

PFA Diagnostics tools and benchmark performance

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and Remi Zaidan

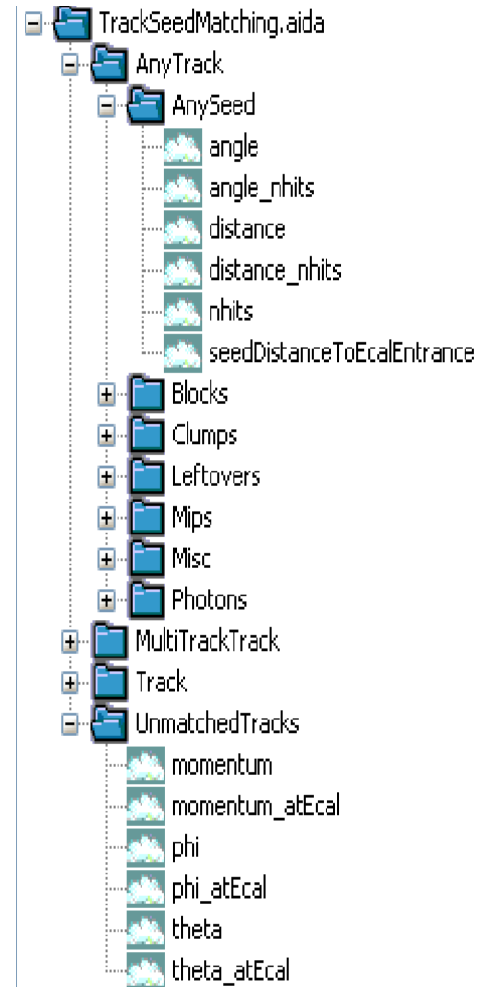
Introduction

- Diagnostic tools are developed to test the PFA performance at each step of the algorithm:
 - Track-seed matching:
 - Matching quality, properties of unmatched tracks.
 - DTree sub-clusters:
 - Purities and energy contributions.
 - Link properties:
 - Variables used for scoring.
 - Scores before and after the first cone.
- Next steps.
- Data:
 - 10'000 500 GeV qq events

Track-Seed Matching

Track-Seed Matching: Definitions

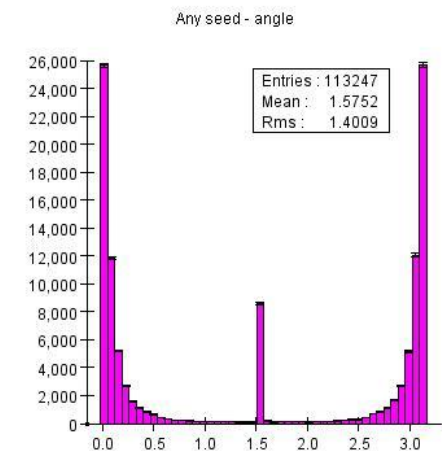
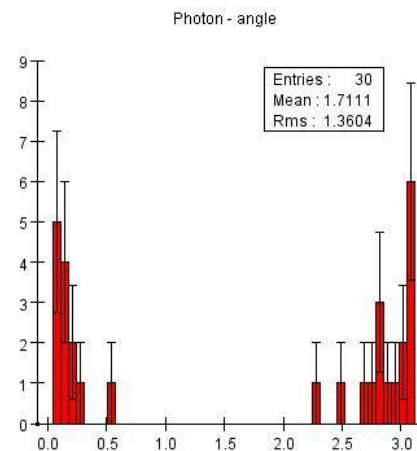
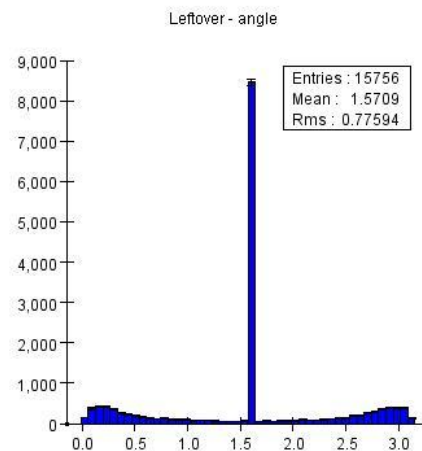
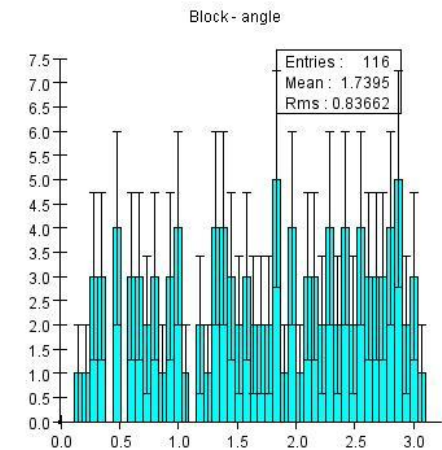
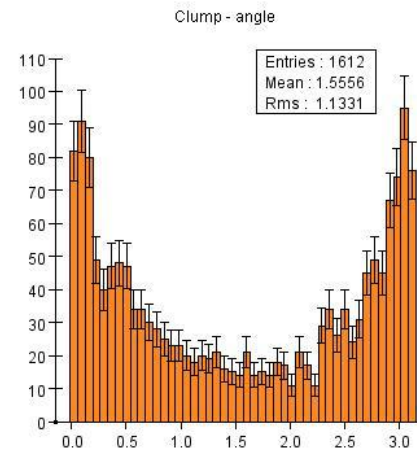
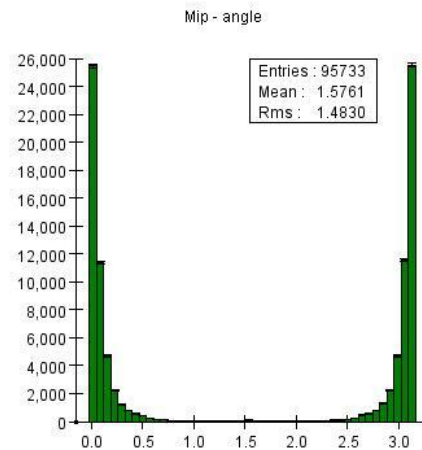
- Tracks are extrapolated to the innermost layer with hits from the seed:
 - Angle is computed between the seed direction from energy tensor calculation and the tangent to the extrapolated track.
 - Distance is computed between the track interception point and the closest hits in the cluster on the same 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.



Track-Seed Matching

Matching efficiency
to a mip:
84.5%

Fraction of seeds
with <4 hits:
7.5%



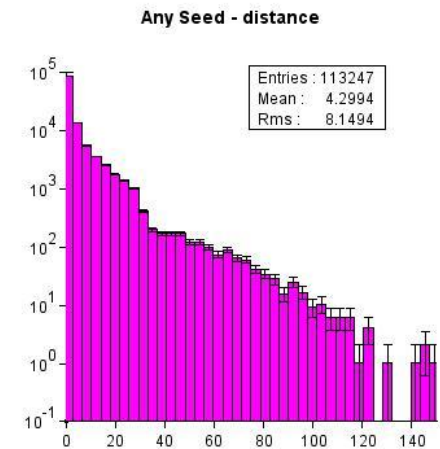
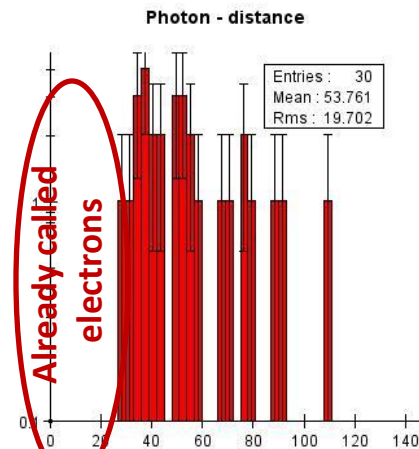
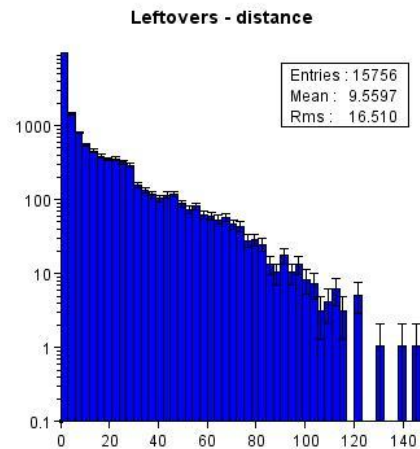
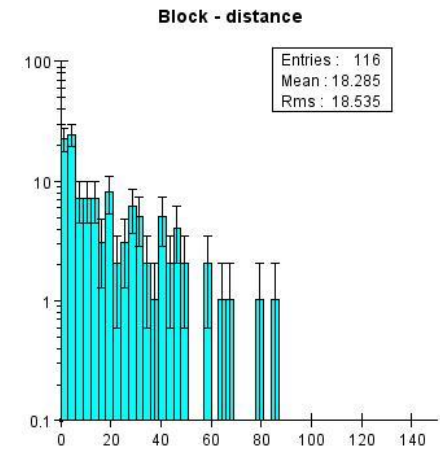
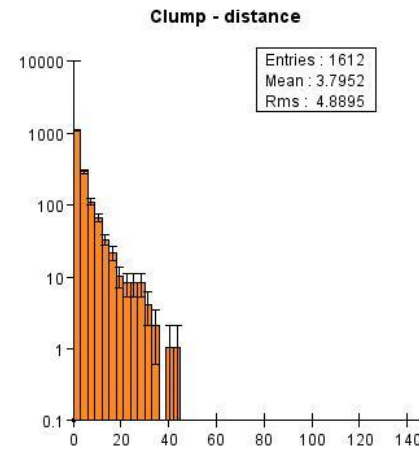
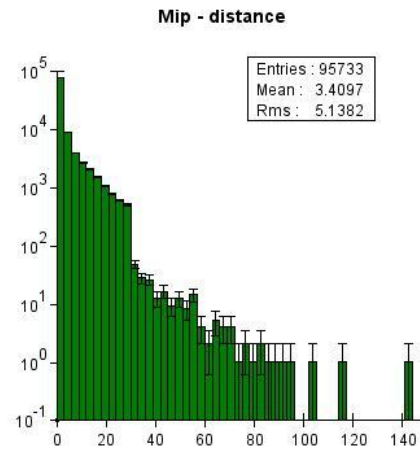
Type	rate
Mips	84.5%
Leftovers	14%
Other	1.5%

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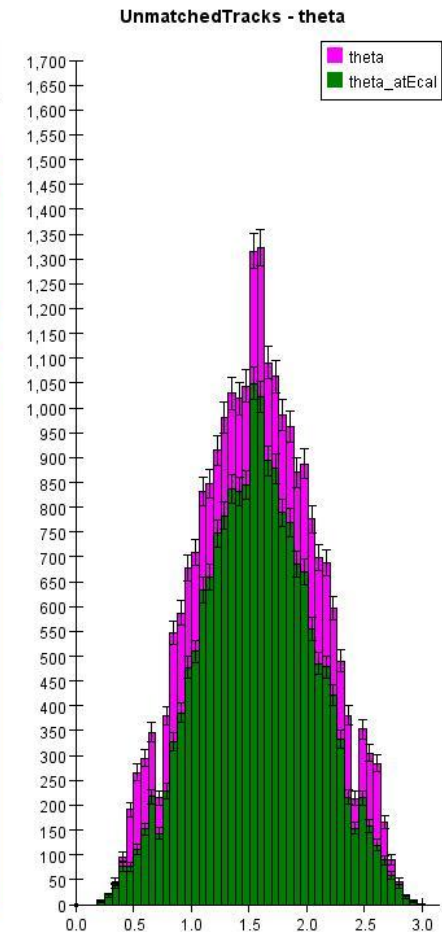
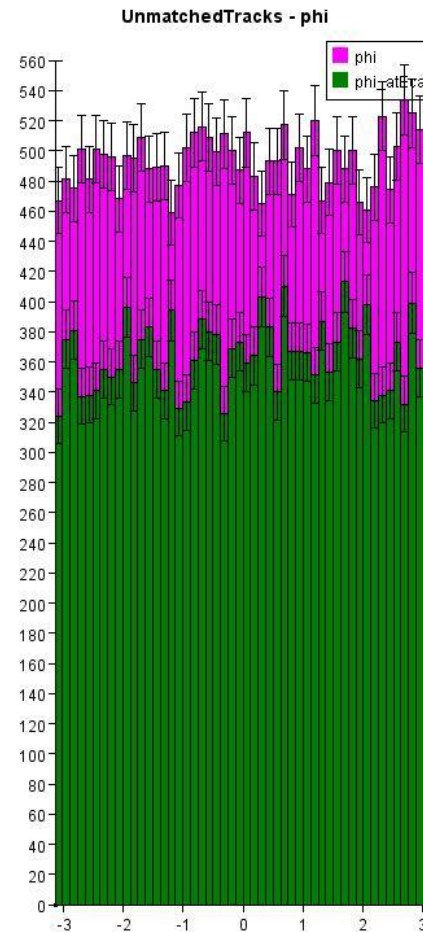
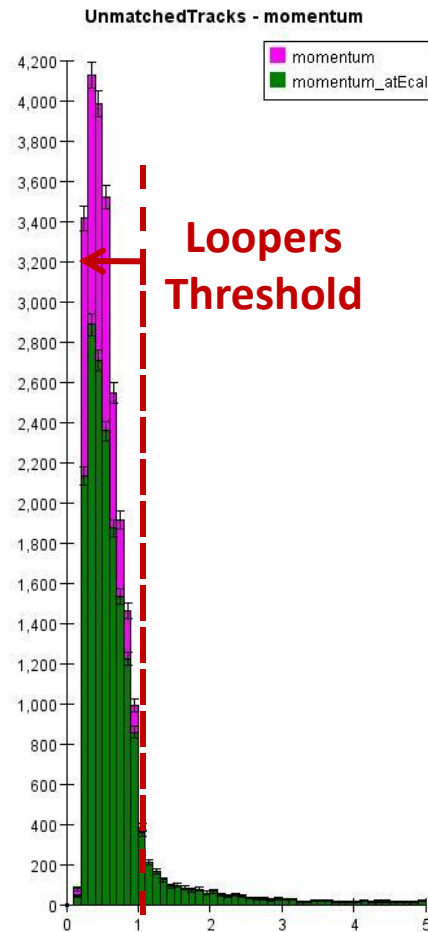


Track-Seed Matching: Unmatched tracks

Fraction of unmatched tracks:
18%

Fraction of unmatched tracks
with $p < 1$ GeV:
90%

Fraction of unmatched tracks
that reach Ecal:
75%



Track-Seed Matching: Unmatched tracks

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Fraction of unmatched tracks with $p < 1$ GeV:

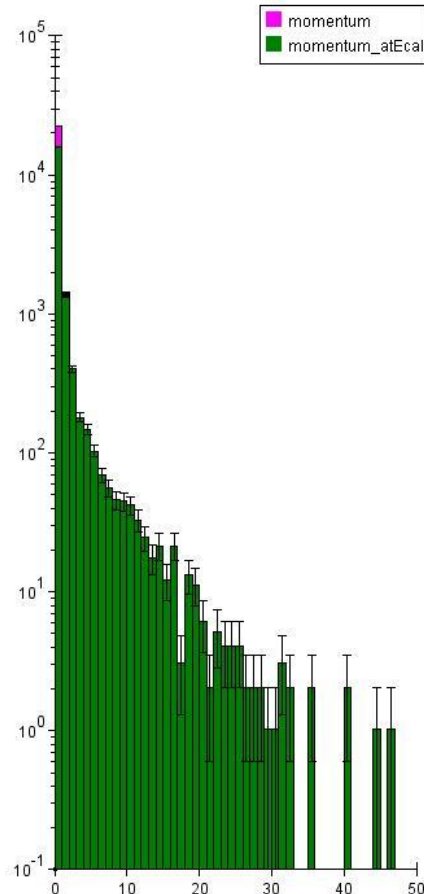
90%

Fraction of unmatched tracks that reach Ecal:

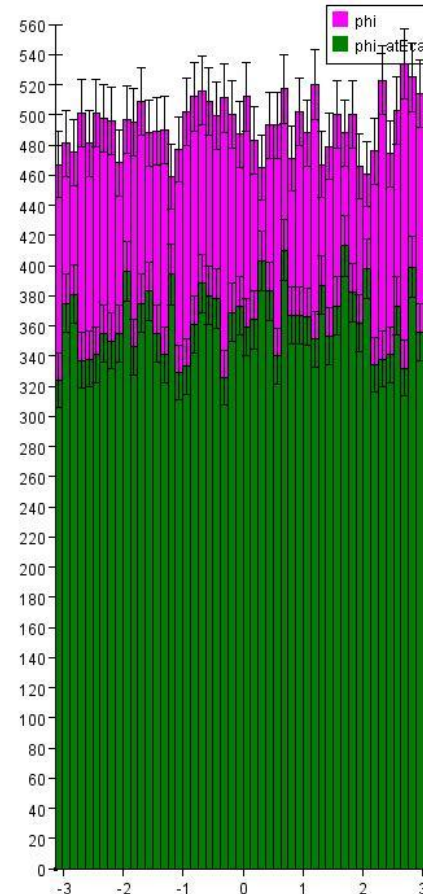
75%

Momentum tail up to 50 GeV

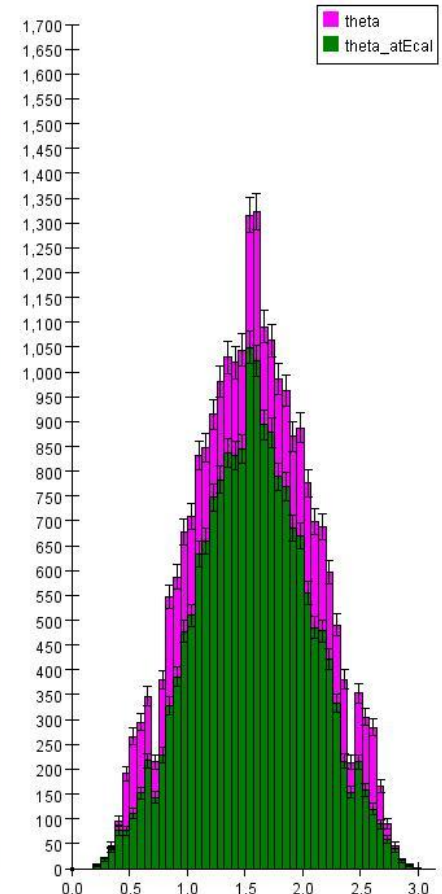
TrackSeedMatching.aida - UnmatchedTracks



UnmatchedTracks - phi



UnmatchedTracks - theta



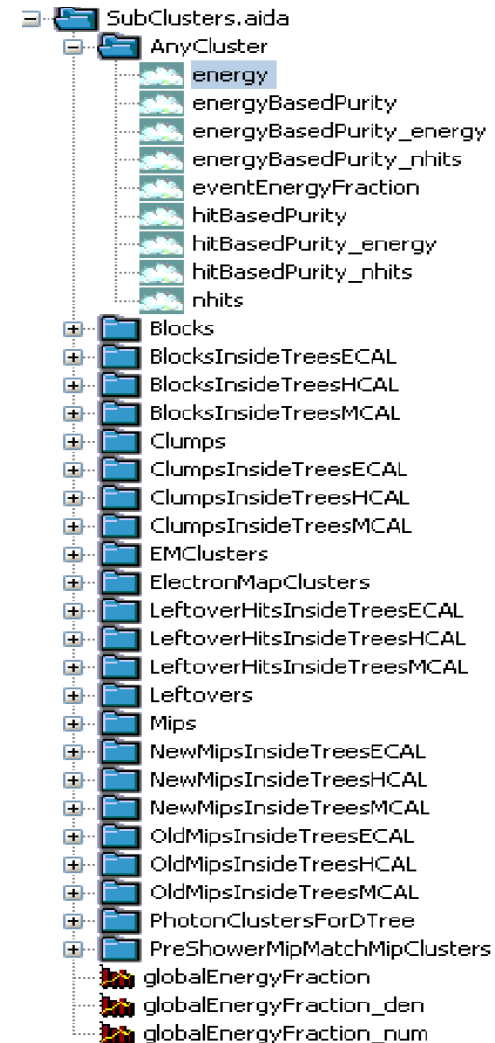
DTree Sub-Clusters

DTree Sub-Clusters: Definitions

- Plots are defined per cluster type.
- Energy fraction ignores energy from non-listed cluster types (missing muons):
 - The total energy is computed by summing up cluster energies from listed types.
- Defined a “per-event” energy fraction and a “global” energy fraction.
- Two definitions for purity:
 - Hit based purity

$$\# \text{ hits from dominant particle} / \# \text{ hits in cluster}$$
 - Energy based purity:

$$\text{Energy from dominant particle} / \text{cluster energy}$$



DTree Sub-Clusters: Energy contributions

Most of the energy goes to clumps:

47.5%

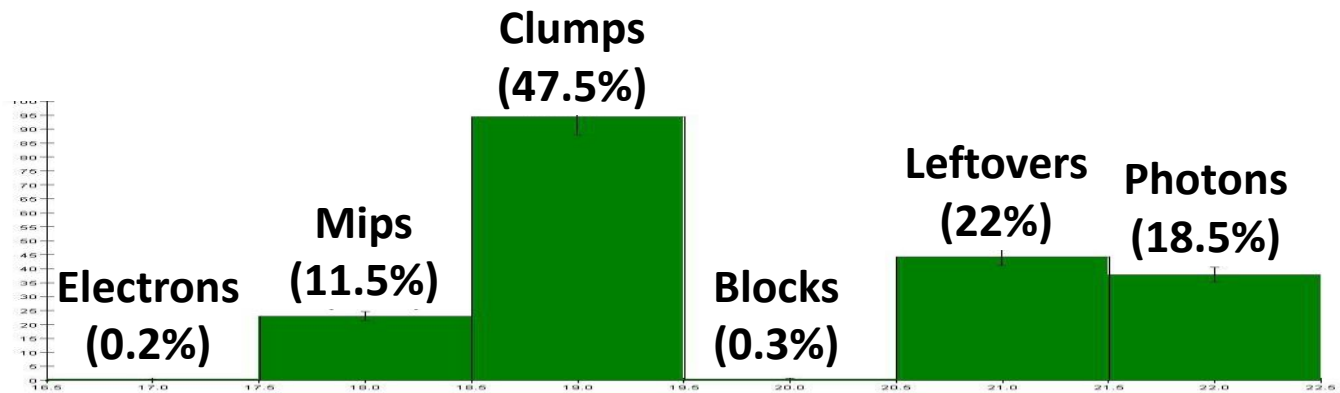
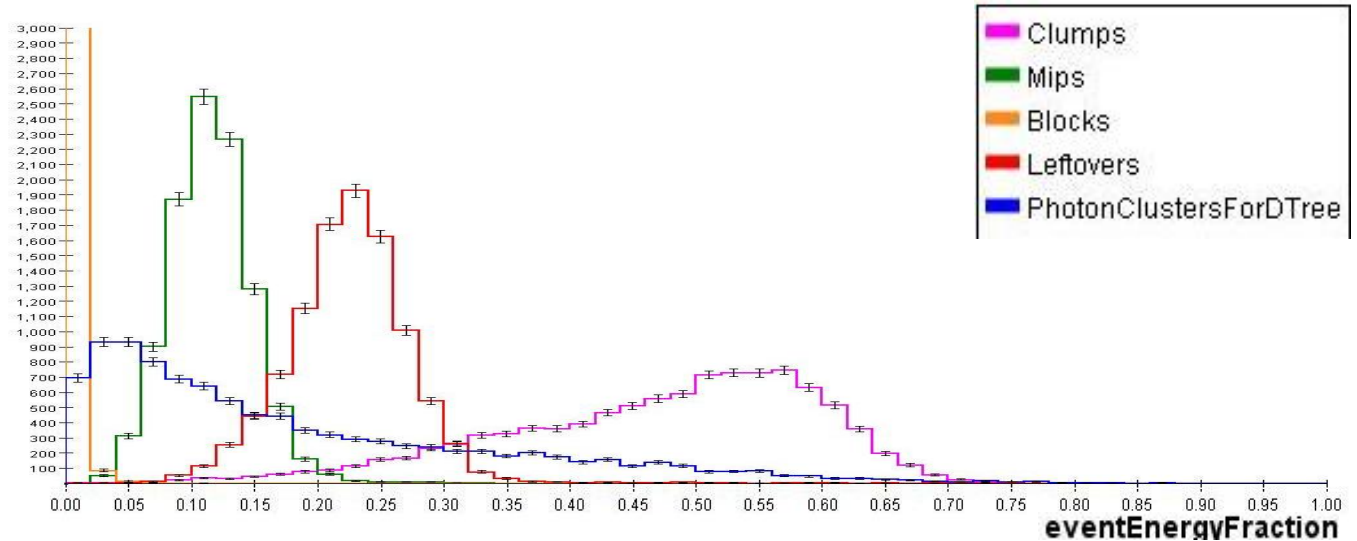
Significant amount of energy is shared:

22%

Blocks are rare:

0.3%

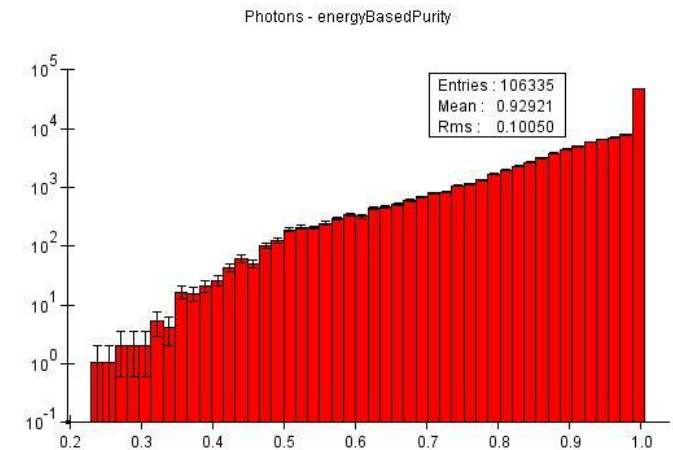
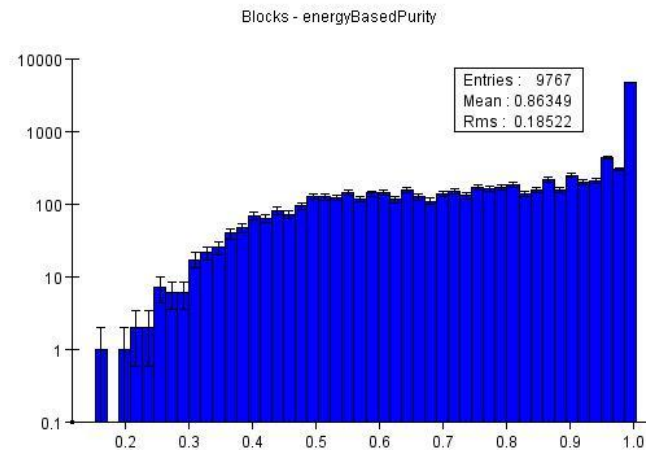
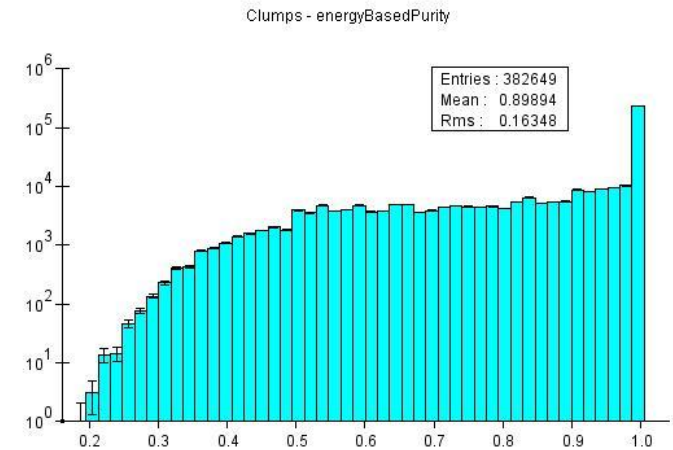
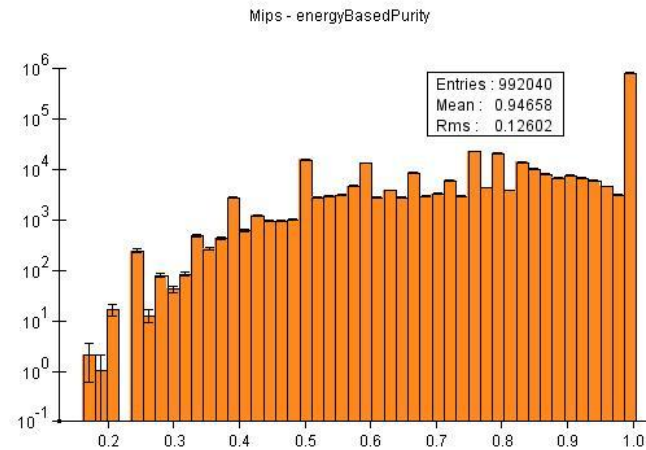
Photon distribution peaks at low fractions but have a large tail.



DTree Sub-Clusters: Purities

Showing energy based purities.

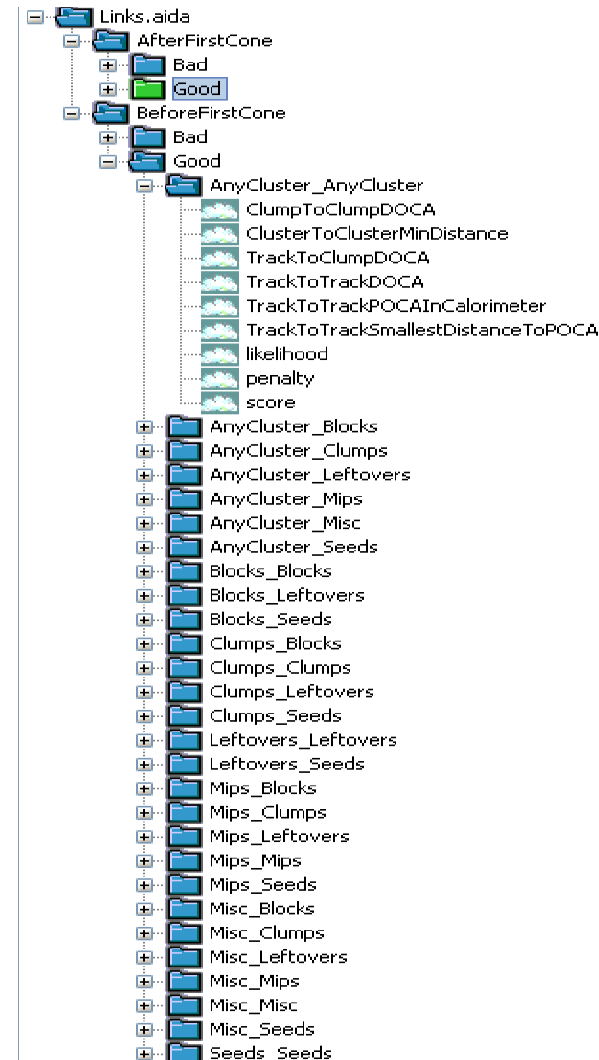
Type	Purity
Mips	95%
Clumps	90%
Blocks	86%
Photons	93%



Link Scoring

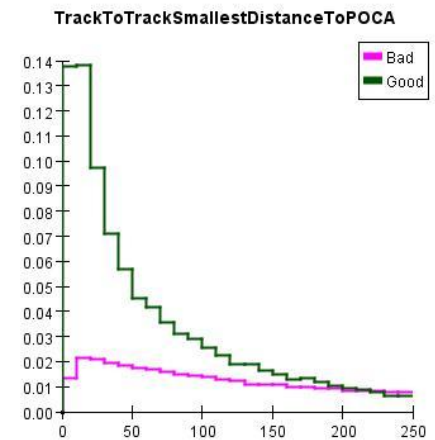
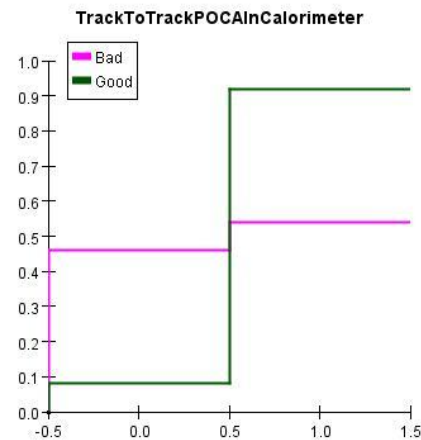
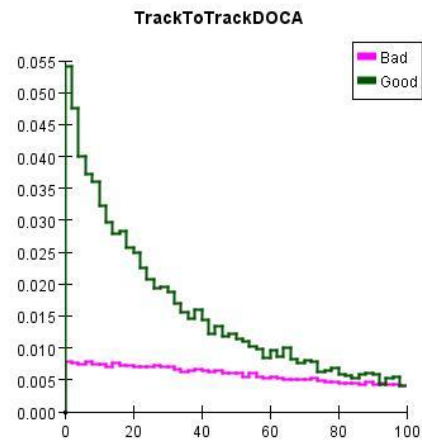
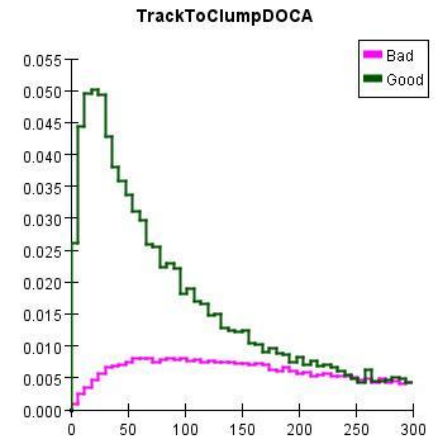
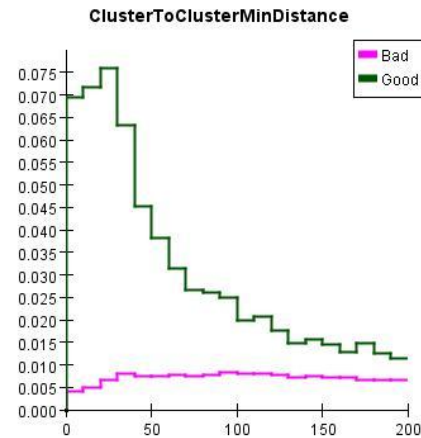
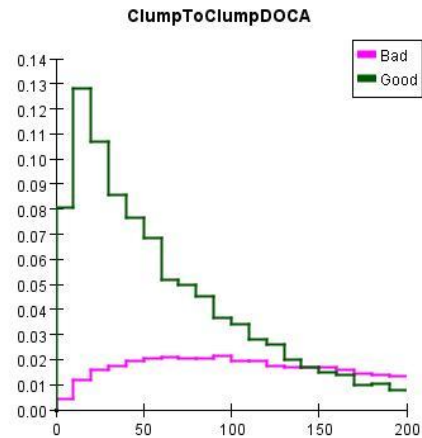
Link Scoring: Definitions

- Plots made per link type.
- A “good” link is a link where both sub-clusters have dominant energy contributions from the same MC particle.
- Made plots for variables used in likelihood:
 - To be compared with the plots in the Data-base.
- Some penalty factors are applied during scoring:
 - Penalty for belonging to separate DTree clusters: $0.8 * \cos(\text{angle})$
 - Penalty for proximity (not applied for mip-mip links): a/R^2
 - Other penalties depending on link type.
 - $\text{penalty} = \text{score} / \text{likelihood}$
- Clump-Clump likelihood is not used !?!
- Score only computed based on angle and proximity + other types of penalties.



Link Scoring: Variables

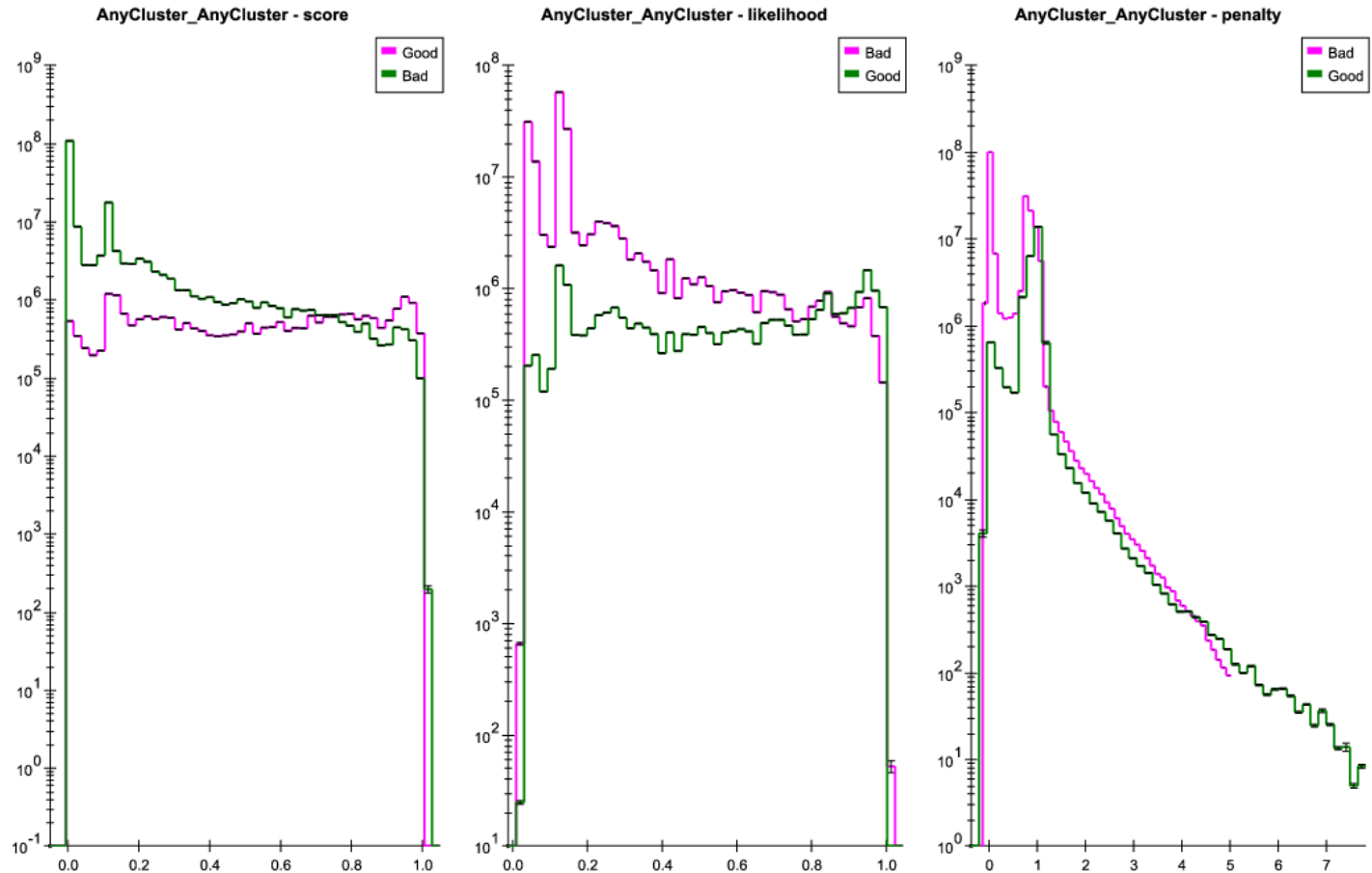
Only relevant links
enter each
distribution.



Link Scoring: Scores

All links

Scoring can be improved!

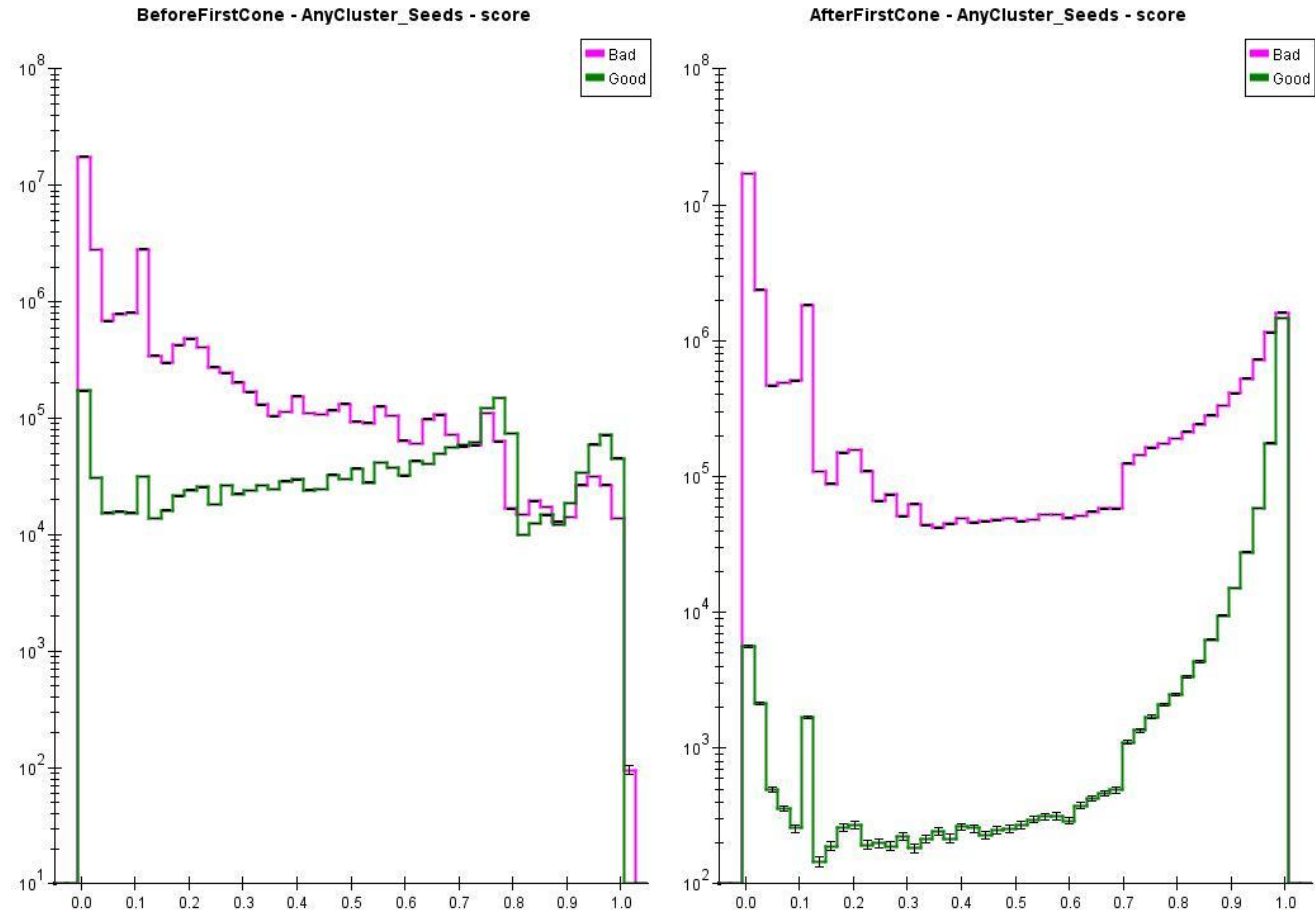


Link Scoring: Scores

Links to seed before/after cone

The cone algorithm is rather aggressive.

We already know that!!!



Next steps

Conclusion and next steps.

- Diagnostic tools for PFA performance quantification are ready.
- Benchmark performance on 500 GeV qqbar events with current PFA setup done.
 - Tacks-seed matching seems to perform OK:
 - Most of unmatched tracks are below 1 GeV.
 - DTree re-clustering performance in terms of purities:
 - Need to know if 22% of leftover hits is problematic or not for the PFA.
 - Need to know if 90% purity in sub-clusters is enough for the PFA.
 - Looking at performance for single pions as well.
- Next steps:
 - Link scoring needs to be given a “quick” look at:
 - Need a better definition for a “good” link: no great ideas yet!
 - Revisit likelihood calibration: now done using a different DTree re-clustering algorithm than the one used in the PFA.
 - Should not be a show-stopper at this point.
 - Start implementing algorithm changes as described in the previous meeting.