BCAL Reconstruction

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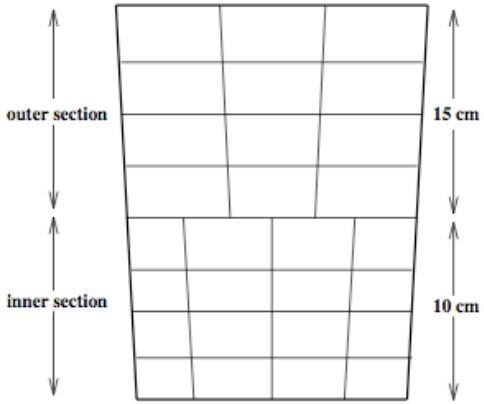
Code and Documentation

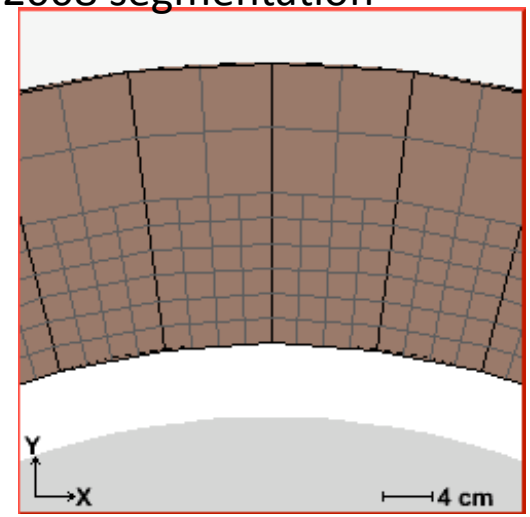
- Code originally ported from KLOE code by Chuncheng Xu (Regina)
- Algorithm documented by Mauricio Barbi *et al*. in Gluex-doc-569-v1 Dec. 2005
- First DANA version submitted to repository in Feb. 2006
- Readout segmentation updated in Apr. 2007 by David L.
- Significant overhaul in July 2007 by Matt S.
  - Performance improvement by factor of 10
  - DBCALMCResponse added
- More work on readout by Matt S. in July-Aug. 2008
  - Readout segmentation updated to current geometry
  - Smearing/threshold parameters updated based on 2006 beam test results
- Dark current and SiPM response updated and tweaked Feb.-July 2009 by Blake L. and Matt S.
- Timing of BCAL and FCAL updated and propagated to DPhoton Aug. 2009 by Mihajlo K.
- Additional photon merging stage implemented Mar. 2010 by David L.

BCAL Reconstruction Algorithm

2005 segmentation



2008 segmentation



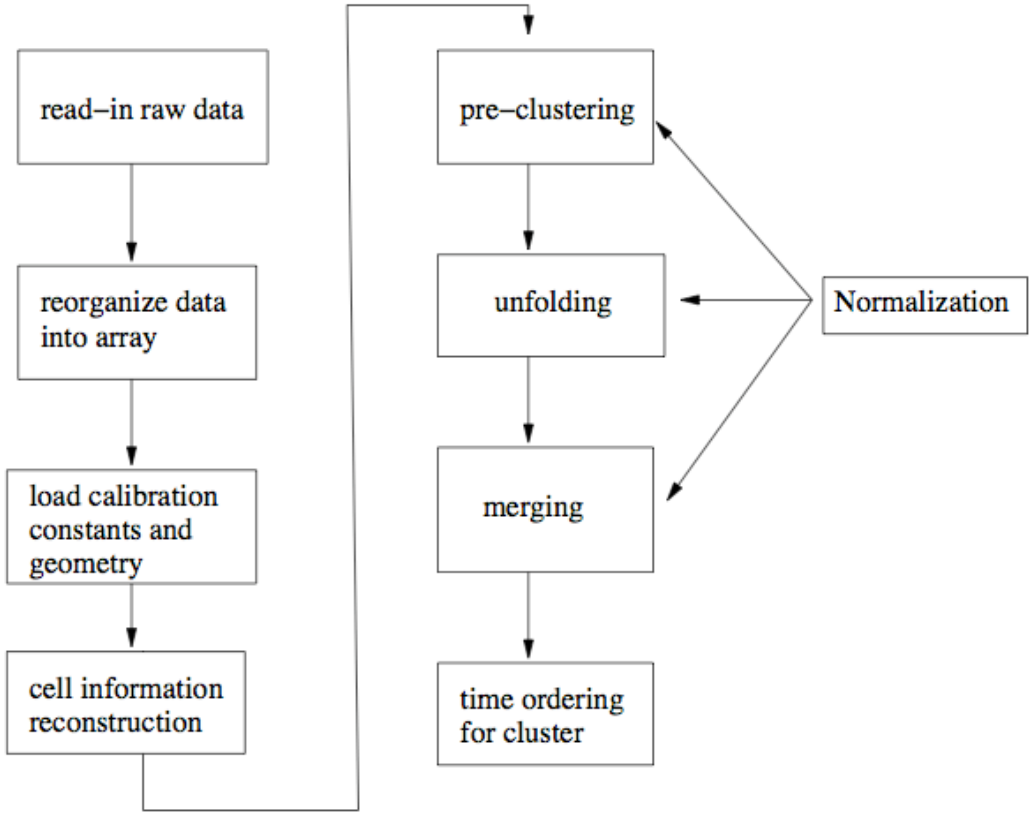


Figure 2: *The schematic for the KLOE reconstruction code.*

Cell Information Reconstruction

- Large arrays are used to hold all hits in event
  - Individual arrays for each end hold:
    - Amplitude (non-corrected)
    - Time
  - Arrays can hold only 1 hit per event
  - Arrays cleared at beginning of every event
  - Hits copied into appropriate array elements (leads to very sparsely populated arrays)
  - Loop over every readout cell to look for ones with both ends hit
    - If both ends are hit, average values are calculated and copied into another set(5) of arrays
      - Both ends "hit" means both over threshold and time difference less than 80 ns (hard-coded)
    - If either end not hit or no timing coincidence, zeros are copied into the cell arrays.
- Every cell is again looped over (in *CeleToArray()*) to copy hit cell info into sparse list of hits with energy, time, and location(xyz)

Pre-clustering

- Hit cells are looped over and ones that are adjacent are made into a cluster
- “Adjacent” is determined by indexes (module, layer, column)
- *z-information is not used at this point!*
- Number of modules hardcoded, but others come from DBCALGeometry factory
  - `if(modiff==1||modiff==-47)`

Unfolding

- Clusters that overlap in x/y but not in z (*or t*) are identified and separated
- Since the z-coordinate is determined by time, the time spread of the cluster on both ends is used to decide if unfolding is required

$$\sqrt{(T^a_{rms})^2 + (T^b_{rms})^2} > 5.0\ ns \qquad (14)$$

- During unfolding, cells are sorted into 4 groups, each of which may become a new cluster

$$(a)\ \ T^a_i > T^a,\ \ T^b_i > T^b \qquad (b)\ \ T^a_i > T^a,\ \ T^b_i < T^b$$

$$(c)\ \ T^a_i < T^a,\ \ T^b_i > T^b \qquad (d)\ \ T^a_i < T^a,\ \ T^b_i < T^b$$

- Motivation of this algorithm was apparently not fully understod by GlueX:

> The reason for this classification is not clear yet, as it could not be provided by the KLOE group, since the person who introduced this logic has left the KLOE collaboration. However, it is known that this logic has been used in the KLOE reconstruction code, and therefore it is assumed that it leads to a good cluster reconstruction resolution. Further studies on this selection are still to be performed, and new options for the cells' classification will be investigated in the near future.

From GlueX-doc-569-v1

Merging

- Merging of clusters is meant to address 3 cases:
  - Over-unfolded clusters
  - Shared showers between BCAL/FCAL (not implemented)
  - Detached cells due to bad channels
  - Parameters used for merging in the DBCALShower factory are given below:

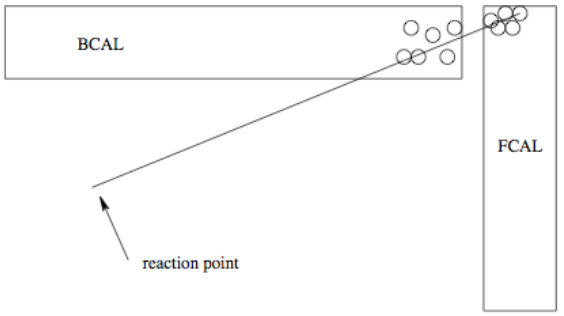


Figure 6: *A track hits both the barrel and forward calorimeters, resulting in showers in both detectors.*

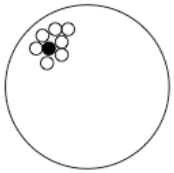


Figure 7: *If the filled circle in the figure is a dead channel, then one or more good cell (open circles) might not be considered as part of the group of adjacent cells belonging to a cluster, and some informations are therefore lost in the pre-clustering process.*

```
// these four parameters are used in merging clusters
MERGE_THRESH_DIST   = 40.0;  // CENTROID DISTANCE THRESHOLD
MERGE_THRESH_TIME   =  2.5;  // CENTROID TIME THRESHOLD
MERGE_THRESH_ZDIST  = 30.0;  // FIBER DISTANCE THRESHOLD
MERGE_THRESH_XYDIST = 40.0;  // CENTROID TRANSVERSE DISTANCE THRESHOLD
```

Note: The merging in the DBCALPhoton factory using only:
z-dist<30cm
xy-dist<15cm
(no time or total distance requirement)

Angular Determination by Line Fit

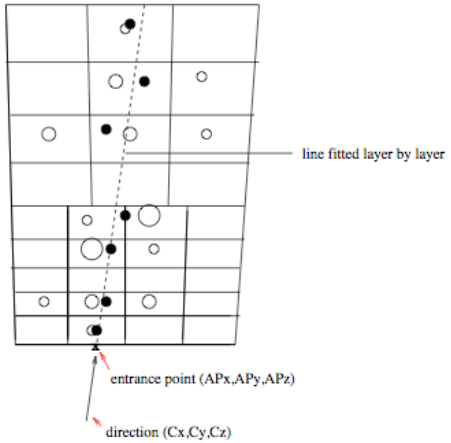


Figure 4: *A particle (full line) enters the BCAL at the apex point* (AP_x, AP_y, AP_z) *and with direction* $\vec{C} = (C_x, C_y, C_z)$*, leaving energy deposition in some of the BCAL cells (open circles). The filled circles represent the energy-weighted average positions of all cells with energy deposition in a given BCAL layer. The dashed line depicts the result of a fitting to these positions.*

- Cells in the same layer of a cluster are combined to get a single 3-D space point for the layer
- Space points are fit to a line to determine the direction of the photon
- The fit values are copied into the DBCALPhoton objects later, but NOT into the Lorentz vector kept in *DKinematicData* base class
- The photon direction in *DKinematicData* is determined by shower position and hard-coded center of target

Splitoffs were a known issue

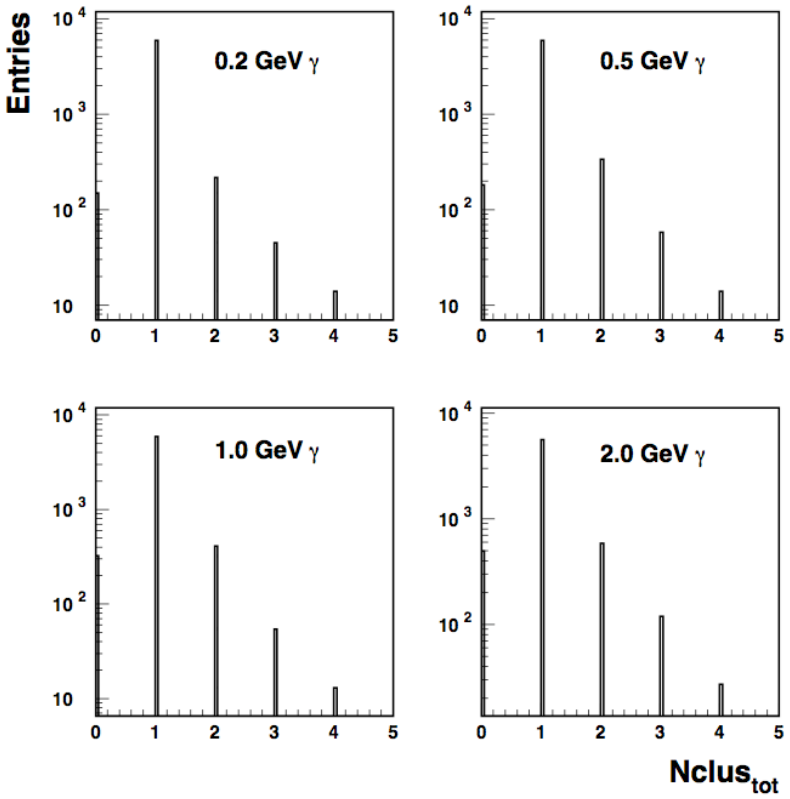


Figure 9: *Reconstructed total number of cluster $Nclus_{tot}$ distribution for single γ MC events. The events were generated with pz/p in [-0.4,0.9] so that the γ particle is at good angle to hit the BCAL. Some events have more than one cluster identified. The percentages of such events are 4.5%, 6.7%, 7.5% and 11.6% for 0.2 GeV, 0.5 GeV, 1.0 GeV and 2.0 GeV events respectively.*

From GlueX-doc-569-v1

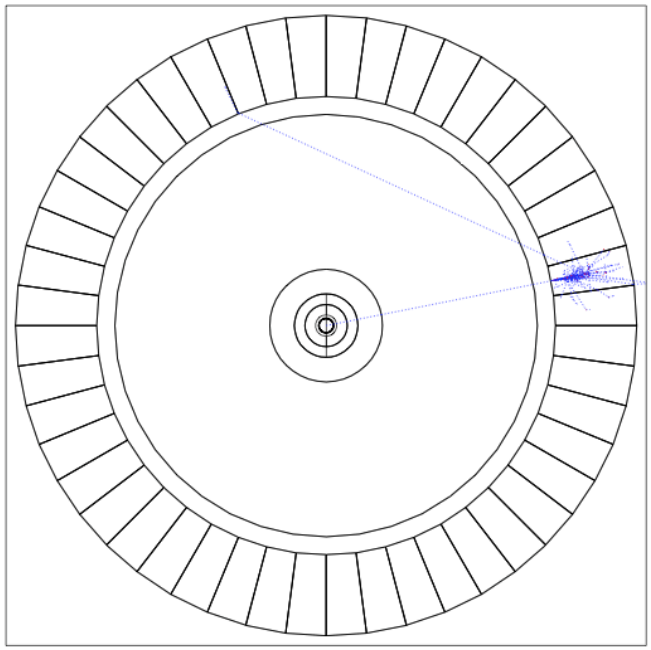
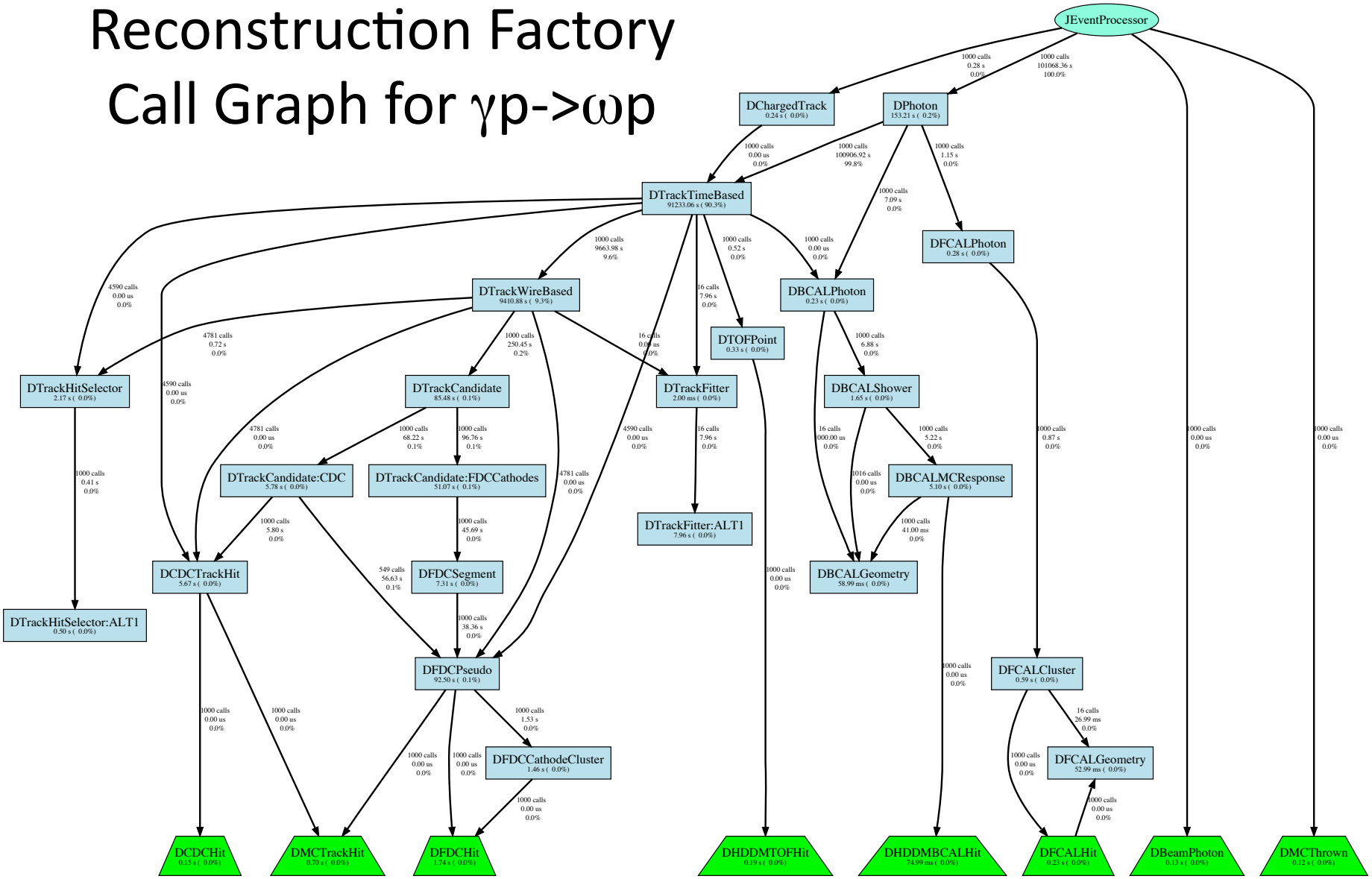
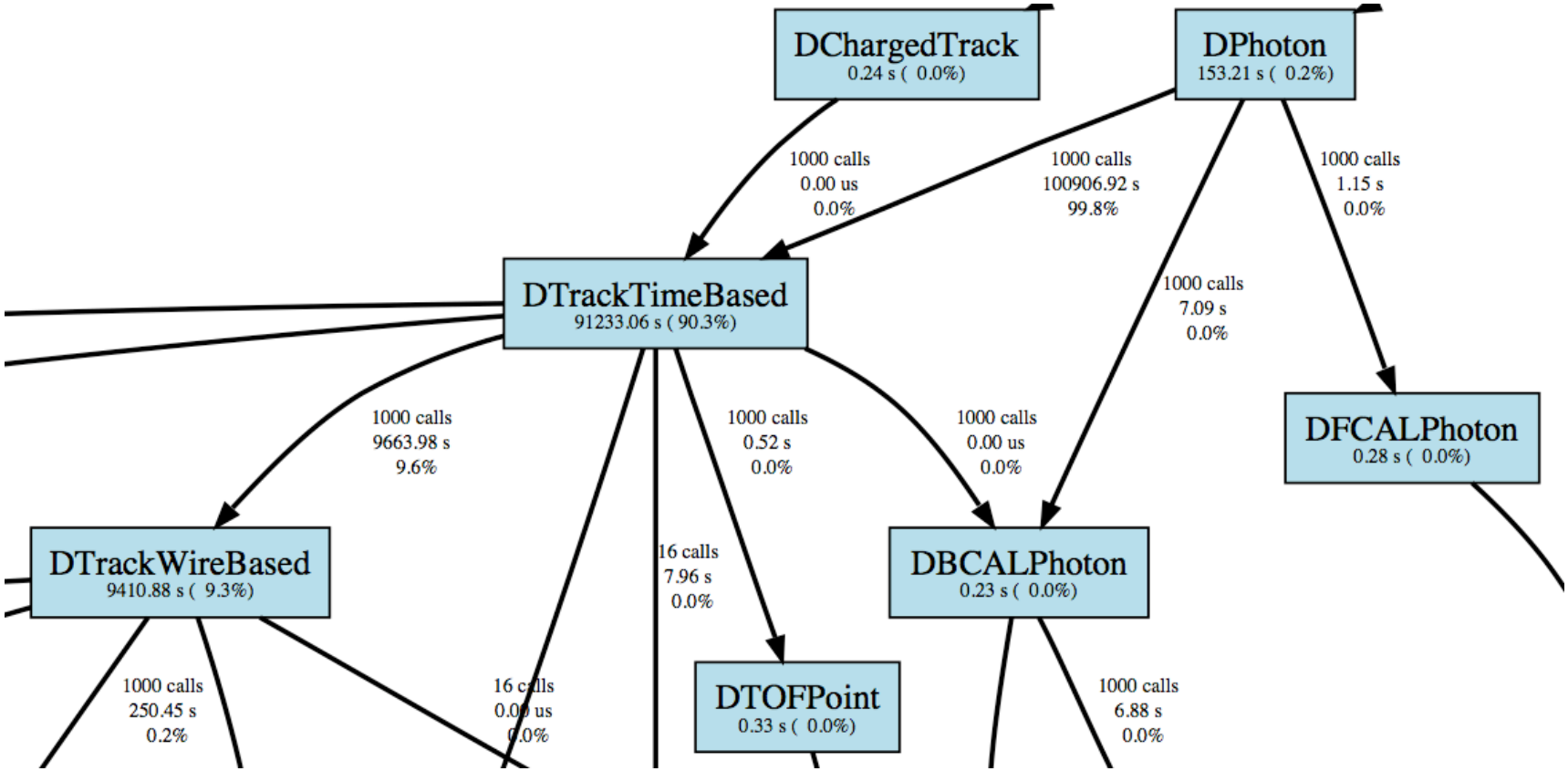


Figure 12: *Event display of a 0.5 GeV γ event. Processes like this one, in which a photon is ejected into a different part of the BCAL, helps to explain the long tail on the energy spectrum and also the additional clusters in fig. 9.*

Reconstruction Factory Call Graph for γp->ωp



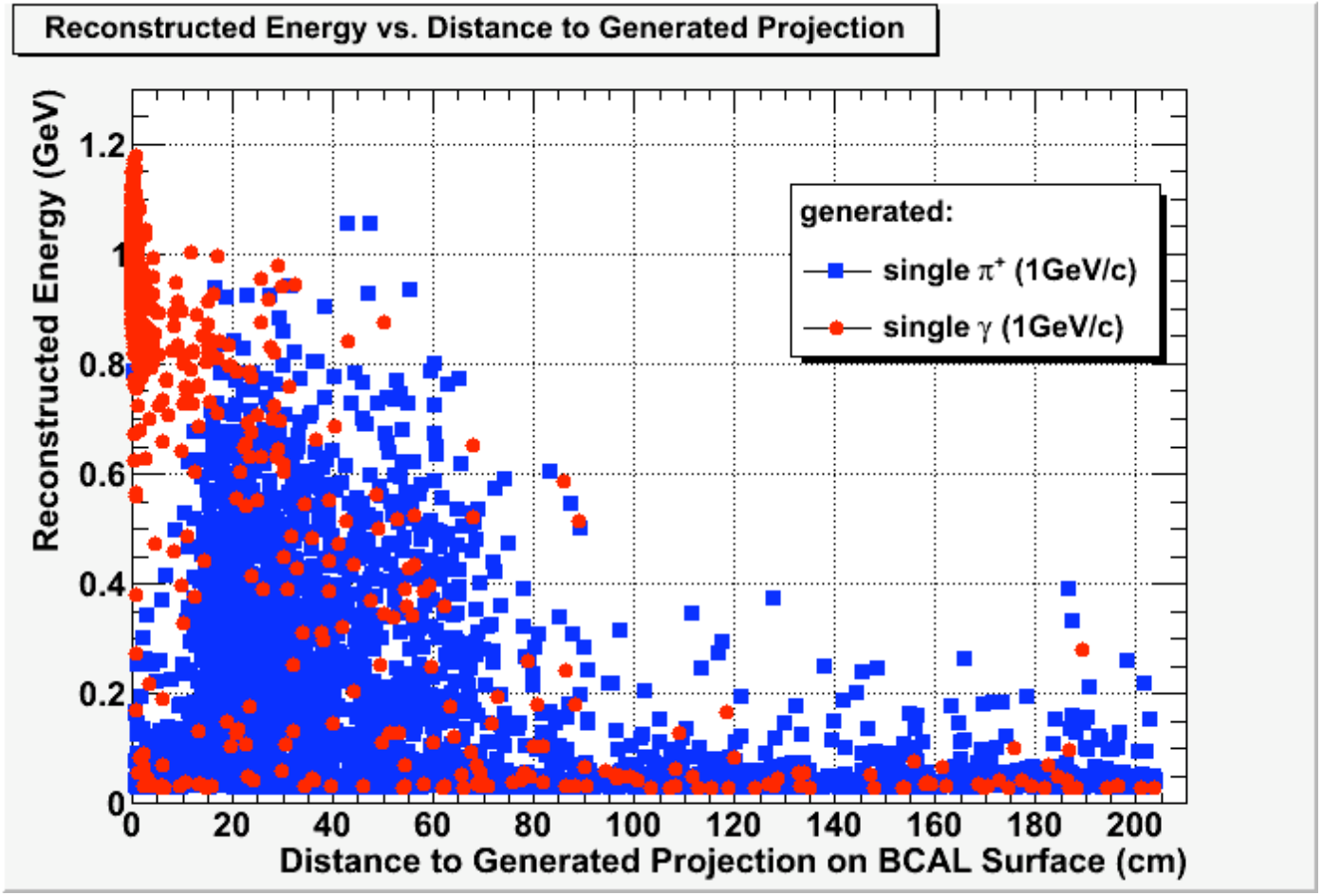
Reconstruction Factory
Call Graph for γp->ωp



Summary

- Some documentation exists (GlueX-doc-569) but authors are no longer active in GlueX and were not original authors of the code.
- Merging of BCAL clusters exists in 2 places. Parameters should be optimized and one of them removed.
- Unfolding procedure not fully understood making it a potential area for improving the multiple clusters issue
- No special treatment of hadronic showers (similar to FCAL).
- No outside vertex info used leading to unrealistic polar angle resolutions when throwing from the center of the target.
- Several places in code where additional optimization could be done, but code is reasonably fast compared to other packages (tracking)

Splitoffs


Reconstructed Energy vs. Distance to Generated Projection
Reconstructed Energy (GeV)
Distance to Generated Projection on BCAL Surface (cm)
generated:
single π⁺ (1GeV/c)
single γ (1GeV/c)
0
0.2
0.4
0.6
0.8
1
1.2
0
20
40
60
80
100
120
140
160
180
200