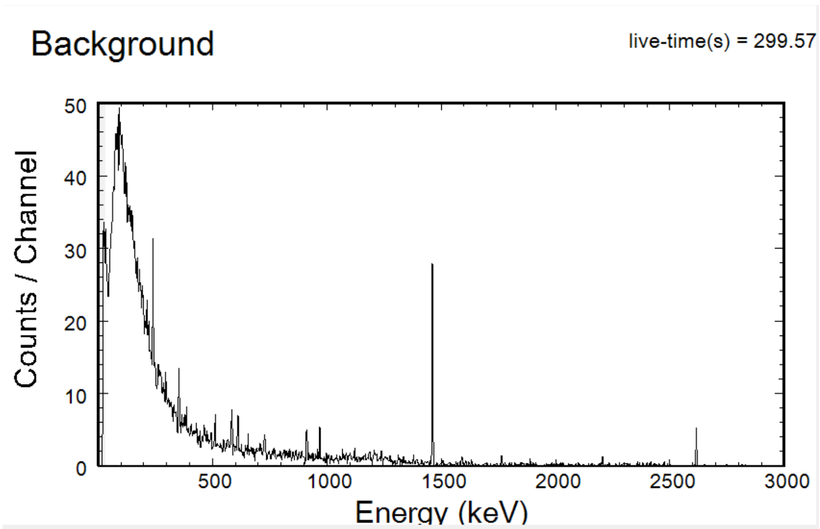


Figure 7 Example of what a Background Spectrum would look like

Analyzing Emission Spectra

Now, we will use Interspec to analyze the spectra. What you should have done already is generate a ton of inject files. Log into Interspec and click File, Upload Spectrum, and Background. Your spectra will be displayed on the right. On the left are three sections, Foreground, Background, and Second Foreground. This allows you to have three spectra displayed at the same time. Set the Background to your background Record 1 and the foreground to your spectra of interest.

I will not go too in depth of how to use Interspec, as there is documentation for that. All we care about is finding the MDA, and to do that, first identify the photopeaks of the isotope we are currently investigating. Then, locate those peaks on the display in Interspec. Double-click on the peak to fit it to a Gaussian. If you right-click the peak and select peak editor, you can fit the peak even better. Once the peak is fit to your content, hover over the peak to get statistical information about it. The peak area is the number of counts in that peak. The cont. area, or continuum area, is the total area, and thus the total counts, below the peak. In general, cont. area will be the background counts, because the background usually fits well under the foreground. However, this is not always true, so you will likely have to go to the background spectra and fit areas onto it to find background counts.

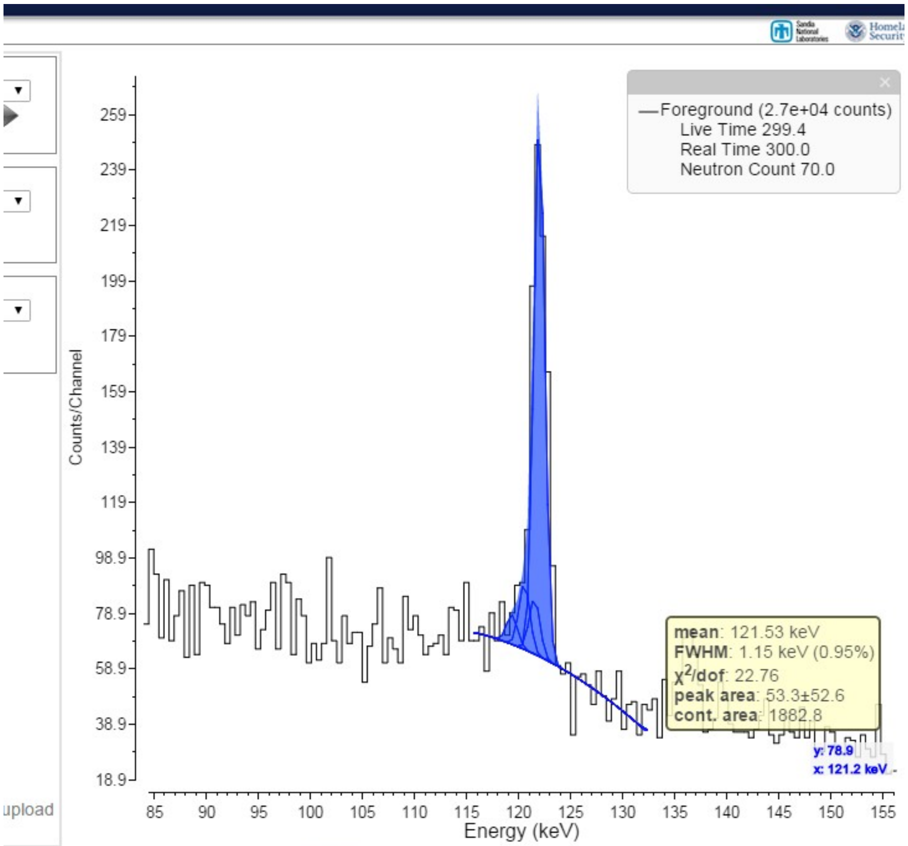


Figure 8 Peak fitting in Interspec

Once we have all of that information, we can calculate how far above the mean counts this particular activity gives. The example above shows a peak area of 517 and a cont. area of 1882. Using the formula, we get

$$\frac{517}{\sqrt{1882}} = 43.4$$

This means that this particular activity gives a photopeak that is 43.4 standard deviations away from the mean, and is thus very statistically significant. However, this does not tell us what the minimum detectable activity is. We have to use an inject file with a smaller activity, decreasing the peak height until the above value is around three. Then, we take that activity value to be the minimum detectable activity.

In the code for the visualization, there are 3 important fields to be filled in: the mda, the physical half-life and the biological half-life. Once these fields are filled in, the visualization can be generated.