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July 1985

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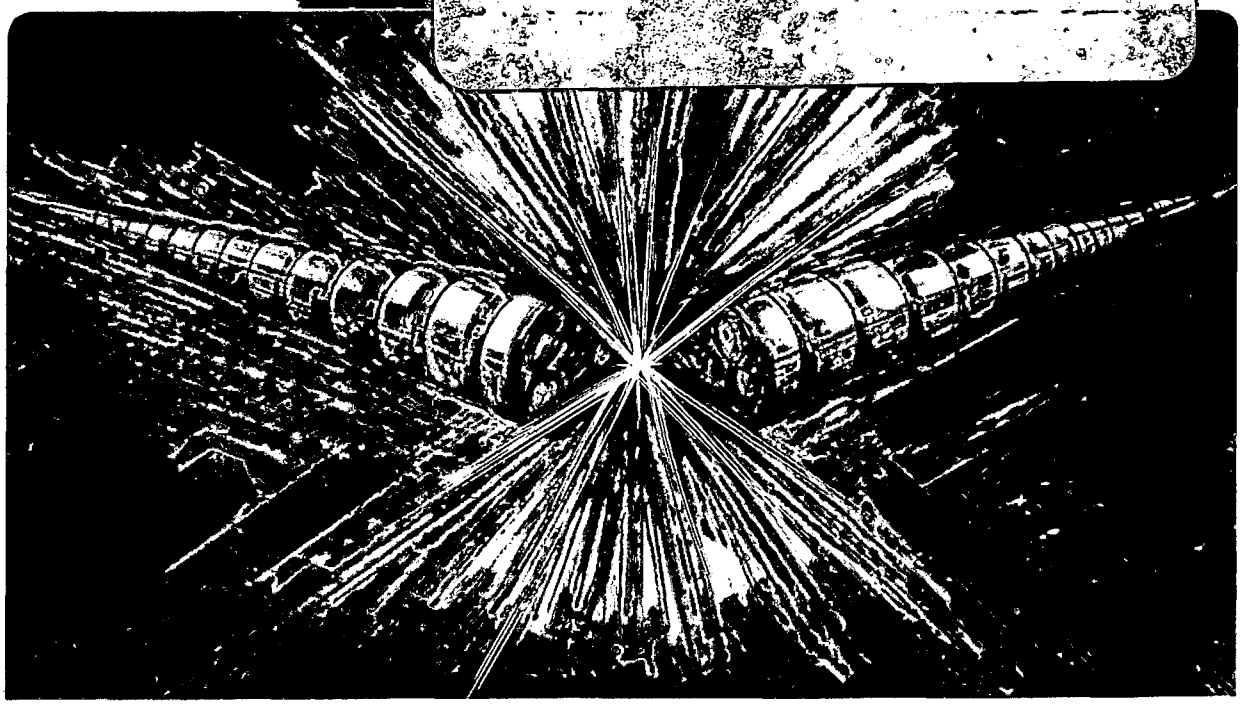

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Neutral-Beam Species Determination from Nuclear Reaction Products*

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Abstract

A review is presented of recent measurements designed to measure neutral-beam species by nuclear reaction analysis. The detection system is described as well as several experiments intended to improve resolution and reduce noise. Results obtained at the Neutral Beam Engineering Test Facility are discussed and compared with the predictions of optical Doppler-shift spectroscopy.

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Introduction

An important consideration in the efficient injection of energetic neutral beams into fusion reactors is the ratio of atomic to molecular ions extracted from the ion source. An on-line diagnostic for this ratio is required as a part of an operational neutral beam injector. This paper concerns the development of one means of satisfying this requirement.

The relative concentrations of D^+, D_2^+, and D_3^+ from neutral-beam ion sources can be determined from the analysis of nuclear reaction products produced in the neutralizer region. The reaction of interest is D(d,p)T. Both the protons and the tritons are characterized by a 3-peak distribution, which can be related to the contributions of D^+, D_2^+, and D_3^+ from the ion source. Details of the nuclear multichannel analysis (NMA) method have been published by Smith and Strathman,[1] and by Markevich and Smith.[2] The purpose of this report is to update certain aspects of the experimental system, and to review some results obtained at the Neutral Beam Engineering Test Facility (NBETF).

Detection System

The detection system has been considerably simplified compared to that described in Refs. 1 and 2, with no loss in resolution. Neither the detector nor the preamplifier is now cooled, and the preamplifier has been removed from the vacuum system. The remainder of the counting system consists of a booster amplifier, also in the accelerator room, and of several other components located in the accelerator control area. The latter include the detector-bias power supply, a final amplifier, and a 1024-channel pulse-height analyzer which is coupled to a computer (Hewlett-Packard Model 9845B) used for data

storage and analysis. A 150 mm^2 Au surface barrier detector (Octec Model BR-17-150-300-S) is used in a reverse-mounted configuration, i.e., a 240 $\mu g/cm^2$ light-tight aluminum electrode faces the incoming particles, and the detector is negatively biased. A multichannel collimator consisting of a single stack of stainless-steel-mesh sheets (see Ref. 1) has been placed in front of the detector. The detector and its housing are electrically insulated from the neutralizer section of the neutral-beam source by means of a plastic mating flange (see Fig. 1).

Experimental Results

Considerable operating experience has been obtained using NMA at the NBETF with accelerator voltages in the range 80-120 kV, and with pulses in the range 0.5-4.0 s. Fig. 2 shows a typical spectrum taken at 120 kV, with an accelerator current of 53 A, and with 2-second pulses. Figs. 3 and 4 show details of the proton and triton distributions with the curve representing a fit to 3 slightly sharpened Gaussians, i.e., the power of the exponential has been reduced from 2.00 to 1.65. It may be seen from Fig. 2 that a background is present, which increase exponentially as the particle energy approaches zero. This background is produced by electrical noise associated with the accelerator high-voltage power supply, as evidenced by the fact that it is unaffected either by 1.6 mm of Pb shielding around the detector, or by closing the valve between the detector and the neutralizer. The background was also present when the accelerator was operated on ordinary hydrogen, and it increased in severity with increasing accelerator voltage. The exact source of the background remains to be determined.

A number of tests were performed in an effect to improve resolution and to reduce noise in the detection system, with accelerator conditions maintained

constant. It was found that resolution was not materially benefited by a coincidence gate which allowed the analyser to record only when the accelerator voltage was within prescribed bounds. A typical operating condition for the gate, selected to minimize variations and yet provide a reasonable duty factor during the pulse, was 120 $\pm$ 0.8 kV. Neither the noise nor the resolution was affected by ungrounding the detector, preamp, and booster amp in the accelerator room. Substituting a solid-shield signal cable for a braided-shield cable appeared to have a deleterious effect on resolution. A bipolar signal pulse produced significantly improved resolution over a unipolar pulse, and shortening the shaping time constant had a similarly beneficial effect, down to 0.5 μs. Eliminating the booster amplifier and increasing the final amplifier gain appeared to worsen the resolution.

Several methods[1] have been investigated experimentally which could serve as an on-line diagnostic for species determination. The operational adopted for use at the NBETF is optical multichannel analysis[3] (OMA). OMA data analysis is done automatically, and results are available before the next shot. The method makes use of the Doppler shift in Balmer-α light, based on 2 separate views of the neutralizer--parallel to the accelerator grids, and perpendicular to the accelerator grids. NMA, on the other hand, requires the integration of 3 or 4 shots of 2 seconds duration at 120 kV, and the data are then stored for later analysis. With a detector of twice the present diameter, and some programming adaptation, NMA is capable of supplying shot-to-shot species determinations, just as does OMA.

NMA data continues to indicate a slightly lower D^+ fraction than does OMA. For example, Table 1 compares the average NMA and typical-shot OMA analysis for the shots whose NMA spectra are shown in Figs. 2-4. The extent

of the disagreement has been reduced from its value earlier in the year, because of a recalibration of the NBETF accelerator-voltage measurement circuitry. The resulting reassessment of the acceleration voltage had an opposite effect on the OMA and NMA species analyses. Aside from the remaining difference in predictions, it is important to assess the shot-to-shot variations in the results for the D^+ fraction, when the accelerator conditions are maintained constant. Table 2 shows the average and relative RMS deviations in about 12 OMA and NMA determinations corresponding to 40 shots at 120 kV. It can be seen that relative deviations for OMA and NMA are comparable.

Discussion

Both OMA and NMA attempt to reconstruct the ion species ratios at the exit of the ion source, and each provides two slightly different predictions for the resultant ratios. OMA is capable of providing species ratios for operation with normal hydrogen, whereas NMA is not. Ref. 3 reports good agreement between OMA and mass spectroscopic predictions, using a source similar in size to that employed on NBETF, when the neutralizer is viewed perpendicular to the direction of the accelerator grids. It should be appreciated, however, that both the species ratios of the neutralized component, to which OMA is responsive, and those of the un-neutralized component, to which the mass spectrometer is responsive, require considerable correction before they can be interpreted in terms of the original ion-source output. OMA analysis makes use of the neutralizer model of Berkner, Pyle, and Stearns, which involves a balance of eleven components in the neutralizer. OMA also replies on an extrapolation of the Balmer-α emission cross section

from measured values in the 10-35 keV range, to a value corresponding to 120 keV. By contrast, NMA, because it responds to both ions and neutrals, requires only a calculation based on reaction kinetics and a knowledge of the reaction cross sections, data for which are available throughout the energy range of interest.

Similar to OMA, NMA provides 2 estimates of the species ratios. In the latter case, one estimate is provided by the proton data, and another by the triton data. In principle, the helium-3 peaks could provide still another estimate; howver, the helium-3 ions have relatively low energy and their intensity is comparable to the noise signal on which they are superimposed. The D^+ fraction obtained from proton data is always about 6% less than that obtained from triton data, and the latter usually overlaps the lower of the 2 D^+ fractions obtained from OMA. The source of the discrepancy in the NMA estimates may lie in the fact that the smallest peak is less well resolved in the case of the protons than for the tritons. This is illustrated quantitatively in Table 3, which applies to the data shown in Figs. 2-4.

Burrell[4] has discussed a phenomenon which could constitute a source of the OMA-NMA discrepancy, namely, charge exchange which occurs in the acceleration region, i.e. pre-neutralization. Such an effect would provide a continuum which could be taken into account in the analysis of both OMA and NMA data, but, in practice, is not. In the model proposed by Burrell to account for this effect, the OMA predictions are inappreciably changed by this effect (at 80 keV), but the correction would tend to lower the molecular-ion component by 10-15%, as predicted by the usual NMA analysis. Thus, when the continuum is ignored, Burrell predicts that there should be a discrepancy between OMA and NMA, and in the direction in which it is actually observed.

Finally, one may ask for a best estimate of the species from the existing on-line methods of measurement. The importance of the pre-neutralization effect is not known but it tends to raise the atomic-fraction estimate as predicted by NMA. Agreement between OMA and mass spectroscopy seems to favor the lower-atomic-fraction estimate provided by OMA. The higher atomic-fraction prediction obtained from NMA and the lower obtained from OMA are in good agreement, and, we believe, represent the best estimate of the species ratios.

Table 1

Species Fractions for the Data of Figures 2-4

Method	D^+	D_2^+	D_3^+
OMA Parallel	0.78	0.17	0.05
OMA Perpendicular	0.72	0.22	0.06
NMA Protons	0.70	0.21	0.09
NMA Tritons	0.76	0.19	0.05

Table 2

Average D^+ Fractions and Relative RMS Deviations

Method	D^+ Fraction	RMS Diviation
OMA Parallel	0.785	1.5%
OMA Perpendicular	0.746	1.8%
NMA Protons	0.701	2.0%
NMA Tritons	0.741	1.6%

Table 3

Peak Characteristics for the data of Figures 2-4

Nucleon	D^+ Ch	D_2^+ Ch.	D_3^+ Ch.	Width	$(D_2^+-D^+)/W$	$(D_3^+-D_2^+)/W$
Protons	899.3	917.4	926.7	4.893	3.70	1.90
Tritons	224.1	251.3	263.4	4.707	5.78	2.57

Figure Captions

1. Detector chamber is a "tree. Top flange contains a pumpout valve and a retractable alpha-particle source.
2. NMA Spectrum at 120 kV.
3. NMA Proton Peaks and Computer Fit.
4. NMA Triton Peaks and Computer Fit.

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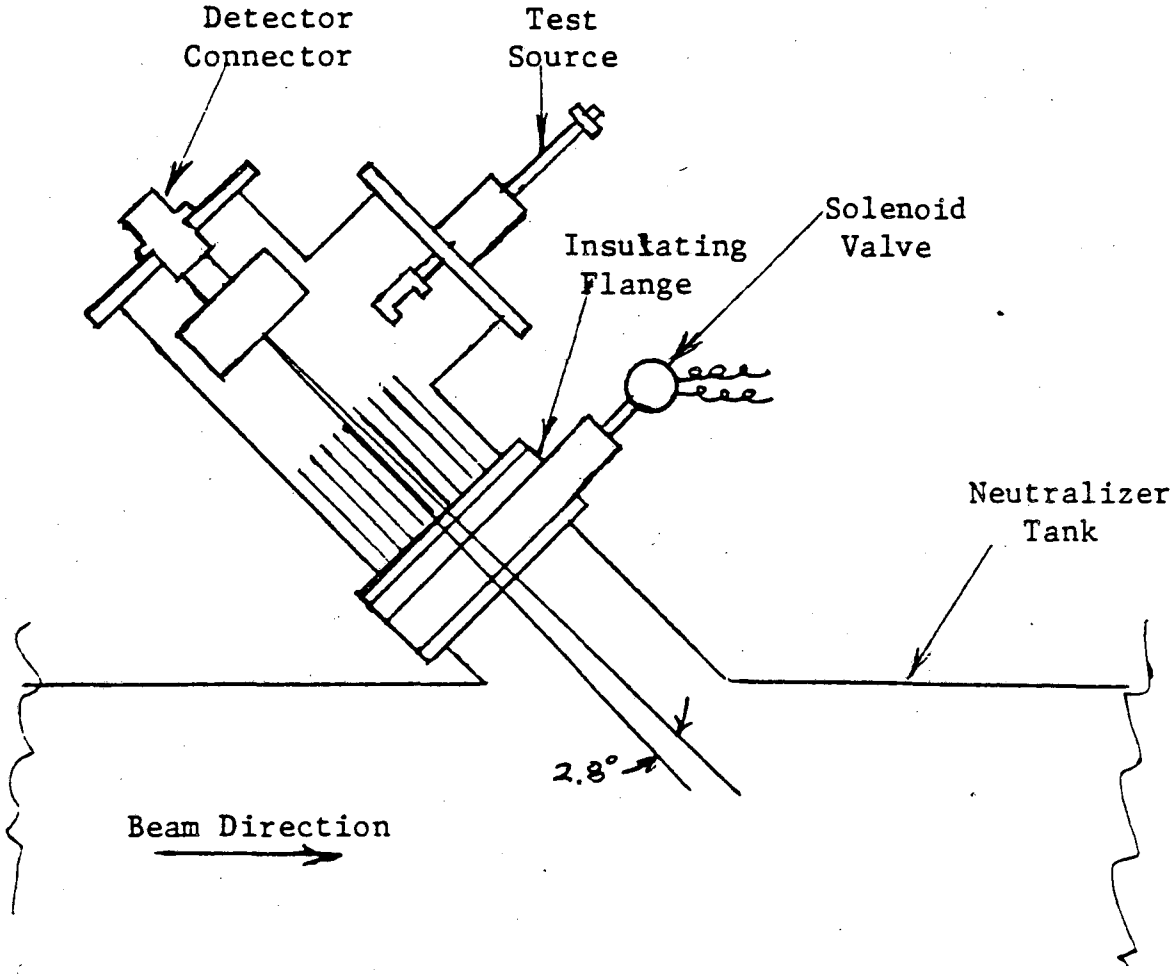

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Fig. 1

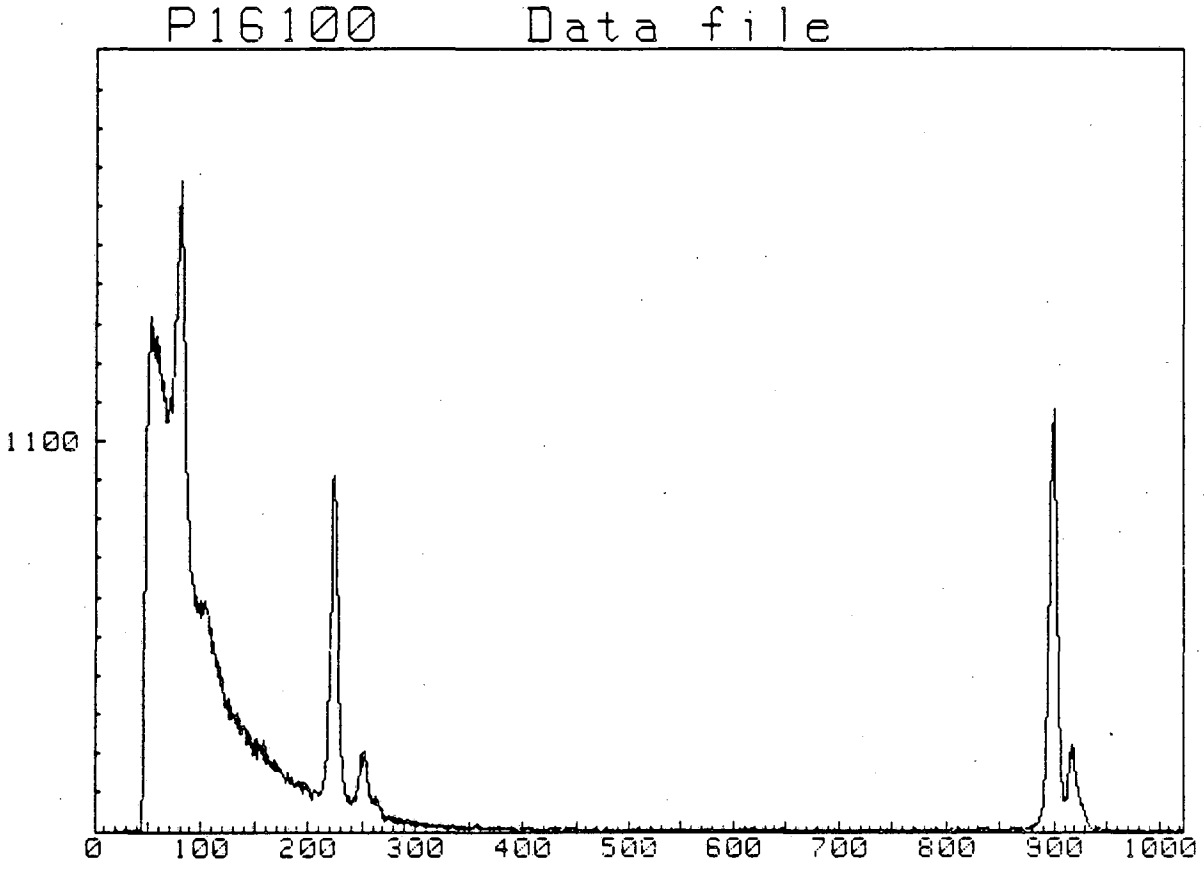

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Fig. 2

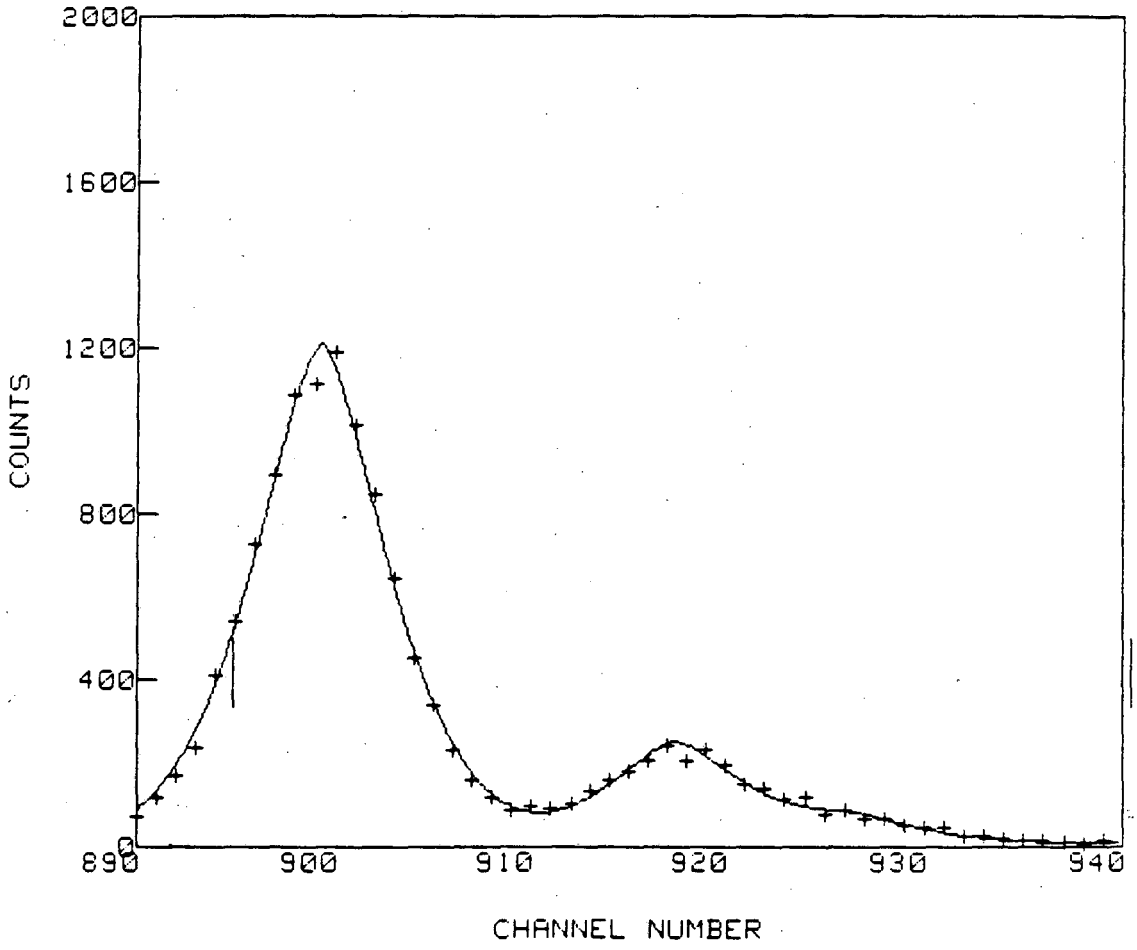

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Fig. 3

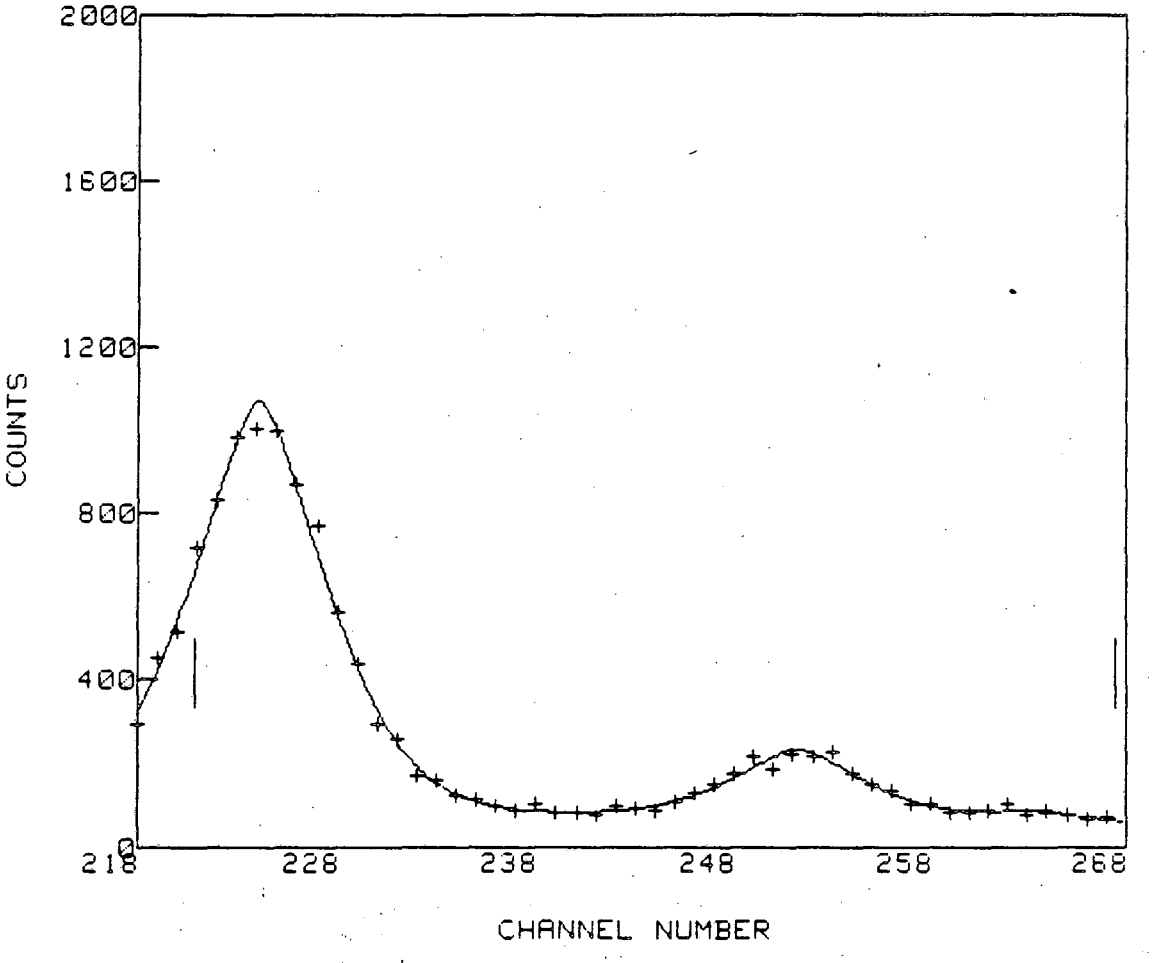

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Fig. 4

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