

PFA status

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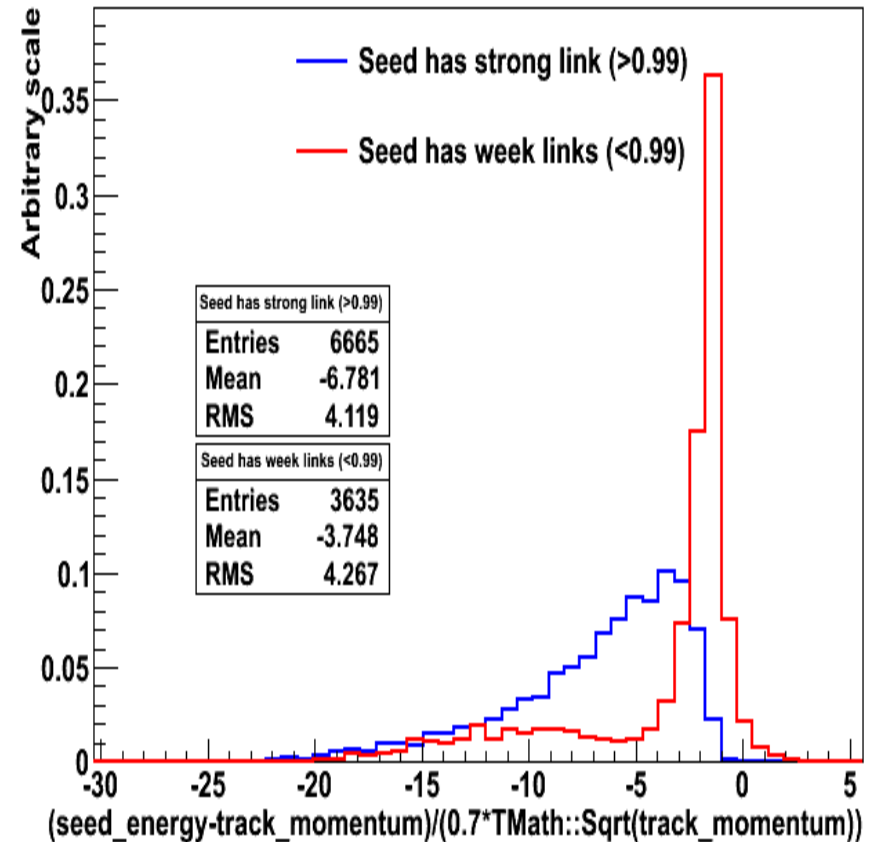
SiD PFA meeting

Tracks with bad seeds

- Run a perfect shower building algorithm:
 - Use seed's MC match as a reference.
 - Use tracks MC match as a reference.
- Large tail in the event energy due to bad seeds.

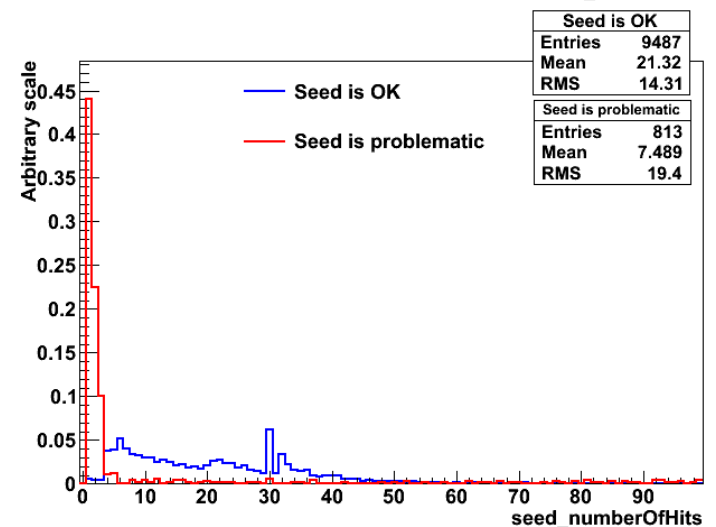
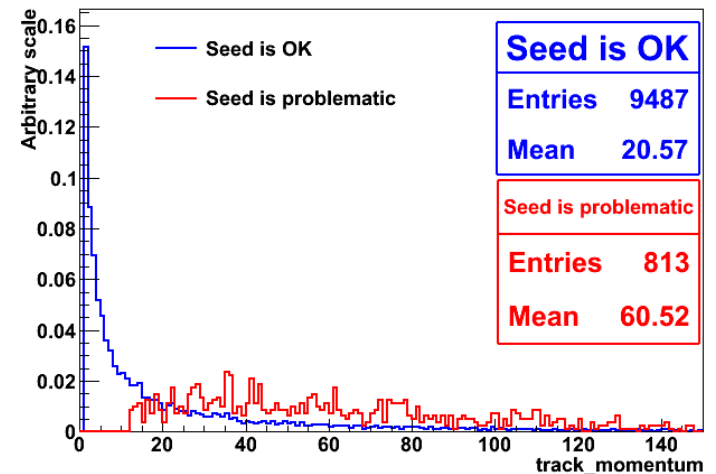
Identifying problematic seeds

- Split seeds into two categories:
 - Seed with at least one strong link (score > 0.99).
 - Seed with only weak links (score < 0.99).
- Two components in the seed with no strong link:
 - The seed itself satisfies the E/P balance (low momentum tracks).
 - The seed energy is too low compared to the track momentum ($E-P < -5 \sigma$)
 - The latter are problematic seeds



Properties of the problematic seeds

- 8% of matched tracks have problematic seeds:
 - On average 1/3 of events have one or more problematic seed.
- They have high momentum:
 - 60 GeV on average instead of 20 GeV for all tracks.
- They have low number of hits:
 - 90% of them have less than 4 hits.
- There is a big photon nearby:
 - See next slide

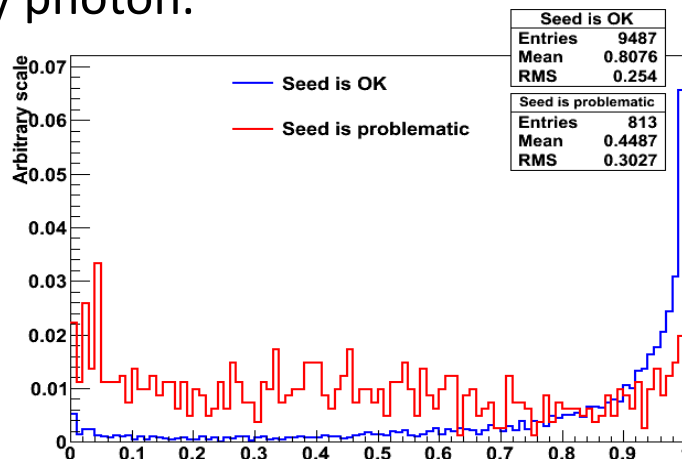
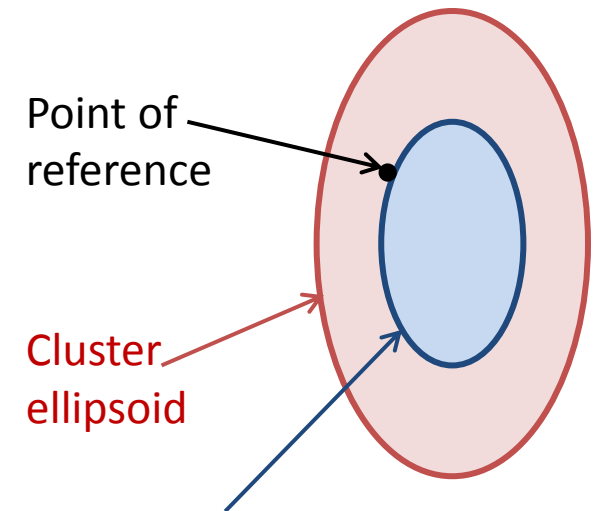


Track/photon proximity

- Shallowness of a point in a photon:

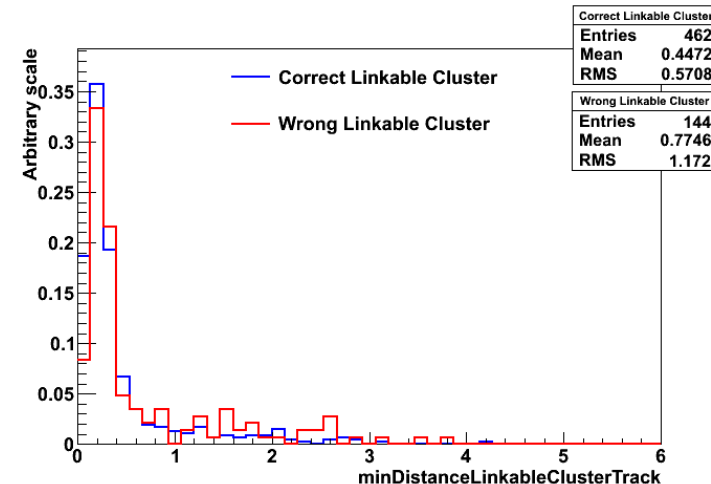
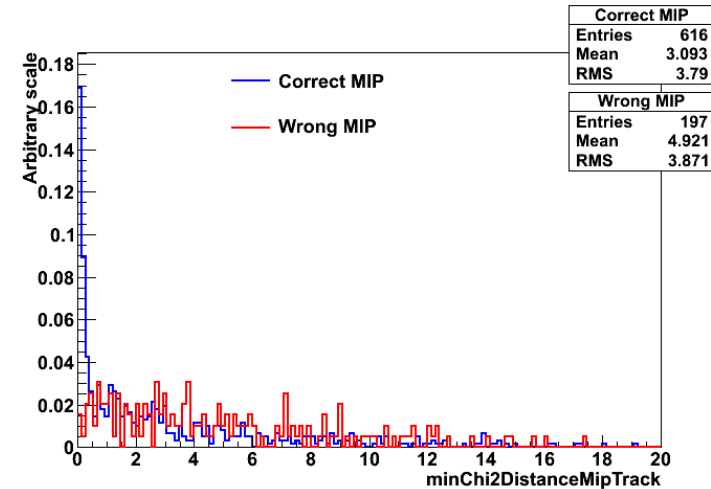
$$\text{shallowness} = \frac{\text{Energy IN}}{\text{Energy IN} + \text{Energy OUT}}$$

- Shallowness of a track in a photon:
 - Extrapolate the tracks at each layer of the photon, and compute the shallowness of the intercept point in the photon.
 - Compute the minimal shallowness over all photon layers.
- Compute the minimal shallowness of the track to any photon.



Fix by extrapolation

- Extrapolate the track into the calorimeter and try to match to a MIP:
 - Matching criteria is a χ^2 between the MIP and the track extrapolation taking the size of the cells as position uncertainty.
 - About 25% of the cases a match is found.
 - About 95% of the found MIPs actually belong to the track.
- Then try to match to a clump:
 - Extrapolate the track and pick-up the first clump it finds within a certain distance.
 - The distance is between the track extrapolation to a given layer and the closest hit of the clump on that layer.
 - Limit distance calculation to the first 3 layers of the clump.
 - About 75% of the found clumps actually belong to the track.
- Overall, about 80% of the found new seeds actually belong to the track.



Alternatives to the extrapolation

- Define a track seed matching based on a likelihood.
- A simple cone algorithm has the same performance as the likelihood:
 - The cone is taken at the extrapolation of the Track to the Ecal entrance with an opening of 4.5 degrees around the track tangent at the Ecal entrance.
 - Take the cluster which is closest to the track extrapolation (negative pole) as a new seed.
 - About 78% of the new seeds actually belong to the track.

Conclusion

- We just (today) got the first result of this within the PFA code:
 - We don't understand the resolution numbers we are getting and we suspect a broken piece of the code is causing wrong numbers.
 - The resolution numbers we are getting are unphysical and inconsistent with the diagnostics at intermediate steps of the PFA:
 - In particular the confusion matrix.