5 Event selection and reconstruction

The reconstruction of an event proceeds in two main steps. First, the energies of the photon in the incoming beam are calculated from the momentum loss of the electron. Secondly, the trajectories and energies of the photons and proton produced by the reaction are calculated from the hits found in the two calorimeters. Although the properties of TAPS and the Crystal Barrel are different, the reconstruction is similar for both calorimeters.

5.1 Tagger reconstruction

5.1.1 Clustering

To reconstruct the incoming photon energy, we first have to determine which fibers were hit. A fiber is hit whenever its TDC’s has recorded a value, and since the TDC’s can record multiple hits, one fiber can be hit multiple times in one event. Secondly, the fiber hits in the tagger need to be clustered. This entails finding the largest continuous group of fibers that recorded a hit. If one fiber is missing in between two fibers which were hit, the two fibers are still considered to be part of the same cluster. Because a fiber can have more than one hit, one fiber can be assigned to multiple clusters in the same event.
The hits in the fibers forming a single cluster must be coincident in time. The time window used for this cut ranges from -5 ns to 5 ns and is depicted in figure 5.1. Fibers that fall outside of this timing window are used to form a separate cluster. The typical cluster consists of one or two fibers.

To calculate the energy value of a cluster, its central fiber is calculated by averaging over the fiber numbers of the cluster members. This average fiber number is inserted in the polynomial that relates the fiber number to the photon energy. This polynomial was obtained in the calibration phase (see section 4.3.2).

5.2 TAPS reconstruction

The TAPS reconstruction software used in this experiment was based on the RoseBud package [56], but was completely rewritten to meet the specific requirements of the CBELSA / TAPS experiments. Detailed documentation has been written using Doxygen [57] and is available with the software package.
5.2.1 Clustering

For the reconstruction of the hits recorded by TAPS the first step is the application of a cluster-finding algorithm. A cluster in TAPS is defined as the largest possible group of adjacent \( \text{BaF}_2 \) crystals in which an energy higher than the CFD threshold was deposited. The crystal in the cluster that recorded the highest energy deposit is referred to as the central crystal.

Secondly, the software discards all crystals with an energy deposit of less than 10 MeV. As it is somewhat higher than the average CFD threshold, this cut serves to reduce the spread in the individual CFD thresholds. Some CFD thresholds are set higher than 10 MeV, but Monte Carlo simulations show that the resolution would start to suffer at higher cuts.

Thirdly, clusters with a total energy deposit of less than 25 MeV are discarded in order to reduce split-offs. Split-offs are energy deposits caused by a part of an electromagnetic shower which has split off from the main cluster. If the energy deposited in an intermediate detector is too low to be detected, such a split-off may form a small and low energy cluster close to, but separate from the main cluster.

In addition to the above requirements which are placed on a cluster, all detector modules making up a cluster are required to be coincident. The relative time difference between the central detector and the other members of the same cluster is shown in figure 5.2. Whenever this time difference is larger than 5 ns, that particular crystal is discarded.

The chance of overlapping clusters to occur in an event has been studied using a Monte Carlo methods, and is 6%.

5.2.2 Position reconstruction

The position of all particles in TAPS is reconstructed by a weighted sum of the position \( \langle x_i \rangle \) of the individual \( \text{BaF}_2 \) modules that make up the cluster. The position \( \overrightarrow{X} \) is given by:

\[
\overrightarrow{X} = \frac{\sum_i w_i \overrightarrow{x_i}}{\sum_i w_i}
\]  

(5.1)

The weights \( w_i \) are based on the energy \( E_i \) deposited in the crystal:

\[
w_i = \text{MAX} \left\{ 0, \left[ W_0 + \ln \frac{E_i}{\sum_j E_j} \right] \right\}
\]  

(5.2)
The value of the constant $W_0 = 4$ is found from GEANT simulations. This logarithmic weighting is described in [58] and has a higher linearity for high energy photons than a simple weighting procedure. This simple reconstruction assumes the shower starts at the front face of the TAPS detector, neglecting the distance the photons penetrate into the detector before an electromagnetic shower is formed. Figure 5.3 illustrates that this assumption causes errors in the position reconstruction, since the shower is reconstructed systematically too far towards the outside of the detector. If the distances $X, Y, Z$, and $R$ are defined as is shown in figure 5.3, the following geometric relation holds:

$$X^4 - 2YX^3 + (Y^2 + R^2 - Z^2)X^2 - 2R^2YX + R^2Y^2 = 0 \quad (5.3)$$

Of the 4 variables $Y$ and $R$ are known, and the average $Z$ as function of energy can be calculated via [59]:

$$Z = X_0 \left( \ln \left( \frac{E}{E_c} \right) + 1.2 \right) \quad (5.4)$$

where $X_0$ is the electromagnetic radiation length (2.05 cm) and $E_c$ is the critical energy (12.78 MeV) for the crystal. This leaves $X$ as the only remaining unknown, and the equation can be solved numerically for $X$. 

Figure 5.2: The time difference between individual crystals within the same TAPS cluster. The gray area shows the cut that was used to select the crystals that belong to the same cluster. Crystals outside this window are discarded.
Figure 5.3: Schematic overview of the error caused by photons entering TAPS under an angle and forming a shower after entering a distance $Z$ into the detector. This causes the distance between the entry point and the beam axis to appear as $Y$, where the true distance is $X$. The reconstruction routines correct for this effect by approximating $Z$ using the energy of the photon.

This new value of $X$ is then used to recalculate the angles of the particle. The final polar angular resolution for photons obtained in this way is 0.022 rad.

### 5.2.3 Time and PSA selection

The time measured by the central detector of a cluster is taken as the time at which the particle was detected. A problem occurs because 10% of all detectors have an unuseable time signal. In these cases the time spectrum shows a broad distribution instead of a sharp peak, which is caused by electronic problems.

Whenever the central detector of a cluster suffers from such problems, the time at which the particle was detected is ill defined. In that case the other crystals of the cluster are inspected, in order of the energy deposited in them, until one is found with a good timing signal.

The PSA value used to identify the particle is defined in the same way as the time value. Due to the same electronic problems, roughly 10% of all detectors did not have a well defined pulse-shape value. It was therefore necessary to look at the PSA value of other crystals in the cluster whenever the PSA value from the central detector was unreliable. For this the same procedure was used as in the definition of the time values.
5.3 Crystal Barrel reconstruction

5.3.1 Clustering

The procedure for clustering the hits found in the Crystal Barrel follows the same procedure as was described for TAPS, but with an additional step. In order to deal with the lower granularity of the detector, a method to separate two overlapping clusters is introduced. This is done by searching for local maxima in the deposited energy across the cluster.

5.3.2 Local maxima and energy constraints

Whenever multiple local maxima are found within a cluster, that cluster is split and the energy in the cluster is divided over the different subclusters, called Particle Energy Deposits or PED’s. This situation is illustrated in figure 5.4. The energy deposited if the crystals which form the local maxima (A and B in the picture) is completely assigned to the PED belonging to that local maximum. The energy deposited in the crystals that only have one of the local maxima as a direct neighbor (C, D, and E in the picture), is also added to the PED which corresponds to that local maximum.

The energy deposited in crystals that have multiple local maxima as neighbors (F, G and H) has to be divided between the different PED’s. The ratio is given by the two sums of the deposited energies over the nine crystals forming the local maximum and its eight immediate neighbors. Finally, for reasons of simplicity, the energy deposited in crystals that have none of the local maxima as a neighbor (I and J) are divided over the different PED’s in such a way that the fraction of the cluster energy that is carried by each PED does not change anymore.

As was done in the TAPS reconstruction, energy thresholds are applied in software to individual crystals (well above the hardware thresholds) as well as complete clusters and PED’s. The energy deposited in a single crystal must be higher than 13 MeV for the crystal to be added to a cluster. Clusters and PED with a total energy below 20 MeV are discarded. The position reconstruction for each PED is completely the same as in the case of TAPS, using the logarithmic weighting procedure that is outlined in section 5.2.2, but with the minimum $W_0$ set to 4.25 MeV instead of 4.0 MeV.
5.4 Event selection

The selection of events is the following step in the analysis. Because the reaction channel of interest has 6 photons and a proton in the final state it is possible to reduce the amount of data significantly by a cut on the cluster multiplicity of an event. For this work only those events containing exactly 7 clusters have been selected. This means the proton in the exit channel must be detected for this analysis. From Monte Carlo calculations, 7.4% of events have a multiplicity higher than 7.

5.5 Results of a first approach to reconstruct the reaction

After selecting the events with a cluster multiplicity of seven, a standard analysis involving cuts on the total energy and momentum of the event, and the three $\pi^0$ masses was conducted. In this way events with a proton and 3$\pi^0$s in the final state were selected. Afterward, the $\pi^0p$ invariant-mass spectrum is calculated and a cut is placed in this spectrum around the $\Sigma^+$ mass (shown in figure 5.5 (right)). The $\pi^0\pi^0$ invariant-mass spectrum for the remaining events is shown in figure 5.5 (left).

In this figure, an estimation of the background is indicated which is obtained by applying cuts in the $\pi^0p$ invariant-mass distribution to the left and the right of the $\Sigma^+$ mass window. The two $\pi^0\pi^0$ invariant-mass spectra obtained in this way do not contain any contributions from $K^0$ mesons, be-
5.6 Kinematic fit

It is immediately clear that, in order to get a more reliable measurement, the resolution of the $\pi^0\pi^0$ invariant-mass must be improved considerably in order to get a much better signal to noise ratio and a better estimate of the background. Therefore the next step has to be applied: the kinematic fit.

The following is a short explanation of the procedure based on [60].

5.6.1 Description of the kinematic fit

The kinematic fit is a least-squares fit with constraints, performed on an event by event basis. The values used in the fit are the measured parameters of the reaction such as the total momentum and angles of the particle trajectories. The constraints are formed by the conservation of momentum and energy and the masses of the intermediate particles. In addition
a number of parameters may have remained unmeasured and must be calculated from the measured parameters using some of the constraints. If \( n \) values were measured and \( r \) parameters have to be calculated, they can be written as an \( n \)-dimensional vector \( \eta_0 \) containing the measured parameters, and an \( r \) dimensional vector \( x_0 \) containing the calculated parameters. The measured parameters contain measurement errors so that not all constraints are exactly fulfilled. The kinematic fit tries to find new vectors \( \eta \) and \( x \) that fulfill the constraints exactly by varying the values of the measured parameters. How much a measured parameter is allowed to vary depends on the measurement error.

The difference between the measured set of parameters \( \eta_0, x_0 \) and the set of parameters \( \eta, x \) which will be determined by the kinematic fit is written as:

\[
\eta = \eta_0 - \delta \quad \text{(5.5)}
\]

\[
x = x_0 - \xi \quad \text{(5.6)}
\]

The calculated parameters and the measured parameters are related to each other via \( m \) constraints, given by conservation of energy and momentum for instance, which can be written as a system of \( m \) equations:

\[
f_{1..m}(x, \eta) = 0 \quad \text{(5.7)}
\]

This set of constraints is called the hypothesis of the fit. Because the constraints might not be linear, we approximate them by a linear function, by making an expansion around the initial values \( \eta_0, x_0 \) as follows:

\[
f(x, \eta) = f(x_0, \eta_0) + \sum_{i=1}^{n} \left( \frac{\partial f}{\partial \eta_i} \right)_{x_0, \eta_0} (\eta_i - \eta_{0,i}) + \sum_{j=1}^{m} \left( \frac{\partial f}{\partial x_j} \right)_{x_0, \eta_0} (x_j - x_{0,j}) \quad \text{(5.8)}
\]

As there are \( m \) such constraints, the above equation is more conveniently written in matrix form, using equation 5.6 and 5.5:

\[
A \xi + B \delta + c = 0 \quad \text{(5.9)}
\]

In this equation \( B \) is a \( n \) by \( m \) matrix containing the partial derivatives for all constraints with respect to each measured variable. \( A \) is an \( r \) by \( m \) matrix containing the partial derivatives of the constraints to all the
calculated variables. The vector $c$ is a column vector with $m$ elements containing the values of $f(x_0, \eta_0)$:

$$a_{kl} = \left( \frac{\partial f_k}{\partial x_l} \right)_{x_0, \eta_0} \quad (5.10)$$

$$b_{kl} = \left( \frac{\partial f_k}{\partial \eta_l} \right)_{x_0, \eta_0}$$

$$c_k = f(x_0, \eta_0)$$

The task is now to perform a least-squares minimization, e.g., to minimize:

$$\delta^T G_y \delta = \delta_1 G_y \delta_1 + \cdots \quad (5.11)$$

where $G_y$ is the weight matrix of the measurement, defined as the inverse of the covariance matrix. In addition, the constraints from equation 5.9 have to be fulfilled. This minimization under constraints is done using the method of Lagrange multipliers. From the minimum function and the constraints, a Lagrange function can be constructed as follows:

$$L = \delta^T G_y \delta + 2 \mu^T (A \xi + B \delta + c) \quad (5.12)$$

where $\mu$ is the vector of Lagrange multipliers. The minimum occurs at the point where the derivatives of $L$ with respect to $\xi$ and $\delta$ vanish. Together with equation 5.9, this gives the following three equations:

$$G_y \delta + B^T \mu = 0 \quad (5.13)$$

$$2 \mu^T A = 0$$

$$A \xi + B \delta + c = 0$$

This system can be solved, giving the solutions:

$$\xi = - (A^T G_B A)^{-1} A^T G_B c$$

$$\delta = - G_y^{-1} B^T G_B (c - A (A^T G_B A)^{-1} A^T G_B c)$$

with

$$G_B = (B G_y^{-1} B^T)^{-1} \quad (5.15)$$

The new estimates for $x$ and $\eta$ follow via equations 5.5 and 5.6. If the constraint equations 5.8 are linear, the expansion in equation 5.8 is exact, and these solutions already give the final result. If they are not linear, we can use the estimates obtained in this way as input for the next iteration, i.e., we equate them with $x_0$ and $\eta_0$. From these results it is possible to calculate a new covariance matrix so that a complete set of new input parameters can be constructed and the procedure can restart from the beginning. This cycle continues until the results have converged, in 4-8 iterations.
5.6.2 The hypothesis

To perform the fit we need to establish the hypothesis we will use, i.e., the contents of the matrix $A$. In this case four constraints on the energy and momentum balances have been used:

$$
E_{\text{tag}} - E_{\text{prot}} - \sum_{i=0}^{6} E_{\gamma_i} = 0 \quad (5.16)
$$

$$
P_{z,\text{tag}} - P_{z,\text{prot}} - \sum_{i=0}^{6} P_{z,\gamma_i} = 0
$$

$$
P_{y,\text{tag}} - P_{y,\text{prot}} - \sum_{i=0}^{6} P_{y,\gamma_i} = 0
$$

$$
P_{x,\text{tag}} - P_{x,\text{prot}} - \sum_{i=0}^{6} P_{x,\gamma_i} = 0
$$

The first term in these equations describe the incoming photon, the second described the outgoing proton, and the sum runs over the six outgoing photons. In addition the invariant masses of the three $\pi^0$’s are used as constraints:

$$
E_{\gamma_1}^2 - p_{x,\gamma_1}^2 - p_{y,\gamma_1}^2 - p_{z,\gamma_1}^2 + E_{\gamma_2}^2 - p_{x,\gamma_2}^2 - p_{y,\gamma_2}^2 - p_{z,\gamma_2}^2 = M_{\pi^0}^2 \quad (5.17)
$$

$$
E_{\gamma_1}^2 - p_{x,\gamma_1}^2 - p_{y,\gamma_1}^2 - p_{z,\gamma_1}^2 + E_{\gamma_3}^2 - p_{x,\gamma_3}^2 - p_{y,\gamma_3}^2 - p_{z,\gamma_3}^2 = M_{\pi^0}^2
$$

$$
E_{\gamma_1}^2 - p_{x,\gamma_1}^2 - p_{y,\gamma_1}^2 - p_{z,\gamma_1}^2 + E_{\gamma_4}^2 - p_{x,\gamma_4}^2 - p_{y,\gamma_4}^2 - p_{z,\gamma_4}^2 = M_{\pi^0}^2
$$

To form the matrix $A$ (see equation 5.8) all the partial derivatives need to be calculated either numerically or analytically. In this work the analytic method was used in order to speed up the calculation. As an example, the derivatives of the constraint on the momentum in the x direction ($p_x(\theta_{\gamma_1}, \phi_{\gamma_1}, E_{\gamma_1})$, the last equation in 5.16) with the respect to $\theta_{\gamma_1}$, $\phi_{\gamma_1}$ and $\sqrt{E_{\gamma_1}}$ of one of the outgoing photons ($\gamma_1$) are:

$$
\frac{\partial p_x(\theta_{\gamma_1}, \phi_{\gamma_1}, E_{\gamma_1})}{\partial E_{\gamma_1}} = 2 \cdot \sqrt{E_{\gamma_1}} \cos \theta_{\gamma_1} \sin \phi_{\gamma_1} \quad (5.18)
$$

$$
\frac{\partial p_x(\theta_{\gamma_1}, \phi_{\gamma_1}, E_{\gamma_1})}{\partial \theta_{\gamma_1}} = (\sqrt{E_{\gamma_1}})^2 \cos \theta_{\gamma_1} \cos \phi_{\gamma_1}
$$

$$
\frac{\partial p_x(\theta_{\gamma_1}, \phi_{\gamma_1}, E_{\gamma_1})}{\partial \phi_{\gamma_1}} = (\sqrt{E_{\gamma_1}})^2 \sin \theta_{\gamma_1} \sin \phi_{\gamma_1}
$$

(5.19)
5.6.3 The pull distributions

The kinematic fit can provide a handle on systematic errors in the measured values. If no such errors exist, the difference between the measured and the fitted values should form a distribution centered at zero, as the fit will be just as likely to increase a specific value as to decrease it. A systematic error will cause a shift in the distribution to either positive or negative values.

Furthermore, if that distribution is normalized to the error put into the calculation, the result should be a Gaussian distribution with a sigma of 1. A broader distribution indicates the measurement errors were estimated incorrectly. Taking the error remaining on the fitted value into account, such a distribution can be formed in the following way:

\[
P_i = \frac{\eta_i - \eta_f}{\sqrt{\sigma^2_i - \sigma^2_{\eta_f}}} \tag{5.20}
\]

which is called a pull distribution. Here \( \eta_i (\eta_f) \) is an element of the vector of the initial (final) values of the measured parameters, and \( \sigma_i (\sigma_{\eta_f}) \) the error on those initial (final) values, which are both inputs (outputs) to the fit. The \( \sigma \) of the resulting Gaussian distribution contains information about the size of the input errors. If the \( \sigma \) of the distribution is equal to 1, the measurement errors were correctly estimated. If the \( \sigma \) of the pull distribution deviates from 1, the measurement errors were either too large or too small.

If no systematic errors were present in the measurement, the pull distribution should be centered at 0. A deviation of the mean from 0 points to systematic errors in the measurement. A non Gaussian form of the pull distribution indicates the measurement errors were not Gaussian distributed.

5.6.4 Confidence level

The results of the kinematic fit satisfy all constraints per definition, and it is therefore no longer possible to use those constraints to separate the signal from the background using conventional cuts. For instance, after the fit the energy balance of the event will be exactly 0 for events in which all particles have been detected, but also for those events in which a particle has escaped detection. It is therefore not possible to separate both types of events via a cut on that energy balance. It is possible, however, to select events using the \( \chi^2 \) value of the fit, which is defined as:

\[
\chi^2 = (\eta_0 - \eta_f)^T G (\eta_0 - \eta_f) \tag{5.21}
\]
The distribution of $\chi^2$ values of all events is $f(\chi^2)$. If all measurement errors were properly estimated and no systematic errors are present, the above distribution should follow the $\chi^2$ that is obtained by adding quadratically a number of Gaussians of $\mu = 0, \sigma = 1$. The number of Gaussians in the sum is equal to the number of degrees of freedom (ndf) in the problem. Such a standard $\chi^2$ distribution is called a $f_{sd}(\chi^2)$ in the following paragraphs.

Events that do not fulfill the requirements imposed by the constraints will have a distribution which peaks at higher or lower $\chi^2$ values than this standard $\chi^2$ distribution. This is illustrated in figure 5.6 (left).

Usually, for control purposes, one inspects the confidence level, which is related to the $\chi^2$ value defined in equation 5.21 via:

$$CL = 1 - \left( \int_0^{\chi^2} f_{sd}(\chi^2) d\chi^2 \right)$$

(5.22)

From this definition it follows that the confidence level runs from 0 to 1, where a high $\chi^2$ value corresponds to a confidence level close to 0, and a low $\chi^2$ value corresponds to a confidence level close to 1. The relation between the $\chi^2$ distribution and the confidence level distribution can be obtained as follows:

$$\frac{d\chi^2}{dCL} = \frac{1}{f_{sd}(\chi^2)}$$

(5.23)

Thus, the confidence-level distribution can be written as:

$$f(CL) dCL = f(\chi^2) d\chi^2$$

(5.24)

$$f(CL) = f(\chi^2) \frac{d\chi^2}{dCL}$$

$$f(CL) = \frac{f(\chi^2)}{f_{sd}(\chi^2)}$$

where $f(\chi^2)$ is the $\chi^2$ distribution of the fitted events and $f(CL)$ is the confidence-level distribution of the fitted events. Further, $f_{sd}(\chi^2)$ is the standard $\chi^2$ distribution for the appropriate number of degrees of freedom.

If the measured values are distributed according to a Gaussian distribution around the values calculated by the fit, and the measurement errors have been estimated correctly, we have $f(\chi^2) = f_{sd}(\chi^2)$ and the confidence-level distribution will be flat.
Figure 5.6: Left: Three $\chi^2$ distributions for a fit with 6 degrees of freedom. The solid line is a fit were the errors are predicted precisely, the dashed line has errors which are 20% underestimated, and the dotted line has errors which are 20% overestimated. Right: The same three fits, now represented as confidence-level distributions. The fit with the exact errors results in a flat distribution, where the other two are peaked at high or low confidence levels.

This situation is illustrated in figures 5.6. The valid events (those that fit the hypothesis) will be uniformly distributed over all confidence levels (indicated by the dark solid line), whereas background events (those that do not conform to the hypothesis of the fit) will have a low confidence level, and can be rejected by a cut.

This figure also shows the importance of a correct estimation of the measurement errors used to form the initial covariance matrix. If the errors have been underestimated, the valid events will be shifted to low confidence levels (the dotted line in the figure), and the cut on the confidence level will reject more valid events. If the errors are overestimated, all events (including the background events) will get shifted to larger confidence levels (the dashed line in the figure) and the confidence level cut will select more background events.

5.6.5 Input values

The initial values for the fit will be all the measured energies of the outgoing photons are used together with the the polar angles $\theta$ and $\phi$ of their trajectories. For the incoming photon the energy measured by the tagger was used, and as the incoming photon beam lies along the $z$-axis, both angles of its trajectory are 0. For the outgoing proton, only the angles of its trajectory, $\theta$ and $\phi$ are usable. The energy of the proton is left as a free parameter in the fit, because protons with a kinetic energy above 450 MeV will punch through the TAPS detector and exit the detector on the back.
This means not all of its energy will be deposited in the detector, and the energy measured by the detector will be wrong.

In total, using the seven constraints and the proton energy as the only free parameter, this results in a fit which is six times over-constraint. One important fact to note is that neither the $K^0$ nor the $\Sigma^+$ mass is used as a constraint in this fit.

### 5.6.6 Input errors

Aside from the measured values and the constraints, it is necessary to form the initial weight matrix in equation 5.11. Because a more exact measurement should carry a higher weight, the values on the diagonal of this matrix are just the inverses of the measurement resolutions. The other values in the matrix are set to 0. In other words, the assumption is made that the error of a measured parameter depends only on that parameter and not on the other measured parameters. This does not hold exactly for all the measured quantities as will be shown below for the case of the resolution for the $\phi$ angle of a particle detected by TAPS, which is dependent on the $\theta$ angle. Finally, the errors are assumed to be Gaussian. As can be seen from the TAPS line-shape in figure 4.3 (left), this is an approximation as well.

Approximations for the resolutions for the energy and direction of the photons measured in the Crystal Barrel have been taken from earlier analyses [21]. The same holds for the resolutions for the direction of the proton measured in the Crystal Barrel. An estimation of the resolutions for the angles $\theta$ and $\phi$ of the photon and proton trajectories as measured by TAPS has been determined using a Monte Carlo simulation, and it is found that those resolutions can be approximated by:

$$\delta \theta = 0.022 \text{ rad}$$

$$\delta \phi = \frac{2.0}{\tan \theta \cdot R} \text{ rad}$$

where $R = 118$ is the distance from the front plane of TAPS to the target center.

The result is shown in figure 5.7 where the difference in $\theta$ and $\phi$ between thrown and reconstructed hits in TAPS is compared with the approximation of the resolution used in the fit. The figure shows that the resolution for $\theta$ gets slightly larger towards the outside rings of TAPS. This is caused by the fact that TAPS is built up as a flat wall, so that in this region particles enter the detector at an angle instead of perpendicularly. This causes
an error in the reconstruction of the $\theta$ angle, which the position correction (see section 5.2.2) is not able to correct completely.

Furthermore, it can be seen that the resolution for $\phi$ is dependent on $\theta$, which is caused by the geometry of TAPS. Near the beam axis only 12 detectors cover the entire $360^\circ \phi$ angle, while on the edge of TAPS farthest from the beam axis 66 detectors cover the same angle. As stated this dependence makes the diagonal covariance matrix an approximation.

The resolution for the energy measurements of TAPS has been well studied [42] and is described by equation 4.3.

To estimate the resolution on the energy measured by the tagger, the difference in corresponding energy between the center fiber of a cluster and both its neighboring fibers is used. The average of these two differences is used as an estimate for the resolution. The situation is schematically pictured in figure 5.8 (left). The resolution is shown in figure 5.8 (right) as a function of the tagged photon energy and is seen to vary between 20 MeV down to 2 MeV.

Figure 5.7: Left: The resolution for $\phi$, for photons detected in TAPS. The scatter plot shows the distribution $\delta \theta$ of errors as determined from a Monte Carlo simulation. The lines show the estimate $\delta \phi$ used as input to the fit. Right: A similar plot showing the resolution for $\theta$. 
Figure 5.8: Left: Schematic overview of the determination of the error on the tagged photon energy. The difference in energy between the hit fiber and both neighboring fibers are averaged to get an estimate of the error. Right: The input errors ($\sigma$ of the distribution) to the fit for the tagged photon energy in MeV as a function of the tagged photon energy.

5.7 Combinatorics

The six photons produced in the reaction can be combined into $3\pi^0$'s in 15 distinct ways, as follows from the formula:

$$N = \frac{n^!\gamma^!}{2^n n^!\pi^!}$$  \hspace{1cm} (5.26)

where $N$ is the total number of combinations, $n_\gamma$ is the number of photons, and $n_\pi$ is the number of $\pi^0$'s. To select the proton out of the seven measured hits, each event is fitted seven times, with each measured hit acting as proton candidate once. The combination yielding the highest confidence level then is selected. It has been verified, by checking the pulse-shape, time of flight, and charged-particle vetoes for the hits identified as proton, that no significant improvement could be made by using these additional methods to identify the proton. This is shown in figure 5.9 where the time of flight of the particles identified as protons is plotted against the deposited energy. The proton band is clearly visible, while the photon band (which should be at 0 ns) is absent.

If the tagger measured more than one hit in the same event, the similar procedure is followed to select the correct hit. For each hit found in the tagger (although usually only one hit is found), there are $7 \cdot 15 = 105$ (the number of proton candidates multiplied by the number of ways to combine the six photons into $3\pi^0$'s) combinations to test.
As explained in section 5.6, the fitting of each combination is an iterative procedure, therefore a lot of computer power is needed to complete these calculations.

To reduce the required time to complete the fitting of the whole data set, some cuts are applied beforehand. First, a coincidence between the tagger and TAPS is required. For this it is necessary that the particle in TAPS used for the coincidence is a photon, as protons need more time to reach the TAPS detector and might therefore fall outside of the cut. Therefore only those combinations that have at least one photon detected by TAPS are selected. The cut on coincidence between the tagger and TAPS was made between -6 ns and 6 ns, or 6σ and therefore has a negligible effect.

The additional requirement that at least one photon needs to be detected in TAPS, which is introduced here, is taken into account when calculating the acceptance. More details can be found in section 6.3.

To further reduce the number of combinations that need to be fitted, only those combinations are considered where the measured two-photon invariant masses of the three π^0's are within reasonable limits of the known π^0 mass of 134.98 MeV. The limits to accept the event are rather wide, 90 MeV - 170 MeV, compared to the two-photon invariant mass resolution of TAPS. This avoids problems caused by any broadening or shift of the π^0 mass that might occur due to the lifetime of the K^0 and the Σ^+. This effect is treated in detail in section 6.4.3.
5.8 RuG Linux cluster

Even after selecting the data according to the requirements described, the time needed to complete the fit for the entire data set is roughly one CPU year. As this is not feasible to do on a desktop machine, all fitting has been done on the Beowulf Linux cluster at the Rekencentrum of the Rijksuniversiteit Groningen. It consists of 96 single and 16 double CPU machines, connected via a 100 Mb/s network. The CPU’s used run at 1.7 GHz and the cluster as a whole can reach 0.22 Tllops/s. Because the CBELSA / TAPS reconstruction software has not been developed specifically for cluster computations, the cluster has been used in a simple manner. Each node of the cluster was used as a stand alone computer that was unaware of the other nodes. The only cluster specific feature used was the job queuing system that distributes jobs over the individual nodes. Operating in this way a node can reconstruct roughly 100 compressed data files, corresponding to 12 hours of measurement time, in 24 hours. About ten percent of the total processing time was used to transfer the data and the results to and from the node. As the cluster has to be shared with other researchers, it was feasible to run 10 jobs per day on average, bringing the total processing time of the data to roughly one month. Therefore the kinematic fit was optimized on a subset of data before the total data set was fitted.

5.9 Kinematic fit results

The $\pi^0\pi^0$ invariant-mass spectrum that results after the kinematic fit is shown in figure 5.10 and should be compared to figure 5.5 (left). After the kinematic fit the peak is clearly separable from the background, and its width ($\sigma$) has been reduced from 30 MeV to 10 MeV. A similar improvement is observed for the $\eta \rightarrow 3\pi^0$ channel where the width of the $\pi^0\pi^0\pi^0$ invariant-mass peak was reduced from 21 MeV before to 8 MeV after the kinematic fit. In section 5.10 it will be shown the kinematic fit has not changed the peak intensity.

5.9.1 Confidence level

In figure 5.11 the confidence level for all events is shown. To select correct events, a cut is placed on this spectrum at 0.10, discarding all events with lower confidence levels. The steeply rising part of the confidence-level dis-
Figure 5.10: The $\pi^0\pi^0$ invariant-mass spectrum after the kinematic fit. The resolution of the $K^0$ invariant-mass peak has improved from roughly 30 MeV (see figure 5.5 (left)) to 10 MeV (sigma).

tribution, which corresponds to the background events, will therefore be rejected, while the good events, which are distributed evenly over all confidence levels are kept in the sample. Although most of the background events are contained in the peak at low confidence levels, it can be seen from the figure, that some of the background is still above the 10% cut.

5.9.2 Pull distributions

In figure 5.12 the pull distributions of the $3\pi^0$-fit are shown, together with a Gaussian fit. To obtain these results the confidence-level cut of 10% has been applied. The pull values for the six photons in each event have been added together in one histogram. The values of the mean and sigma of the Gaussians of the pull distributions have been collected in table 5.1. The measured proton energy is not used as an input value to the fit, but instead is calculated from the other measured values. Therefore it has no pull distribution.

From the distributions it can be seen that the pull distributions of the energies of the photons are slightly non Gaussian and exhibit a shift to higher values. This is caused by the low energy tail (which can be seen in figure 4.3 (left)) of the energy response of the $\text{BaF}_2$ and $\text{CsI}$ crystals used by TAPS and the Crystal Barrel, respectively. The energy of the incom-
Figure 5.11: The confidence-level distribution of the $3\pi^0$ kinematic fit. A cut is placed at 0.10 to select correct events.

Figure 5.12: The pull distributions (black solid line) for the $3\pi^0$ kinematic fit. The dashed gray line is the result of a Gaussian fit with $\sigma = 0$. 
CHAPTER 5. EVENT SELECTION AND RECONSTRUCTION

<table>
<thead>
<tr>
<th>Type</th>
<th>$\theta$</th>
<th>$\sqrt{E}$</th>
<th>$\phi$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Photon</td>
<td>0.93</td>
<td>0.043</td>
<td>-0.09</td>
</tr>
<tr>
<td>Proton</td>
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<td>0.205</td>
<td>-0.02</td>
</tr>
<tr>
<td>Tagger</td>
<td>1.01</td>
<td>-0.087</td>
<td>-0.12</td>
</tr>
</tbody>
</table>

Table 5.1: Sigma ($\sigma$), mean ($\mu$), and skew (third moment) of all pull distributions. The photon pulls for all six outgoing photons have been added together. The proton energy is a calculated and not fitted and therefore no pull distribution exists.

The proton shows a complementary shift of the pull distribution to lower values, which is a consequence of the energy conservation constraint. The proton $\theta$ pull is slightly displaced towards higher values. This is probably caused by the fact that most protons are detected by TAPS, and the algorithm that tries to correct for the penetration depth of photons (see section 5.2.2) is also applied to the protons. Since this algorithm was tuned to photons, and the protons have a different interaction with the detector, it results in a small residual systematic error in the $\theta$ angle of the proton.

All pull distributions have a width ($\sigma$) either close to or slightly less than 1., meaning that the kinematic fit has not changed the energy and angle of the detected particles beyond the detector resolutions.

5.10 Invariant-mass shifts

To check that any invariant-mass peaks are not artificially enhanced by “pushing” background events into the peak it is useful to select the reaction:

$$\gamma p \rightarrow \eta p \rightarrow 3\pi^0 p \rightarrow 6\gamma p$$

and inspect the $\pi^0\pi^0\pi^0$ invariant-mass spectra for the events before and after the fit. For this purpose a selection of events was made that satisfied cuts on the total energy and the total transverse momentum in order to reject background. The spectrum was then generated once using the measured values and once using the kinematically fitted values. The results are shown in figure 5.13. It can be seen that the background does not change, although the peak has become much sharper. The sigma of the $\eta$ invariant-mass peak decreases from 21 MeV to 8 MeV, while the peak contents stay the same: integration yields 53207 ± 231 versus 53201 ± 230 counts. For the $K^0\Sigma^+$ channel this direct check is not possible with enough
Figure 5.13: Comparison of the \( \eta \) peak in the \( \pi^0\pi^0\pi^0\) invariant-mass spectrum after a kinematic fit (solid spectrum) and before (dashed spectrum). The fit improves the invariant-mass resolution for the \( \eta \) peak, without altering the background.

accuracy, as the invariant-mass peaks calculated from the measured values are not clearly separable from the background. Note that, as stated, neither the \( K^0, \Sigma^+ \), nor \( \eta \) mass enters in the fitting procedure so there is no reason to assume that it is possible for the fit to generate or enlarge such an invariant-mass peak.