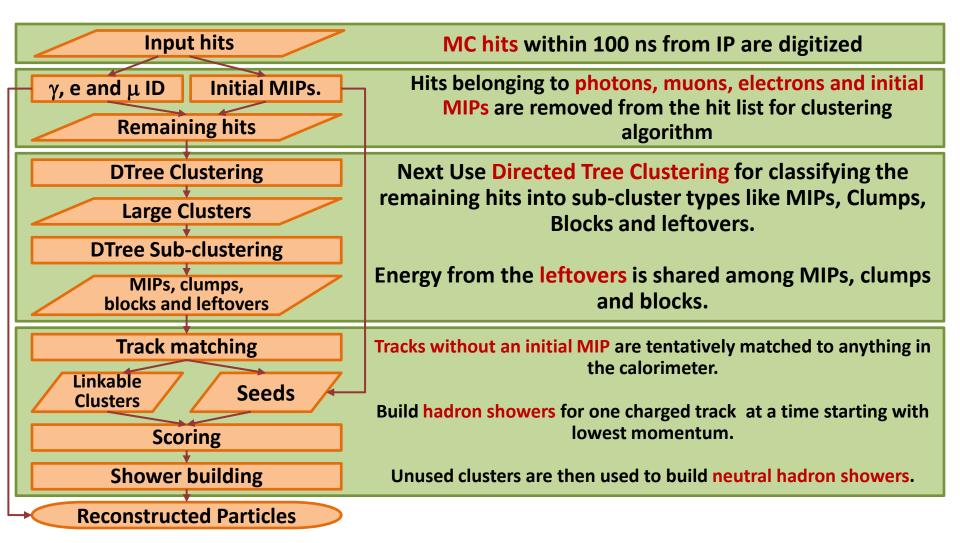
#### Status of the SiD/Iowa PFA

R. Cassell, M.Charles\*, U. Mallik, Remi Zaidan Nov 15, 2010 SiD Workshop, University of Oregon, Eugene

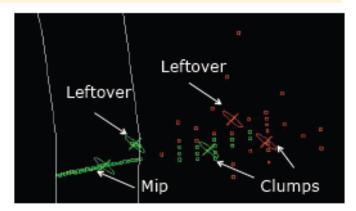
#### Basic Building Blocks of the (Iowa) PFA



## Categorizing: DirectedTree Clustering

| Ecal Digi Hits(Barrel, Endcap) |                                |   | Hcal Digi Hits (Barrel, Endcap) |      |                                |                                |
|--------------------------------|--------------------------------|---|---------------------------------|------|--------------------------------|--------------------------------|
| Photon,<br>Electron,<br>Muon   | DTree cluster<br>(Ecal Barrel) |   | DTree cluster<br>(Ecal Endcap)  | Muon | DTree cluster<br>(Hcal Barrel) | DTree cluster<br>(Hcal Endcap) |
|                                |                                | MIPs A continuous sequence of single hits                       |                                 |      |                                |                                |
| DTree cluster                  |                                | Clumps Group of hits with high density                          |                                 |      |                                |                                |
| Direc ciu                      | stei                           | Blocks No structure, if(>= 20hits in ECal, >=15 hits in HCal)   |                                 |      |                                |                                |
|                                |                                | Leftover No structure, small number of hits (Share with others) |                                 |      |                                |                                |

 Leakage
 Some of high energy shower escapes Hcal, reaching Muon Detector. Adding the energy by using Muon Endcap as tail catcher give better resolution. (Currently not using Barrel)



## Cluster Building

- Extrapolate (each) track to the ECAL surface
- FindSeed: sub-cluster directly connected to extrapolated track (other than MIPs)
- Each track typically has one seed
   Special cases: track without seed, or when it does not reach the calorimeter
- Now start connecting other sub-clusters to the seed of each track
- Start with lowest and then progressively higher momentum tracks
- Up to ten iterations until all track-cluster match satisfy (E p) within tolerance

#### Connecting sub-clusters

Scoring: (a poor man's) Probability of a link

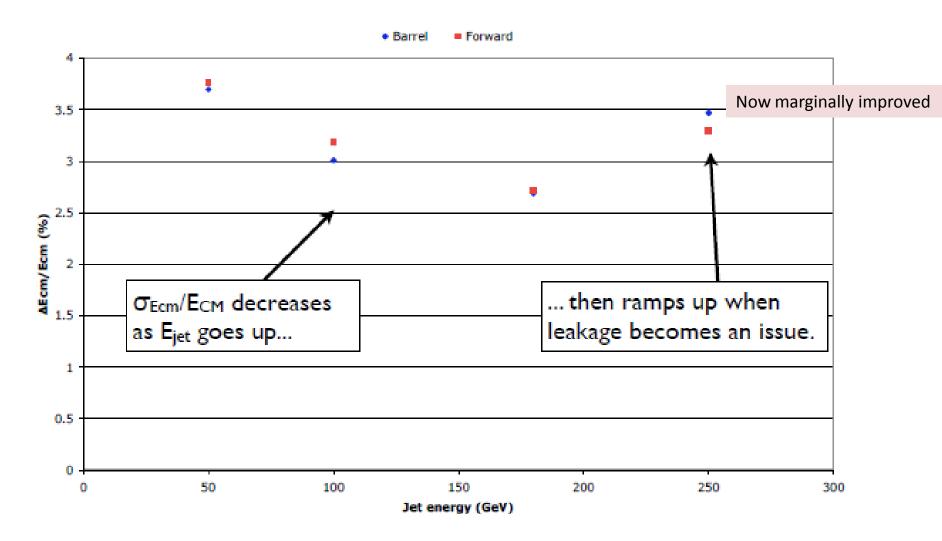
Based on the sub-cluster type and geometric proximity a score between 0 and 1 is assigned between any two sub-clusters starting with the cluster in consideration

The higher the score the higher the probability of a link To pick up secondary neutral hadrons, a cone-like algorithm is used

A cut-off threshold is obtained for an energy by tuning with events

### Energy dependence

#### Performance at LOI, 4/2009



At higher energies resolution worsened partly due to leakage but also due to algorithm

#### Intermediate history

Threshold Accepting Method applied by Christoph Pahl Showed initial promise; but ambitious

Zaidan took a good look at the PFA to understand in depth

- improved cone algorithm and applied a likelihood
- fixed several bugs
- > modified the iterations, relaxed E/p chceks
- allowed sharing of hits by multiple tracks
- modified track-seed matching, using direction of track
- removed primary neutral hadron clusters to test algorithm for only charged tracks

#### No magic bullet found

Modification of each single step was being foiled by some later steps because on interdependence and built-in "cures" in the algorithm

Conclusion: No obvious "simple" solution

#### Meeting of the minds:

at end of September at CERN for a few days (Cassell, Charles, Mallik, Zaidan)

#### Plan of attack:

Develop diagnostic tools to measure success/failure quantitatively Starting from the top:

Test sub-clustering immediately after Directed-tree clustering

Is sub-cluster purity good enough? Evaluate

Are extensions of tracks and MIPS done with high efficiency?

Is scoring done well enough? Should use same algorithm

Is Photon finder efficiency good enough?

Is the Photon veto good enough (overlap with initial MIPs (seeds)

or muons)

Is calibration good enough?

Where can we gain most: Where is the biggest problem (upstream)

#### Frequent meetings as needed

#### Diagnostics Tools: (Zaidan)

- track-seed matching match-quality, properties of unmatched tracks
- Dtree sub-cluster qualities and performance, purities and energy dependence
- link properties
   variables used in scoring (before and after first cone)
- shower properties efficiency, purity, energy-momentum comparison

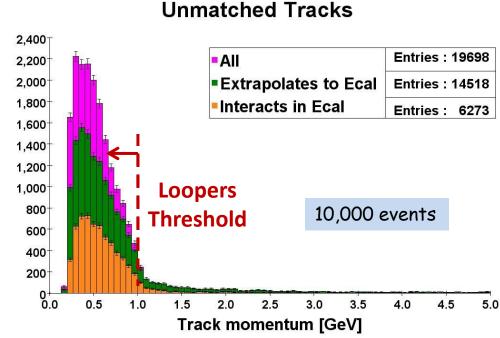
Completed in early October

### Some results from the studies: Track-seed matching:

most of the seeds are MIPS

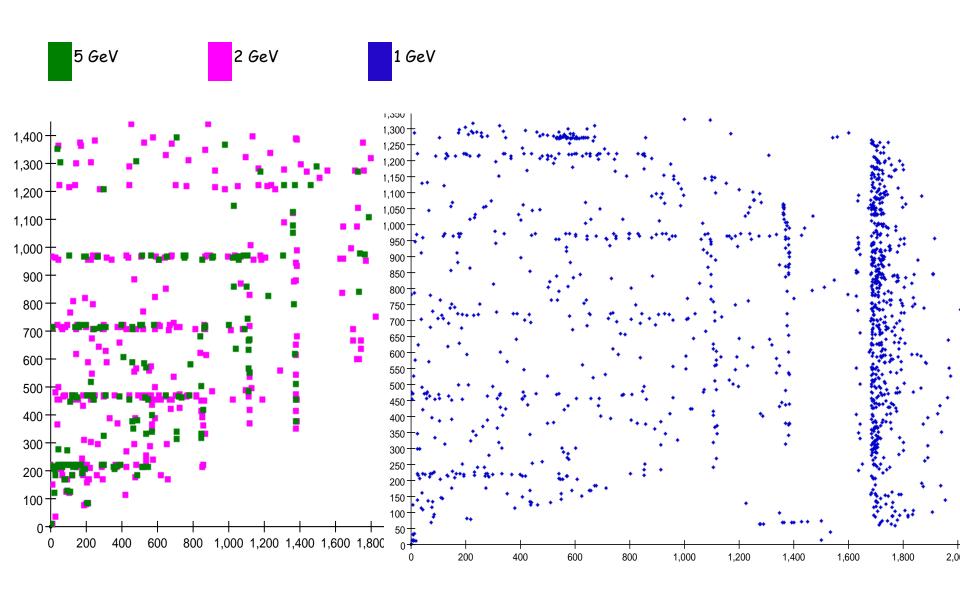
| Seed      | Match-rate |
|-----------|------------|
| MIPs      | 84.5%      |
| Leftovers | 14%        |
| Other     | 1.5%       |

Seeds with < 4 hits are 7.5%



Fraction of unmatched tracks  $\Rightarrow$  18% Of these most are loopers, fraction with p < 1 GeV  $\Rightarrow$  90% Of these 18%, fraction which should reach Ecal  $\Rightarrow$  74% Only 32% actually reaches Ecal (int in tracker)

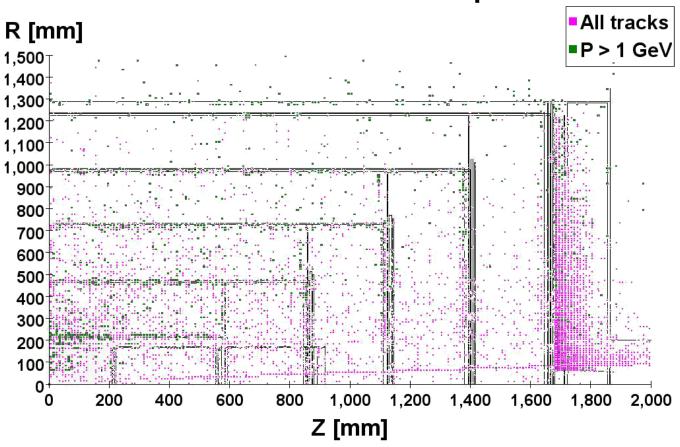
Few electrons get tagged as photons when there is a miss in match between a seed and a near-by track (0.03%)



End points of tracks with single pions (Cassell) at several energies

## Track-Seed Matching





qqbar at 500 GeV, 500 events

## Compare with single pions

track-seed matching looks better for single pions at a first glance

|             | Efficiency | Matching to MIP |
|-------------|------------|-----------------|
| qqbar       | 82%        | 84.5%           |
| Single pion | 99%        | 91.3%           |

Integrated spectrum

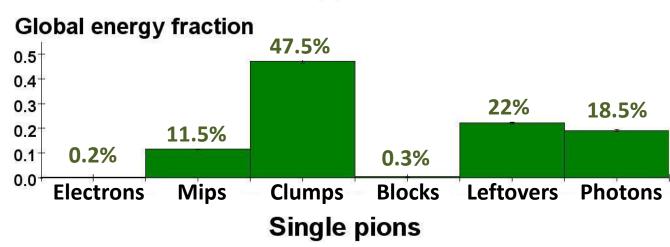
Momentum dependence between the qqbar and the single pion samples are different, no difference once it is properly accounted for

# Dividing up into sub-clusters, comparison

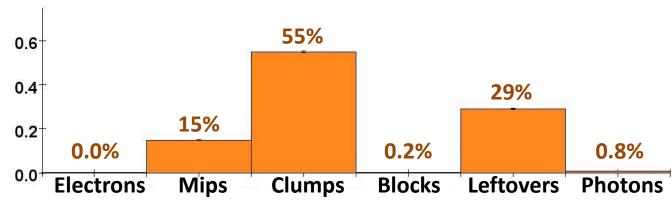
#### energy fractions in total sample

Excess in clumps in appar w.r.t. single pions.

Similar distributions: no photons in single pions.



qqbar



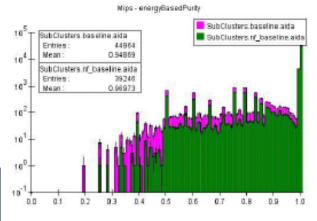
## Sub-cluster purity, not energy weighted

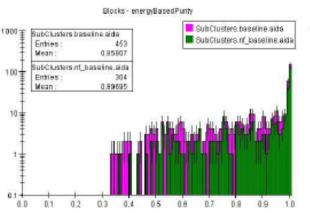
## Are neutral hadrons causing a big problem? Compare performance with and without

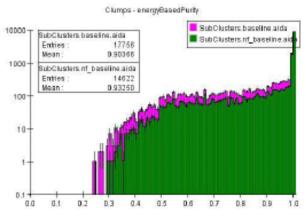
Purple: baseline

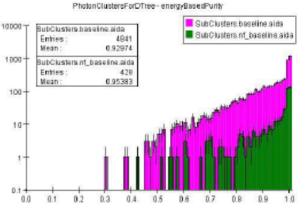
Green: Neutral filter applied

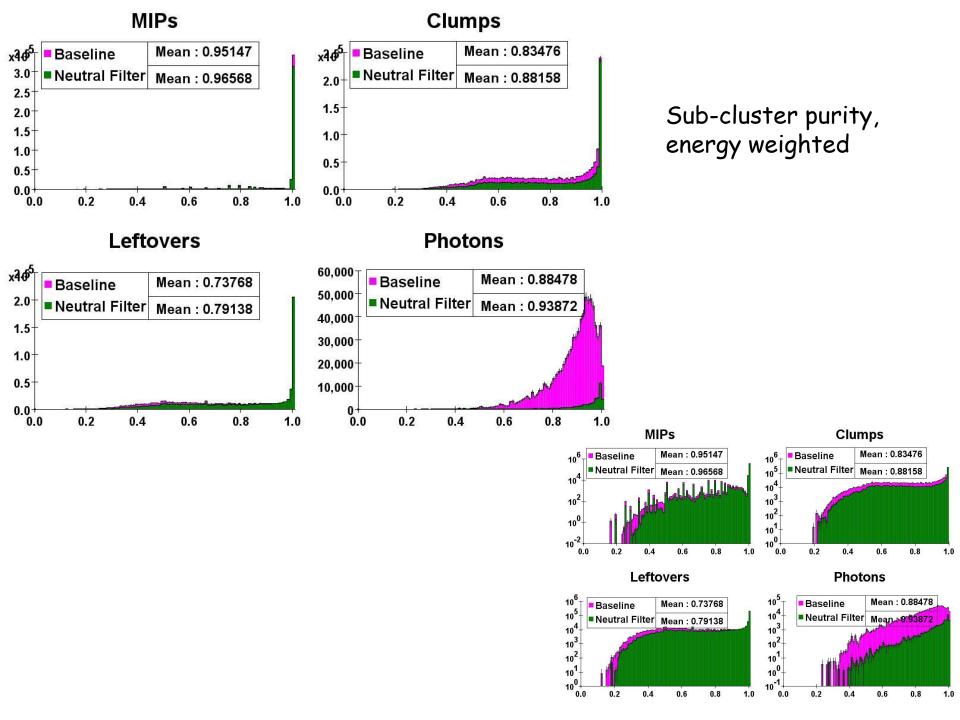
| PFA    | Baseline | Neutral<br>filter |
|--------|----------|-------------------|
| Mip    | 95%      | 97%               |
| Clump  | 90%      | 93%               |
| Block  | 86%      | 90%               |
| Photon | 93%      | 95%               |











## An intermediate summary

Energy distribution among the sub-clusters (in the data sample):

Clumps: 47% of energy Leftovers: 22% of energy Photons: 18% of energy

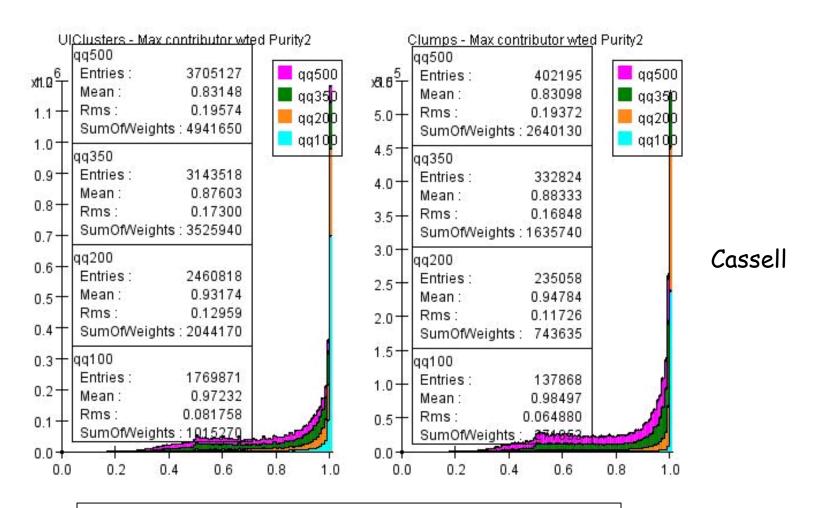
MIPs : 12% of energy

Purity according to sub-clusters, good enough?

| Subcluster | baseline |                 | Neutral hadron filtered |                 |
|------------|----------|-----------------|-------------------------|-----------------|
|            |          | Energy-weighted |                         | Energy-weighted |
| Clumps     | 90%      | 84%             | 93%                     | 88%             |
| MIPs       | 95%      | 95%             | 97%                     | 97%             |
| Blocks     | 86%      | 82%             | 90%                     | 86%             |
| Photons    | 93%      | 89%             | 95%                     | 94%             |

Neutral hadrons are adding some confusion but not that much

## Energy-dependence of purity

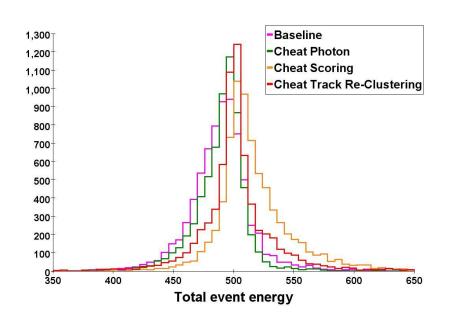


As overlap of showers increases with energy, isolation gets to be challenging, purity suffers

#### Testing each piece step-by-step

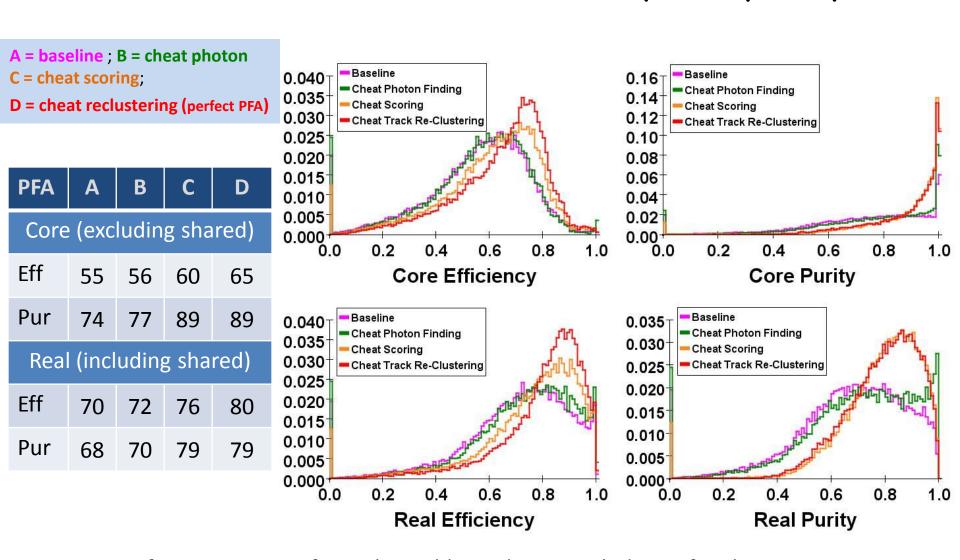
#### Baseline

Cheat-scoring: simply check with MC if it is really a match (score 0 or 1)
Cheat photon finding: perfect photon finder, no photon veto
Cheat reclustering: associate sub-clusters if it belongs according to MC (ignore score) look at the sub-cluster and add to the track where it has dominant contrib
Cheat reclustering + perfect sharing: left-overs added to showers according to MC



| PFA                       | RMS90 |
|---------------------------|-------|
| Baseline                  | 3.4%  |
| Cheat Photon Finding      | 2.8%  |
| Cheat Scoring             | 3.9%  |
| Cheat Track Re-Clustering | 3.6%  |

## Shower reconstruction efficiency and purity

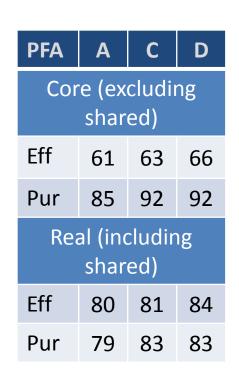


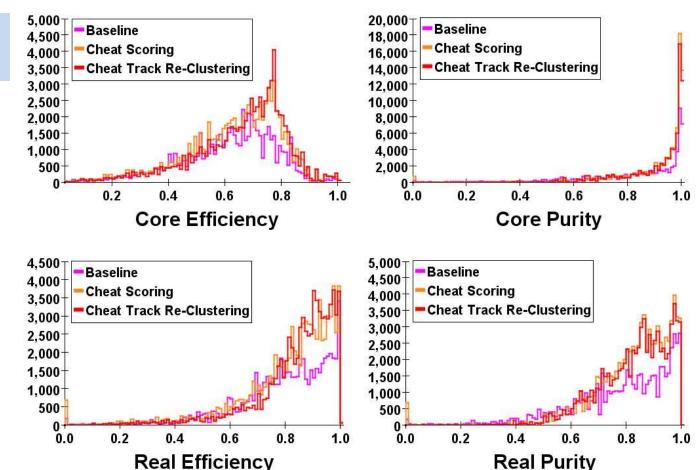
Perfect PFA + perfect shared hits do not enlighten further, except 22% energy in shared hits is not negligible

## Shower reconstruction efficiency and purity

#### Neutral filter applied







Conclusions: Optimize sub-clustering better (works OK at low energy)
Photon finder needs to be improved
(According to MC 26% of energy should be in the photons)
(Cheat photon finder shows large improvement)
Then asses if it should be scoring or algorithm

Where we are: Think we understand quite a few of the problems

Next steps: Where to start

: Attempt at isolation of sub-clusters?

: Attempt at link-scoring?

Remi will explain link scoring, resolution, effects of E/p balance

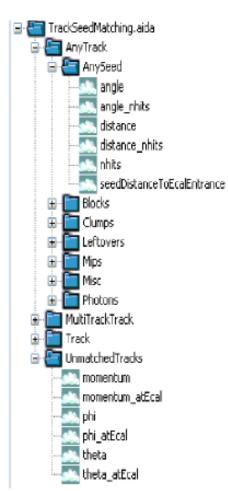
Garabed Halladjian joined the PFA effort on November 1, 2010

# Back-ups

## Track-Seed Matching: Definitions



- Tracks are extrapolated to the innermost layer with hits from the seed:
  - Angle is computed between the seed direction from energy tensor calculation and the tangent to the extrapolated track.
  - Distance is computed between the track interception point and the closest hits in the cluster on the same layer.
- Seed distance to Ecal entrance is the depth of the innermost layer with hits from the seed.
- Plots are made per seed type and also separating simple from multiple tracks.
- Multiple tracks:
  - Angle and distance to seeds are computed using extrapolation results averaged on sub-tracks.
  - Angle is the maximum angle between "sub-tracks" at the extrapolation layer.
  - Distance is the maximum distance between interception points.
- For unmatched tracks:
  - Momentum, theta and phi are plotted for all unmatched tracks and for those that reach the Ecal.







Better track-seed matching for single pi in general

Higher matching efficiency:

qqbar: 82% single pi: 99%

Higher matching to mip rate:

qqbar: **84.5**% single pi: **91.3**%

