ALIGNMENT PROCEDURE FOR THE HYCAL DETECTOR

PRIMEX NOTE 33

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0.1 Objectives

This note describes the procedure for finding the "true" center of the HYCAL detector using the dedicated Compton data acquired during the Fall 2004 run. The center point of the detector as seen by the photon beam is shifted from its nominal value of $(x_0, y_0) = 0, 0$ due to the shift and rotation of the incoming photon beam. We exploit the coplanarity of Compton kinematics in order to find the shifted center as seen by the beam. The resulting (x_0, y_0) values need to be subtracted from the (x, y) coordinates of the reconstructed clusters.

0.2 Procedure

The Compton events were selected using a number of kinematic and geometric cuts. The cuts used in this procedure are likely to be more stringent than necessary, as we are more interested in having a "clean" sample of Compton events than the statistics. The pairs of clusters were selected based on the timing coincidences between the tagger and the clusters. The following cuts were applied to the selected pairs:

1. The central opening of the HYCAL was cut out.
2. The detector modules nearest to the opening were not used.
3. The area mostly affected by pair-production contamination was cut out: $(\phi_1 - 90)^2 + (\phi_2 + 90)^2 > 900$ and $(\phi_1 + 90)^2 + (\phi_2 - 90)^2 > 900)$

4. Only the lead crystal part of the detector was used, excluding the transtion region between the crystal and the glass sections.

5. The separation between two clusters was required to be larger than 18 cm, corresponding to the minimum opening angle (and separation) of the Compton pair at a given beam energy.

6. We required the minimum energy of the clusters to be larger than 1 GeV.

7. Conservation of energy was required: $abs(((e_1+e_2)/e_{beam}-1.)) < 0.05$

8. Only events with one hit in the veto counters were used.

A "shower depth" correction was applied to the coordinates of the clusters that passed all cuts. This correction takes into account the fact that the reconstructed (x, y) of each cluster were not measured at the surface of the detector, but rather, at some distance inside of the crystal, given by the shower depth of the event. The shower depth, d, is a function of energy, and has the following emprical form for the crystal part of the detector: $d = z_0 * log(1 + e/e_0)$, where e is the cluster energy, and $e_0 = 1.1e - 3$, and $z_0 = 0.86$. This correction was applied to x and y of each cluster, so that the new corrected coordinates were: $x \rightarrow x - d$ and $y \rightarrow y - d$. Knowledge of the coordinates of two clusters and Compton kinematics allows to reconstruct the energy of the initial photon, E_c:

$$E_c = \frac{m_e sin(\theta_\gamma}{2sin^2(\theta_{\gamma 2}/2)tan(\theta_e)} - m_e, \tag{1}$$

where θ_γ and θ_e are the polar scattering angles of the Compton photon and electron respectively: $\theta_\gamma = atan(\sqrt{x_\gamma^2 + y_\gamma^2}/z)$ and $\theta_e = atan(\sqrt{x_e^2 + y_e^2}/z)$, and z is the distance from the target to the surface of the detector.

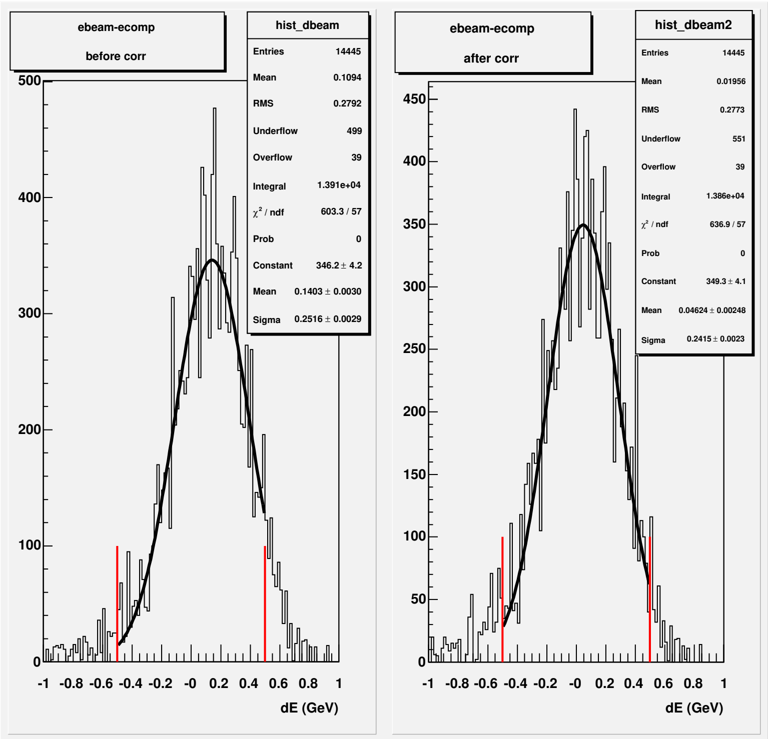

Figure 1: $E_{beam} - E_c$ (GeV) before and after the shower depth correction. All particles within $|E_{beam} - E_c| < 0.5$ are accepted into the "Compton sample".

In order to use this formula, we need to know, in principle, which cluster corresponds to the photon, and which cluster corresponds to the electron, however, at the beam energy of 5 GeV, the electron and photon are kinematically indistinguishable. We assume here that the more energetic first cluster is the electron, even though, swapping the two particles doesnt change out results in this procedure. After the expected Compton energy E_c is calculated, we form the difference between that quantity and the beam energy, as shown in Figure 1. All particles within $|E_{beam} - E_c| < 0.5$ are accepted into the "Compton sample".

The "clean" sample of Compton events is used next to find the "center" of HYCAL. We know that due to the coplanarity of Compton kinematics, the lines connecting pairs of Compton events will cross in the center of the detector, assuming perfect beam and detector alignment. Figure 2 shows some of such crossing lines. Since the beam and the detector are not per-

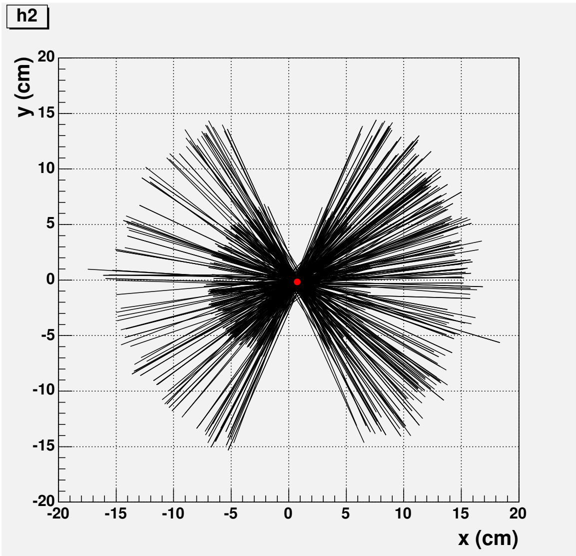

Figure 2: Lines connecting Compton pairs on the surface of HYCAL.

fectly aligned with respect to each other, the crossing points do not coincide exactly. We assume that the point closest to the "true" crossing point is the point of closest approach to each of the lines. The distance, D, between a line (defined by two points (x_1, y_1) and (x_2, y_2)), and a point (x_0, y_0) is given by the following equation:

$$D = \frac{|(x_2 - x_1)(y_1 - y_0) - (x_1 - x_0)(y_2 - y_1)|}{\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2)}} \tag{2}$$

We minimize the sum of squares of the expression for D for all Compton pairs, and solve the pair of linear equations for (x_0, y_0):

$$\frac{\partial}{\partial x_0}[\sum_{i=1}^{i=N} D_i^2] = 0 \qquad \frac{\partial}{\partial y_0}[\sum_{i=1}^{i=N} D_i^2] = 0 \tag{3}$$

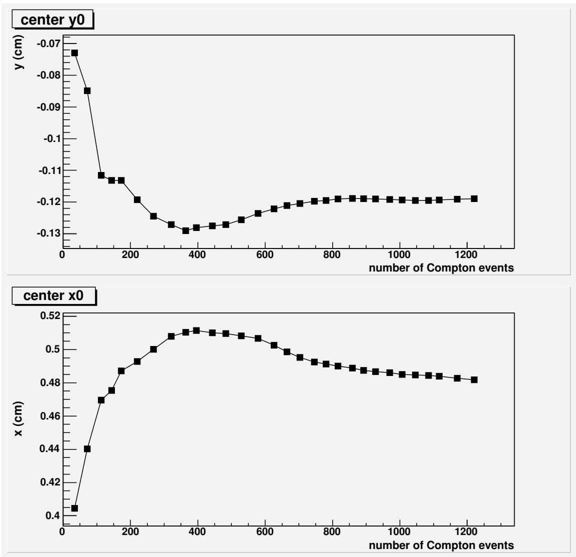

Figure 3: (x_0, y_0) vs N

The minimization procedure is performed over a number of Compton pairs, N, in increments of N. We observe a convergence of (x_0, y_0) as N increases. This is shown in Figure 3.

0.3 Results

The results of this procedure are shown in Figure 4, where we plot the values of (x_0, y_0) vs the run number.

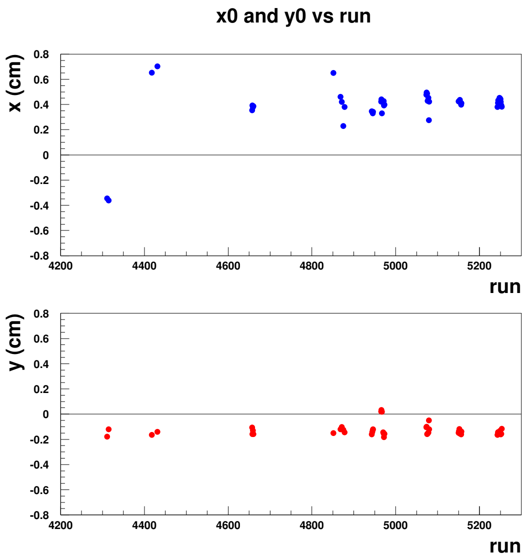

Figure 4: (x_0, y_0) vs N

The average values for the three run groups are shown in Table 1. These values are loaded into the PRIMEX calibration database, system=crystal attribute=alignment, in the format: $x_0\ y_0\ z\ \theta_x\ \theta_y\ \phi\ dt$, where the last 4 items are currently zeros. In order to take the alignment correction into account, the offsets

Table 1: Alignment results for crystals

run range	z (cm)	x_0 (cm)	y_0 (cm)
4293-4345	715.89	-0.35 $\pm$ 0.007	-0.15 $\pm$ 0.03
4346-4535	715.89	0.68 $\pm$ 0.03	-0.15 $\pm$ 0.03
4536-5330	723.51	0.41 $\pm$ 0.06	-0.13 $\pm$ 0.05

need to be subtracted from the reconstructed HYCAL coordinates: $(x, y) \rightarrow (x - x_0, y - y_0)$. The effect of the alignment correction is shown in Figure 5.

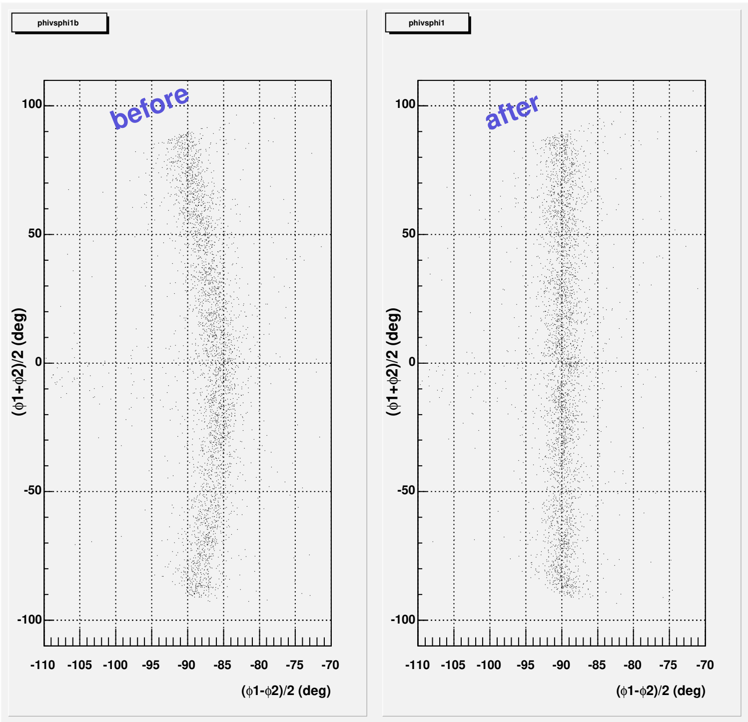

Figure 5: ϕ_1 vs ϕ_2 plot before and after the alignment procedure.