

# Pulse shape analysis for $\gamma$ -ray tracking applying a genetic algorithm

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Gamma-ray tracking arrays such as MARS [1] and GRETA [2] use the energy and the three-dimensional positions of the interaction points to determine the  $\gamma$ -ray scattering sequence of Compton and pair-production processes. The energy and position information can be obtained by an analysis of the signals from segmented HPGe detectors [3].

One of the new approaches for this task, which is based on the application of a genetic algorithm (GA), was tested with measured pulse shapes from the GRETA prototype detector. It was irradiated with a  $^{137}\text{Cs}$  source ( $E_\gamma = 662$  keV) using a coincidence setup which selected events with single interactions at a certain position [3, 4]. Pulse shapes have been measured (at 500 MSamples/s, 8 bit) for 35 positions within segment B4 and 55 positions within the segments B1/B2. The spacing between the positions was 3-4 mm. Since there is no complete parameterization known, we had to adjust the parameters of the drift velocities of the charge carriers in order to match our calculations to the measured signals. The good agreement enabled us to analyze the measured data with the GA using a calculated base system with a higher position resolution (we used a 1.5 mm grid) than the measured base system [3]. For the averaged signals (1 mm collimator), the positions of the interactions could be reconstructed within a positional error of 1.6 mm (B4) and 2.8 mm (B1/B2). This indicates that an accurate calculation of signals for interactions within the front part is more difficult to parameterize. Analyzing the individual noisy signals, the positional error worsens to 2.0 mm and 2.9 mm (2 mm collimator, only one

position [3]) both within segment B4.

In addition, “artificial” double interaction signals were generated by randomly choosing two positions and energies from the measured signals and adding them. Fig. 1 shows the results of the analysis considering two interactions within the same segment or within two neighboring segments (B1/B2).

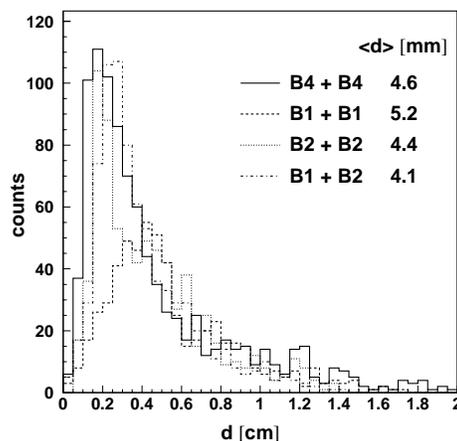


Figure 1: Positional error for “artificial” double interactions

These preliminary results demonstrate that for double interactions a position error of  $\sim 4$ -5 mm can be achieved at this time. The average error of the reconstructed energies (both interactions within the same segment) is around 30%, this clearly has to be improved.

## References

- [1] D. Bazzacco et al., LNL Annual Report 2000.
- [2] M.A. Deleplanque et al., NIMA 430, 292 (1999).
- [3] Th. Kröll et al., LNL Annual Report 1999.
- [4] K. Vetter et al., NIM A 452, 105 and 223 (2000).