Track-Particle Matching Considerations

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Introduction

- □ While studying track resolutions and efficiencies, I noticed that some fraction of reconstructed tracks did not have an associated particle in the ReconstructedChargedParticlesAssociation branch why?
- After some conversation, learned that the algorithm which matches reconstructed tracks with particles (and fills R.C.P.Associations branch) includes an explicit requirement that the track/particle relative momentum be within 10%

□ Issue #450 was opened to address this: <u>https://github.com/eic/EICrecon/issues/450</u>

- Proposal is to effectively remove this relative momentum criteria from the conditions for track-particle matching and make the association purely geometric (set the momentum difference so high as to be negated)
- Following slides are a very quick summary study using reconstructed Pythia-6 files (22.11.3, brycecanyon, 18x275, 1 < Q2 < 10)</p>
- Also document the presence of 'duplicate tracks' two reconstructed tracks with nearly identical momenta

Track-Particle Matching Algorithms

const auto p_mag = std::hypot(p.x, p.y, p.z); const auto p_phi = std::atan2(p.y, p.x); const auto p_eta = std::atanh(p.z / p_mag); const double dp_rel = std::abs((edm4eic::magnitude(mom) - p_mag) / p_mag); // check the tolerance for sin(dphi/2) to avoid the hemisphere problem and allow // for phi rollovers const double dsphi = std::abs(sin(0.5 * (edm4eic::angleAzimuthal(mom) - p_phi))); const double deta = std::abs((edm4eic::eta(mom) - p_eta));

if (is_matching) {

const double delta =

std::hypot(dp_rel / m_cfg.momentumRelativeTolerance, deta / m_cfg.etaTolerance, dsphi / sinPhiOver2Tolerance);

if (delta < best_delta) {

best_match = ip;

best_delta = delta;

m_log->trace(" Is the best match now");

 Default track-particle matching algorithm for ReconstructedChargedParticlesAssociation branch found in: <u>https://github.com/eic/EICrecon/blob/main/src/algorithms</u> <u>/tracking/ParticlesWithTruthPID.cpp</u>

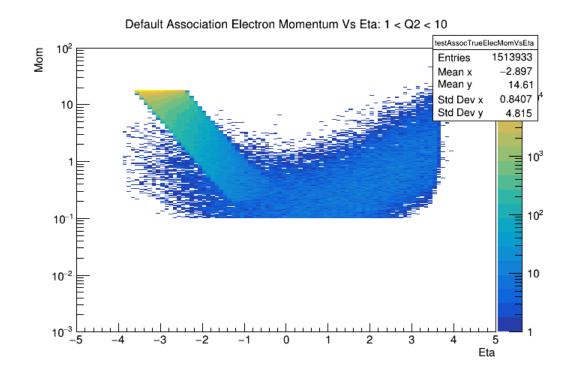
For each track, loop through all particles within certain deta, dephi, and relative dp (0.2, sin(0.5*0.03), and 0.10) – match is particle with closest dR = hypot(dp, deta, dphi)

Issue: Relative momentum difference is used in matching criteria – tracks with a poorly reconstructed momentum (>10%) will not be paired with their particle, even if geo match is close. Poor momentum resolution instead registers as an inefficiency

Look at removing momentum difference as a matching criteria

□ Also look at tolerance of delta phi cut

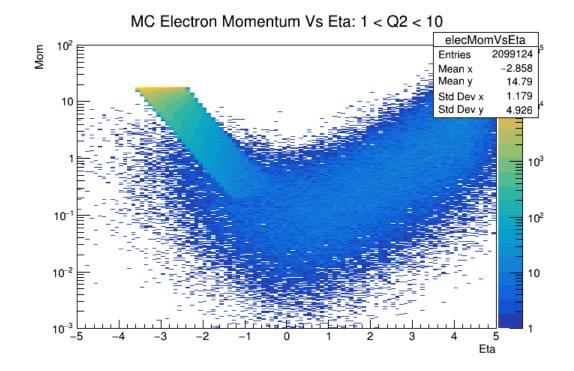
Matched Electrons: True Mom/Eta



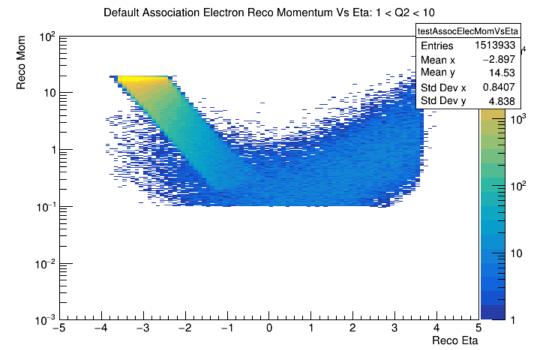
- The above plot shows the true momentum / eta of the track (ie that of the particle the track is matched to) and ratio of this plot to that on the right would give efficiency
- Next, look at momentum / eta of the reconstructed track itself

 Look at electron momentum vs pseudorapidity for pure MC (below) and reconstructed tracks with an associated particle (left)

□ True momentum and eta are plotted



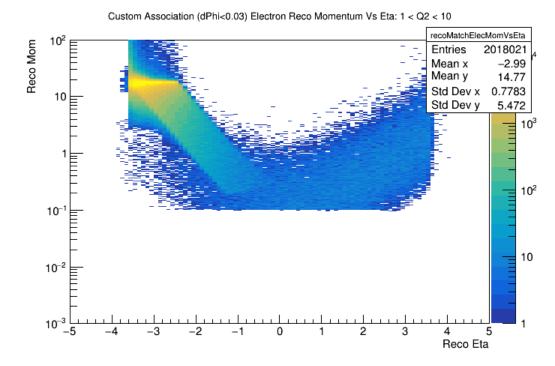
Matched Electrons: Reco Mom/Eta



- Result of removing the momentum requirement in the trackparticle matching can be seen on the right – significant spread, especially around the electron peak
- □ These tracks are still geometrically matched to a particle
- Ability to 'see' where momentum resolution goes bad will be important

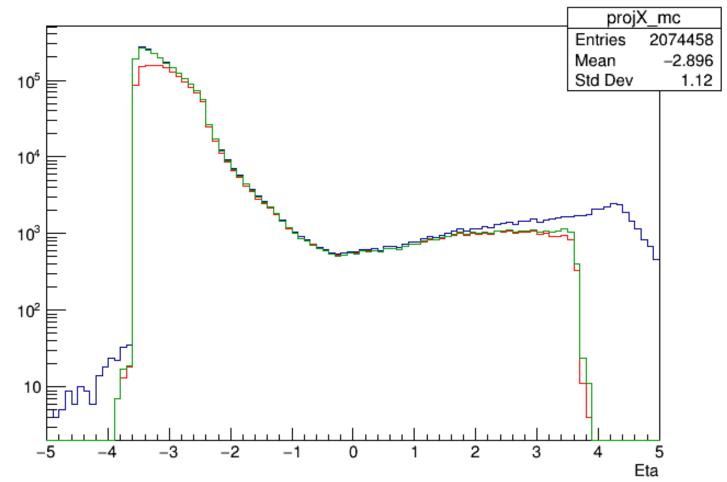
Mild momentum spread is seen around the electron peak when looking at the reconstructed momentum of matched tracks for the default track-particle matching algo (left)

□ Allowed momentum spread is capped at 10%



Electron Efficiency Comparison: Delta Phi < 0.03

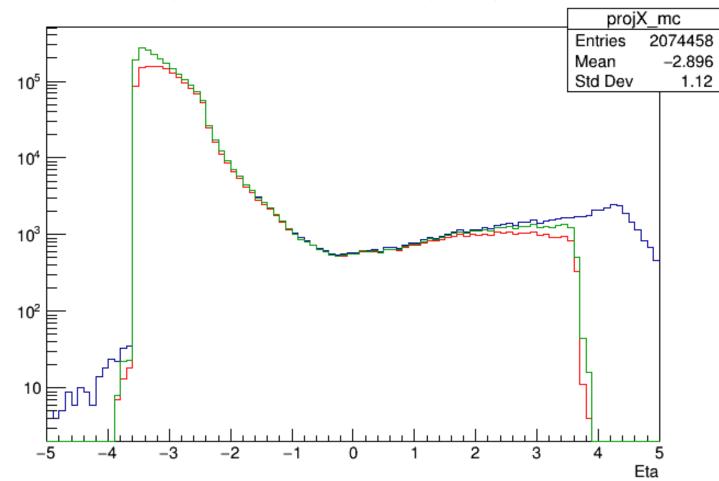
Electron Spectrum: 1 < Q2 < 10: Blue=MC Red=Standard (dPhi < 0.03) Green=Modified



- Project previous plots onto the pseudorapidity axis to see how the trackparticle matching algorithms perform
- True (particle) eta is plotted for matched tracks, but bin migration in eta will be small
- Blue is pure MC, Red is the default matching algorithm which includes the relative momentum cut of 10%, and green is the modified matching algorithm without the relative momentum cut
- Default matching algorithm misses tracks at high |eta|
- Modified algo picks up the unmatched tracks in the electron peak region 6

Electron Efficiency Comparison: Delta Phi < 0.03

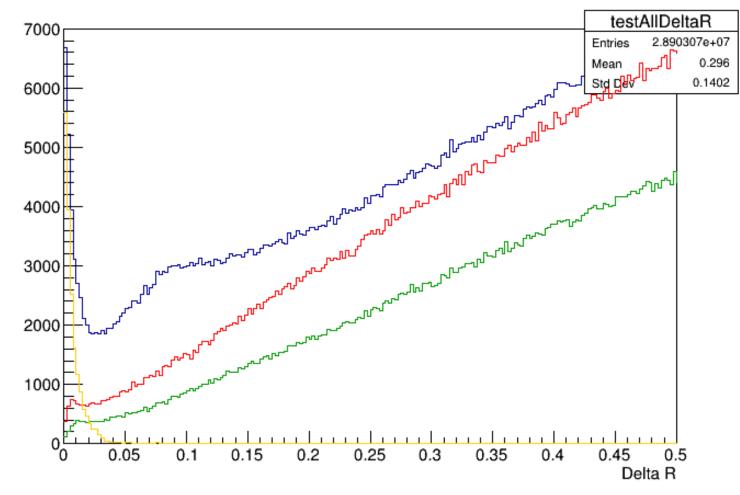
Electron Spectrum: 1 < Q2 < 10: Blue=MC Red=Standard (dPhi < 0.10) Green=Modified



- Default matching algorithm uses a phi tolerance of 0.03 radians and requires track and particle to be within Sin(0.5*0.03) of each other
- This seemed a bit tight, so loosen the tolerance to 0.1 radians in the modified matching algorithm
- See further recovery of matched tracks, especially in eta > 1.5 region

Duplicate Tracks

Pairwise Distances: Blue - All Reco Tracks, Red - MC Particles, Green - Associated Tracks, Yellow - Reco Tracks Same Particle



- Found that some tracks were not matched to a particle by the default algorithm even though all criteria were satisfied
- Discovered these tracks had basically identical momentum, eta, phi as another in the same event
- Loop through all reconstructed tracks and calculate hypot(delta eta, delta phi)
 between each pair –blue curve). See a spike at ~0 Delta R
- Red curve shows the same for all (charged) MC particles and green for all tracks which have a particle associated with them as found by the default matching algo – no spike at zero found
- Yellow curve are track pairs which point to the same particle

Want to raise awareness of this feature

Conclusion

Current track-particle matching algorithm that fills ReconstructedChargedParticlesAssociation branch requires track and particle to have a relative momentum difference < 10%</p>

□ This requirement will cause tracks which are geometrically associated with particles, but with poorly reconstructed momentum to be considered unmatched – confuse efficiency and momentum resolution

Proposal: Remove relative momentum condition from matching – also loosen delta phi tolerance from 0.03 to 0.10

Also discovered some fraction of tracks seem to be duplicates – having nearly the same momentum, eta, phi. This is probably to be expected at some level, but analyzers need to be aware so they do not double count

Duplicate tracks can be avoided by requiring a match to a particle