# Profiler reconstruction code and simulation

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#### Code

- Directory ProfilerCode in INSIDE dropbox
- File README inside

- Main program: Profiler.h,cpp
- Classes:

EventoPix, FiberHit, FiberCluster, Track,KalmanTrack, Pair



### Protons (90 degree)

#### Milano: G. Battistoni, S.Muraro

- Parametrized Monte Carlo proton simulations that uses flux measured at 90° from beam direction at Heidelberg
- Primary particles are generated as if coming from a 220 MeV/u Carbon beam along x axis (Gaussian smearing of 0.8 cm)



#### Fiber Hits

- Fibers are read-out with 0.1 cm readout pitch
- Hits within same fibers are merged and energy is summed



#### **Fiber Clusters**

- X and Y clusters are made by consecutive fiber hits

- 2D clusters are made by combining X and Y clusters within same layer in all possibile ways
  \* there is a fake cluster for each true one due to wrong combination
  \* z coordinate is middle of that of X and Y plane
  - \* energy is sum of fiber hits energy



## Tracking algorithm

- Starting from first hit layer, seeds are created combining clusters from the first two layers
- Seeds are prolonged to subsequent layers: clusters are associated to tracks in decreasing order of "distance" = distance between expected (on the basis of direction determined from seed) and measured position
- Clusters are assigned only to a single track Tracks can share only clusters of seeds
- If there are more clusters than seeds in one layer, some remain unassigned (possibility, now disabled, to initialize new seeds)

Since d1<d2, cluster A is assigned to seed 1



### Pairs

Pairs = all combinations of tracks that share the first hit, have more than two clusters and different angular coefficient

Relevant when study prompt photon interactions



#### **Track candidates**

#### Number of TrkCand per event

#### nTrkCand htemp 10<sup>5</sup> 58678 Entries 0.9459 Mean 0.341 RMS 10<sup>4</sup> 10<sup>3</sup> 10<sup>2</sup> 10 2 6 10 12 14 16 4 8 n nTrkCand

#### Number of clusters per track candidate



### **MC** Association

- MC association track-MC particle is done on the basis of the MC id of the fiber deposits
- Each track has an associated MC particle
- The associated MC particle is the one which shares more fiber deposits with the reconstructed track
  - The output tree contains all the original MC tree
  - True angular coefficient and vertex for each MC associated particle are stored



#### Fit to Track candidates

A chi2 fit and a Kalman fit are performed on each track candidate (with more than two hits). Both fits give  $\sigma(XZ)\sim\sigma(YZ) = 0.033$ 

coefficient Kalman fit resolution on XZ angular coefficient from chi2 fit (similar for Y) (similar for Y) AKFitX-axMC {nHotTrkCand>2} AFitXZ-axMC {nHotTrkCand>2} h2 h1 49940 Entries 49940 Entries Mean 0.009685 10<sup>4</sup> Mean 0.009768 RMS 0.05667 RMS 0.05807  $\chi^2$  / ndf 4051 / 78 χ<sup>2</sup> / ndf 4266 / 80 Prob Prob 10<sup>3</sup> Constant 8669 + 60.8Constant 8716 ± 61.5 Mean  $0.004024 \pm 0.000159$ Mean  $0.004039 \pm 0.000160$ 0.03343 2 0.00018 Sigma  $0.03376 \pm 0.00018$ Sigma 10  $10^{2}$ 10 10 -0.6 -0.4 -0.2 0 0.2 0.4 -0.8 -0.6 -0.4 -0.2 0 0.2 0.4 0.6 0.8 -0.8 0.6 0.8 ax-axtrue ax-axtrue

resolution on XZ angular

### Angular resolution & MS

Two components:

MS before the profiler (in the head, dominant) ~30mrad coerent with angular resolution





#### Determination of proton origin

Proton origin is defined as point of closest approach of the reconstructed track to the beam axis.

If multiple tracks are reconstructed the one with the minimum chi2 from fit is taken



#### Spatial resolution on origin: X



#### Spatial resolution on origin: Y



#### Spatial resolution on origin: Z



#### Spatial resolution on origin: XY

#### x:y true

#### x:y reco



### Spatial resolution on origin

- In a window of  $3\sigma$  (from single Gaussian fits) there are:

N=44608 events

with resolutions in (x,y,z)=(0.4,0.4,0.8) cm for a single proton

- Need to translate single proton resolution in resolution on Bragg peak to estimate real performances
- Monte Carlo sample corresponds to approximately 30 times the protons available in a real treatment fraction per slice.

#### Normalization

- We are considering protons from 220MeV/u Carbon beam
- In a real treatment (fraction) we expect ~10<sup>7</sup> Carbons at this energy. This corresponds to ~2\*10<sup>-4</sup> protons/Carbon in the profiler acceptance => 2\*10<sup>3</sup> protons in the profiler
- In the simulation, 2\*10<sup>-2</sup> protons/generated protons are in acceptance. Since we simulate 3\*10<sup>6</sup> protons in our sample this corresponds to 60\*10<sup>3</sup> protons in the profiler
- Actually, in the real scan there are energies close to 220MeV/u which move the Bragg peak within our spatial resolution. Shall we consider then all these energies for our normalization?

#### More realistic case

#### protons generated in a wider angular cone around the 90° direction



#### Conclusion

- Complete code and simulations for protons coming from a realistic Carbon treatment impinging on the profiler at 90° available
- Single proton resolution is ~(0.4,0.4,0.8) cm in (x,y,z):
   need to define a figure of merit to evaluate resolution on
   Bragg peak and accurately scale statistics to a realistic
   treatment
- To do:
  - \* study case at 60°
  - \* study performances on prompt photons (point-like source should be sufficient)