

Pipeline

GEMini/GEMaxis.cpp

**Identify
Clusters**

Identitfy where and
how many clusters
there are



GEMini/GEMaxis.cpp

**Position
Reconstruction
from Clustters**

Reconstruct where the
position of the electron
from the cluster



GEMTrack.cpp

**Track
Reconstruction**

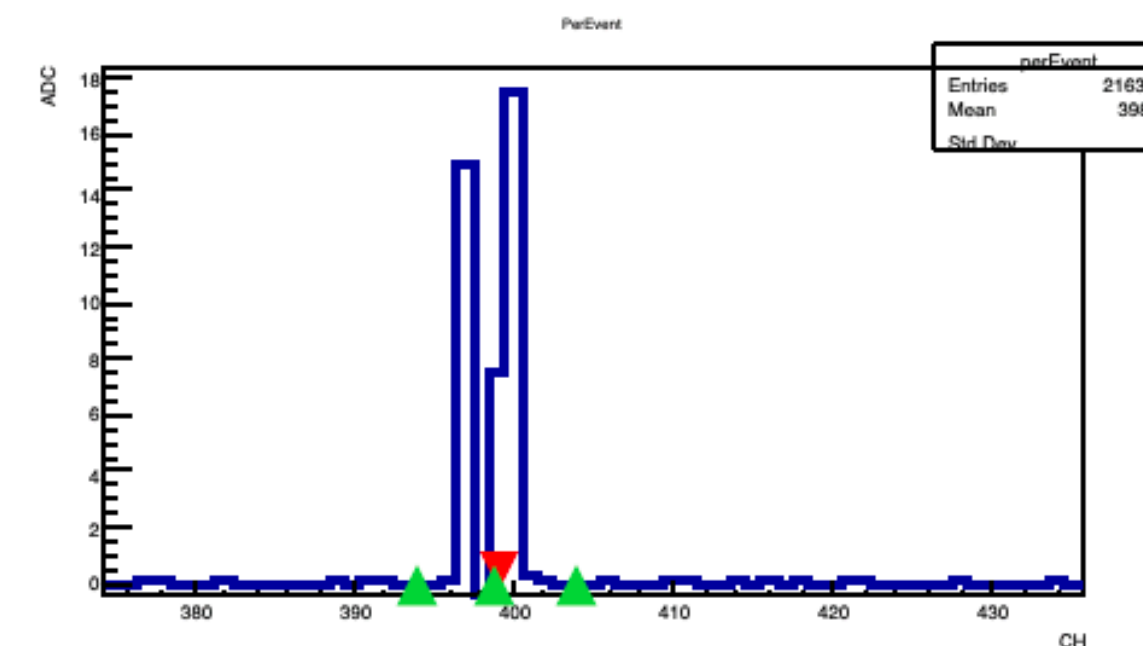
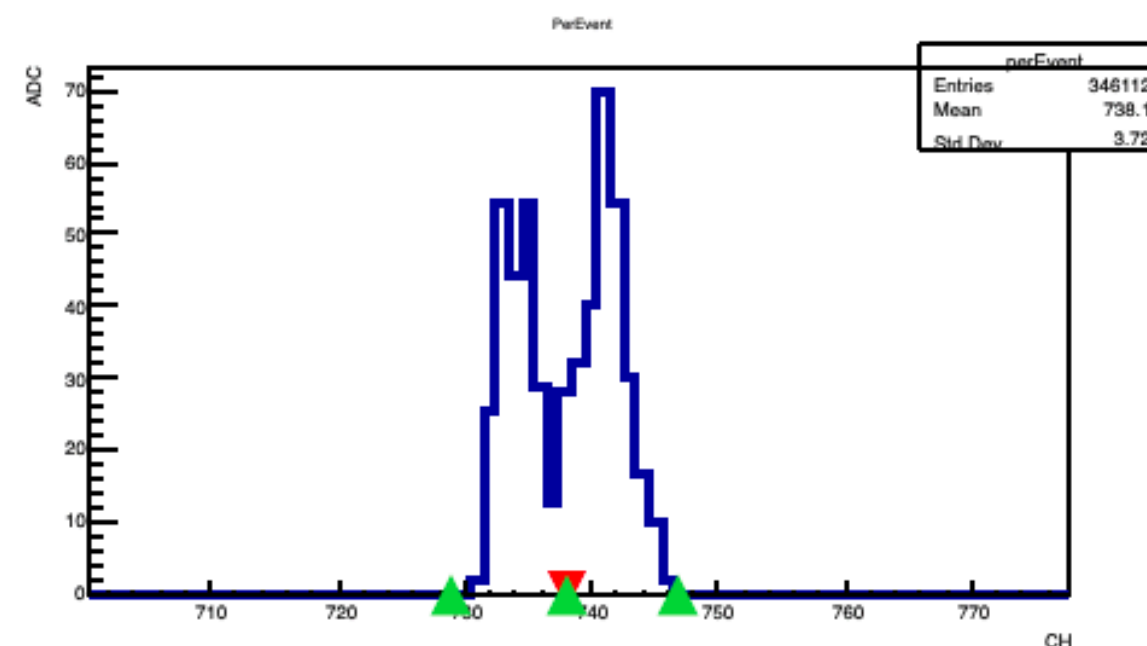
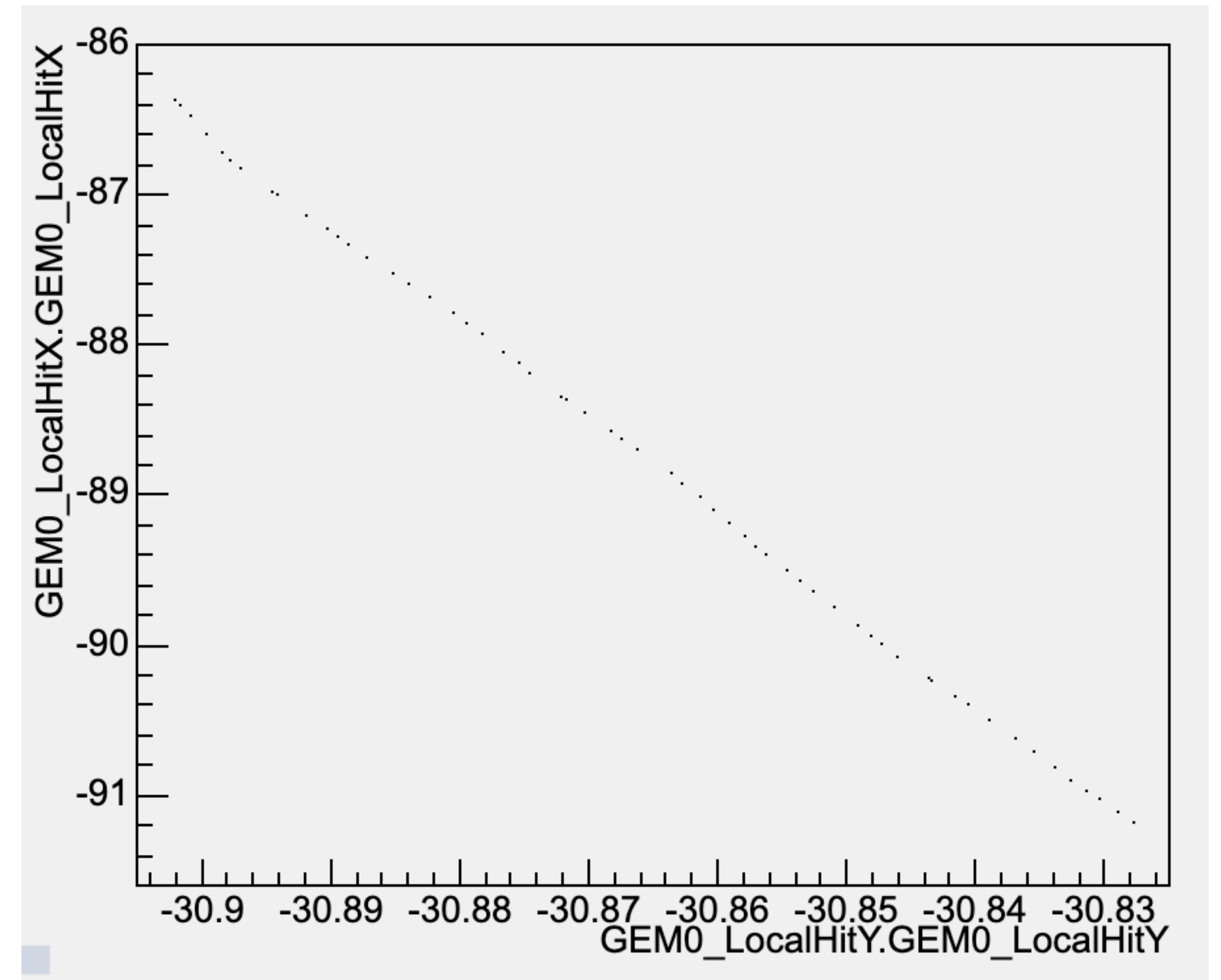
From all cluster
positions, deduce
which track causes
which clusters

Cluster Identification

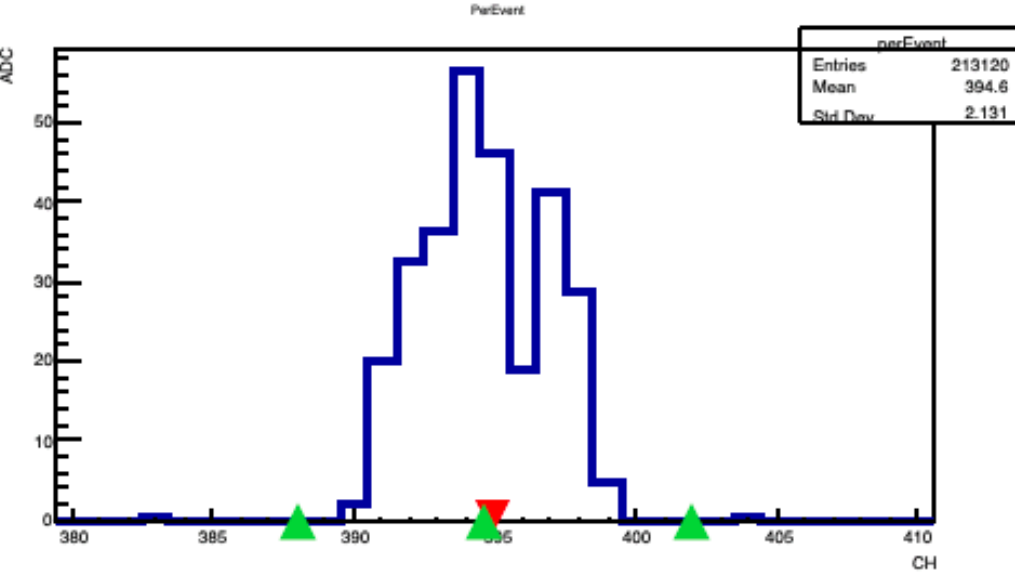
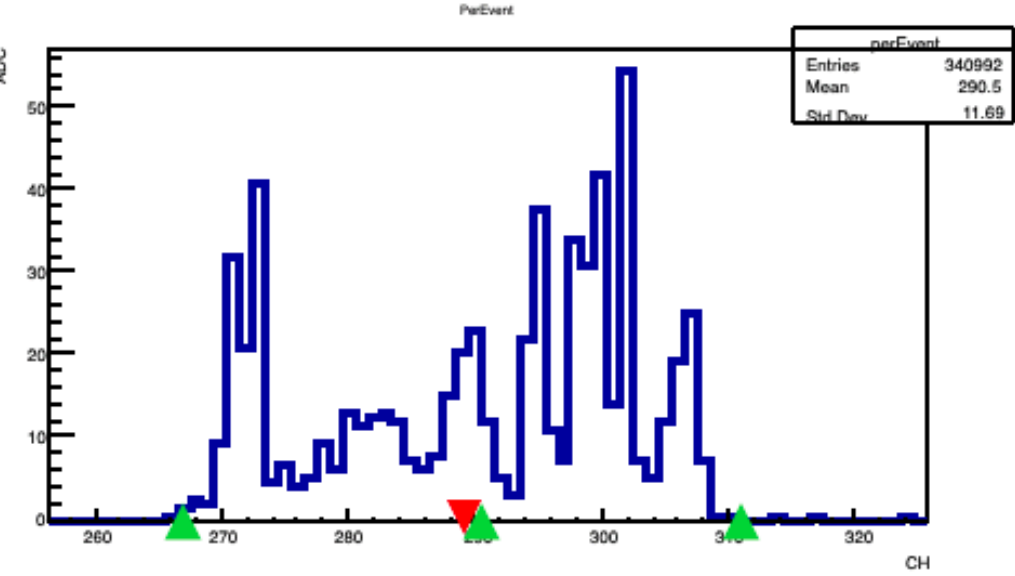
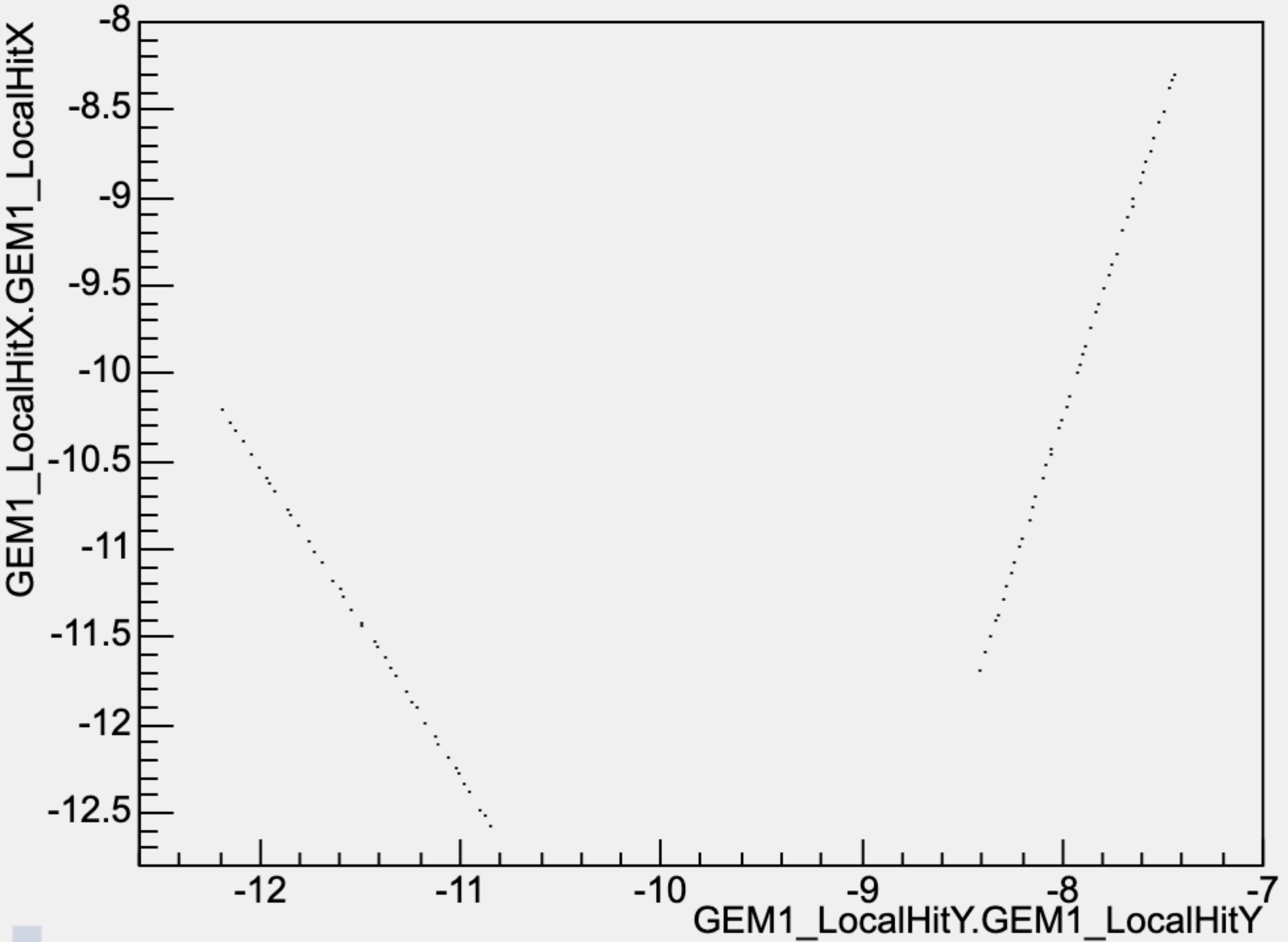
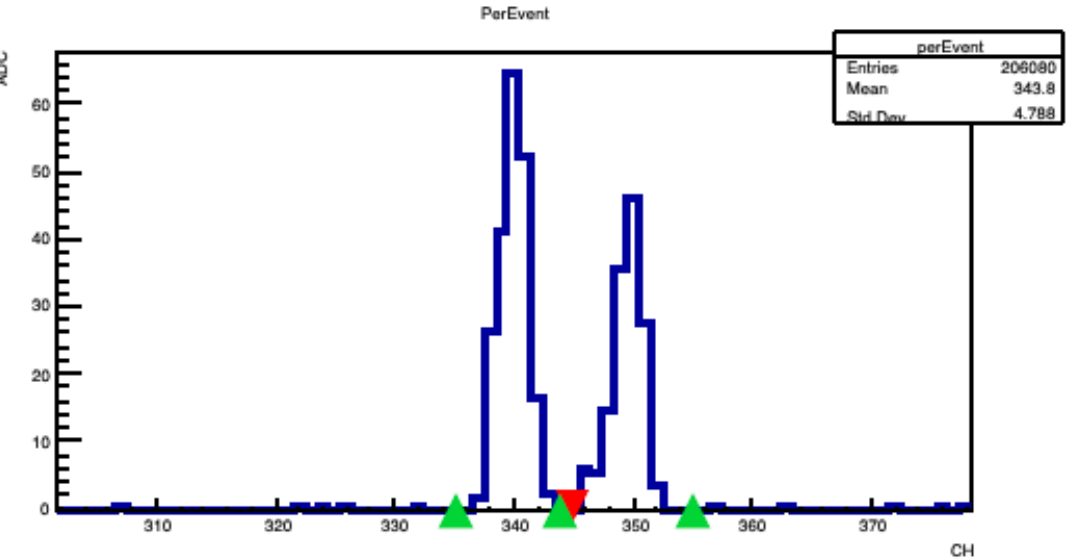
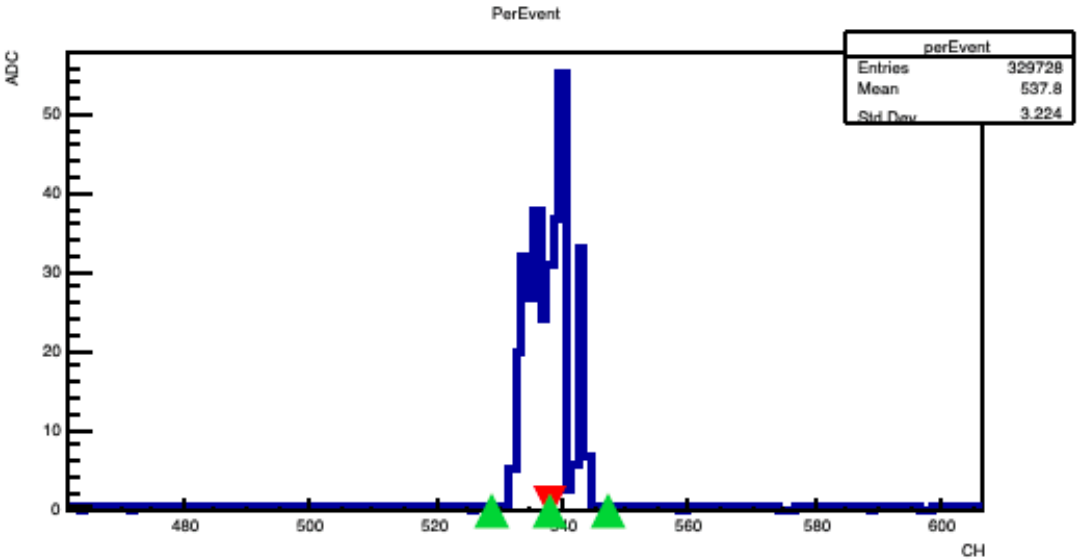
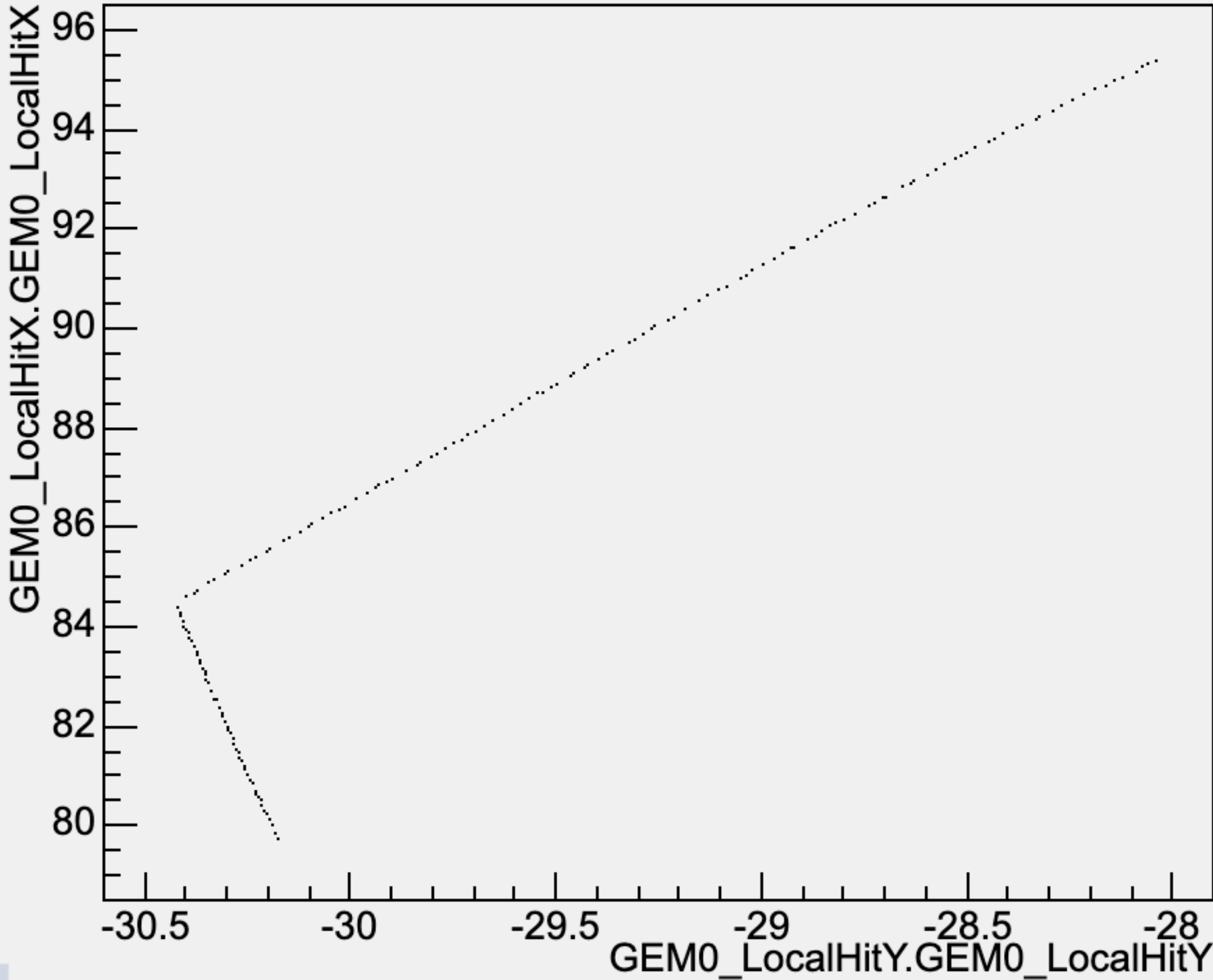
Clusters can be hard to identify at high angles

High angle clusters show multiple peaks

Stochastic probabilities make them very randomized



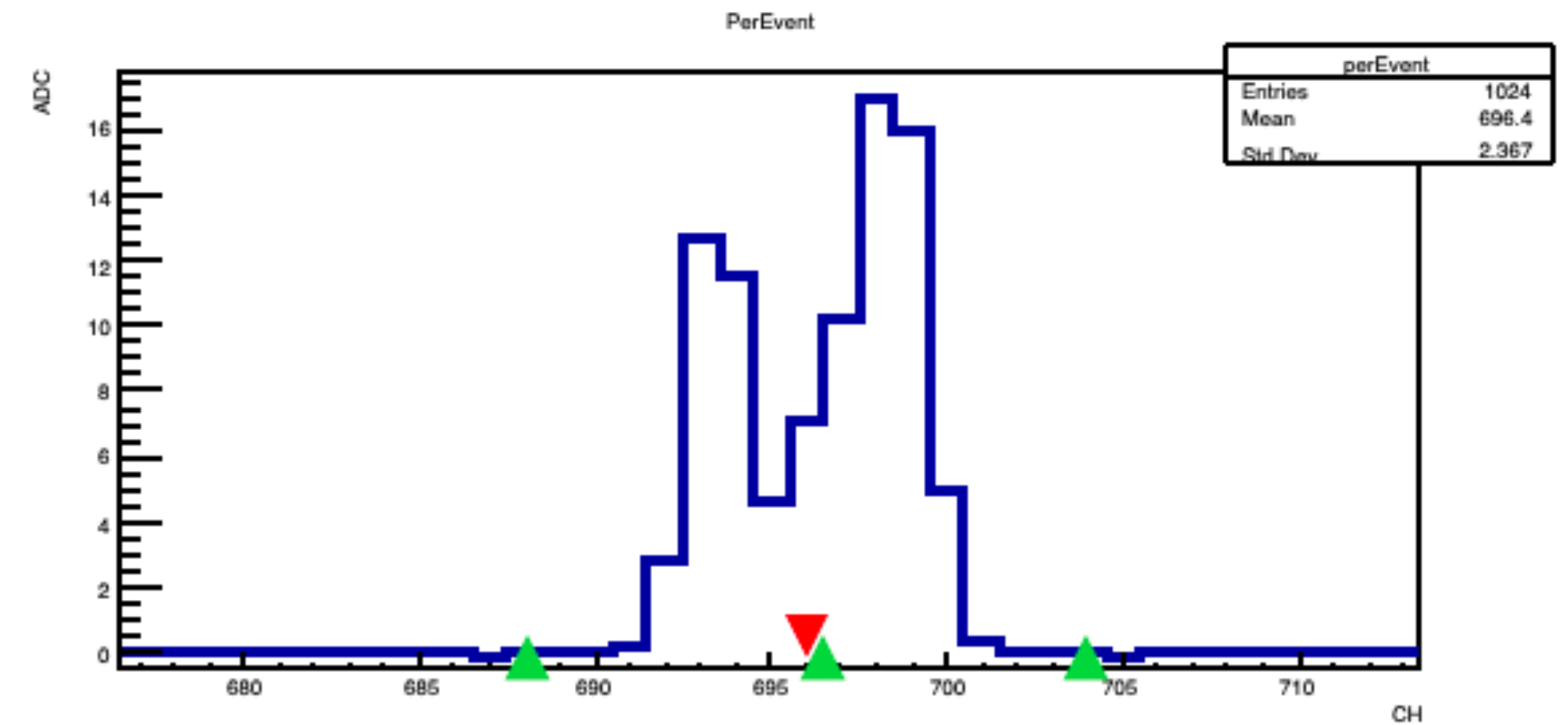
You would think this these are 2 tracks, but is actually one



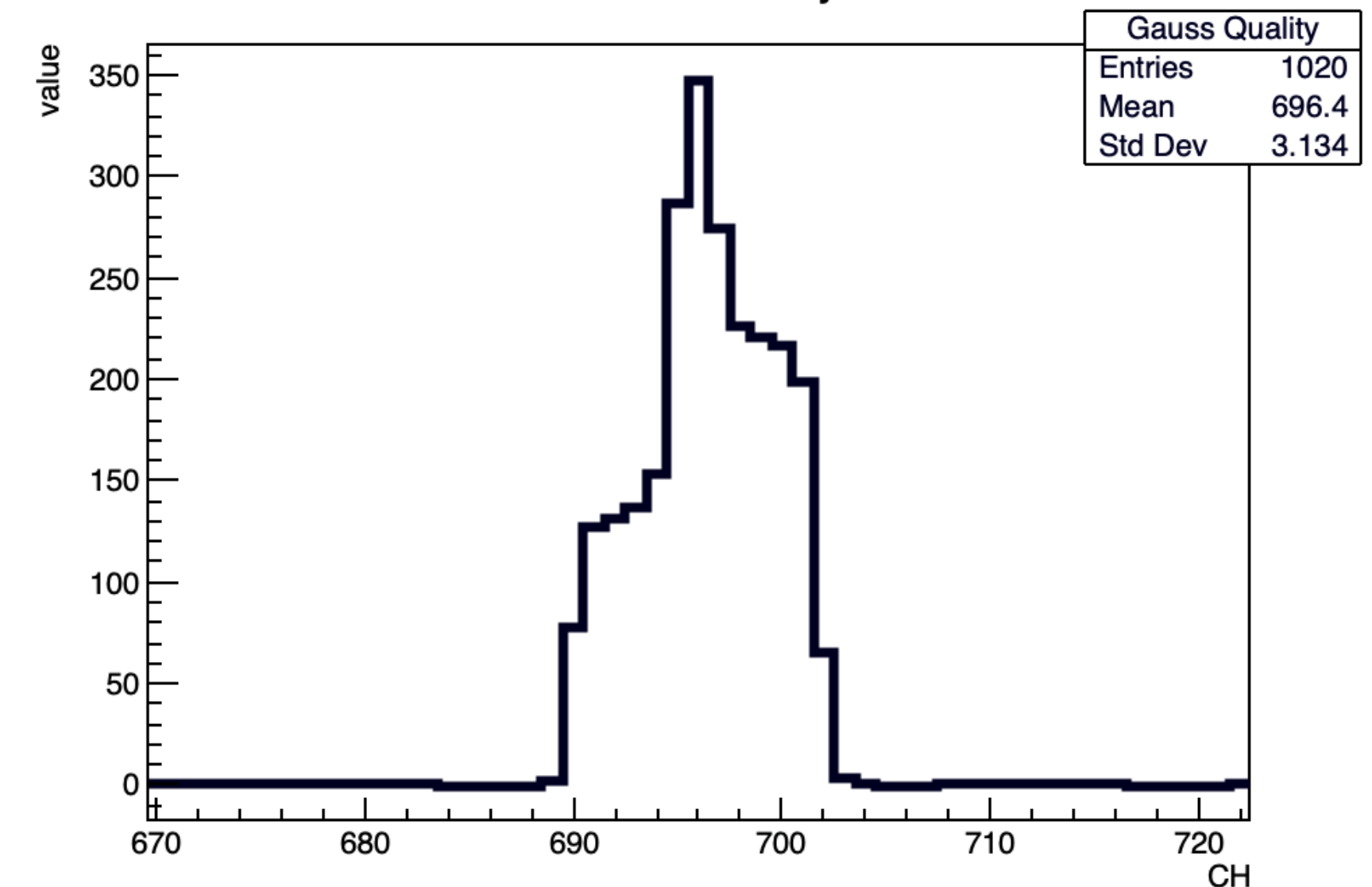
Cluster Identification Method (Previously Implemented)

A gaussian window is overlayed and “slided” across the channels which a chi2 test being done at each point to produce a “quality” factor

The higher the quality factor the more likely the there is a cluster there at that point



Gauss Quality



Cluster Identification

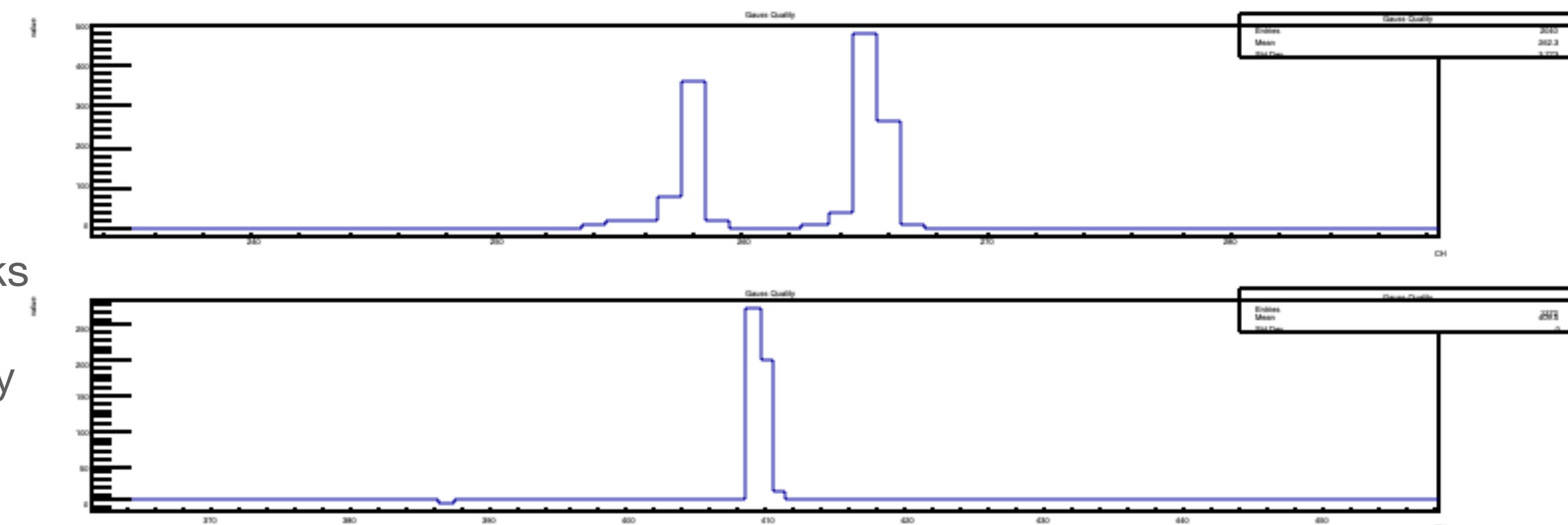
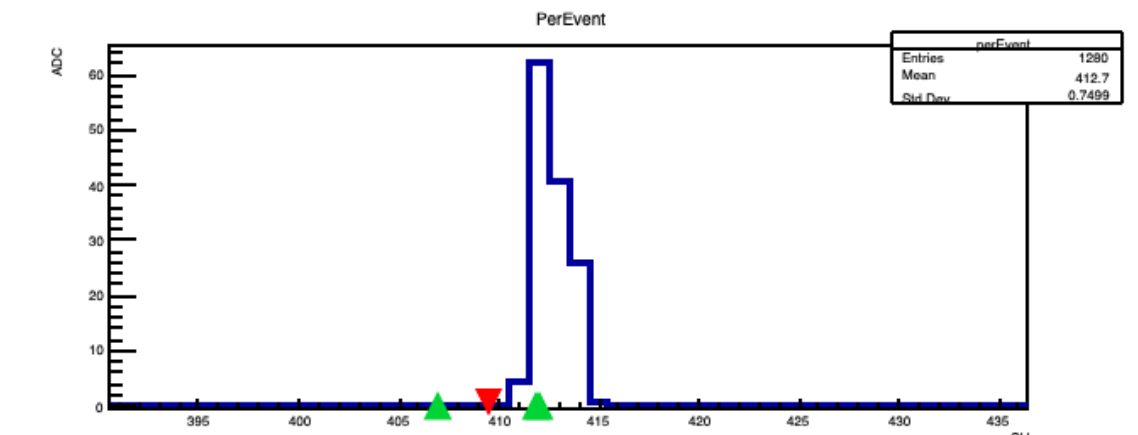
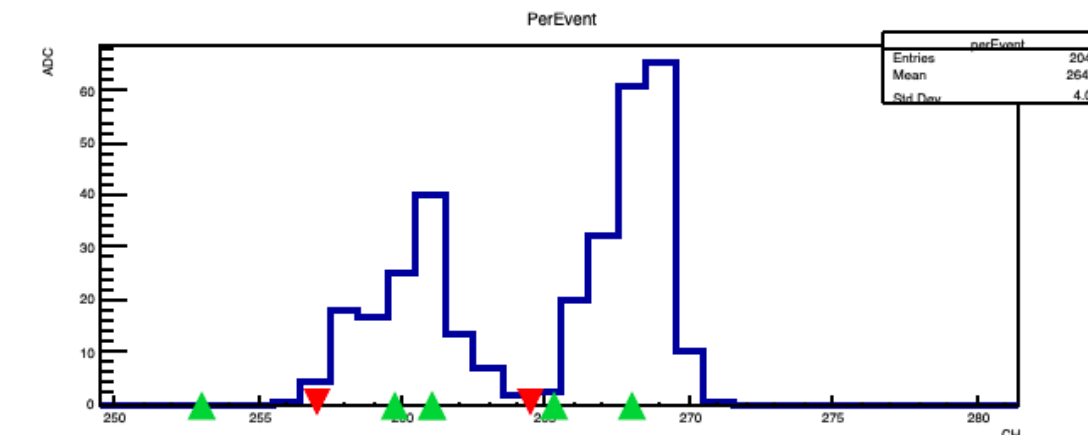
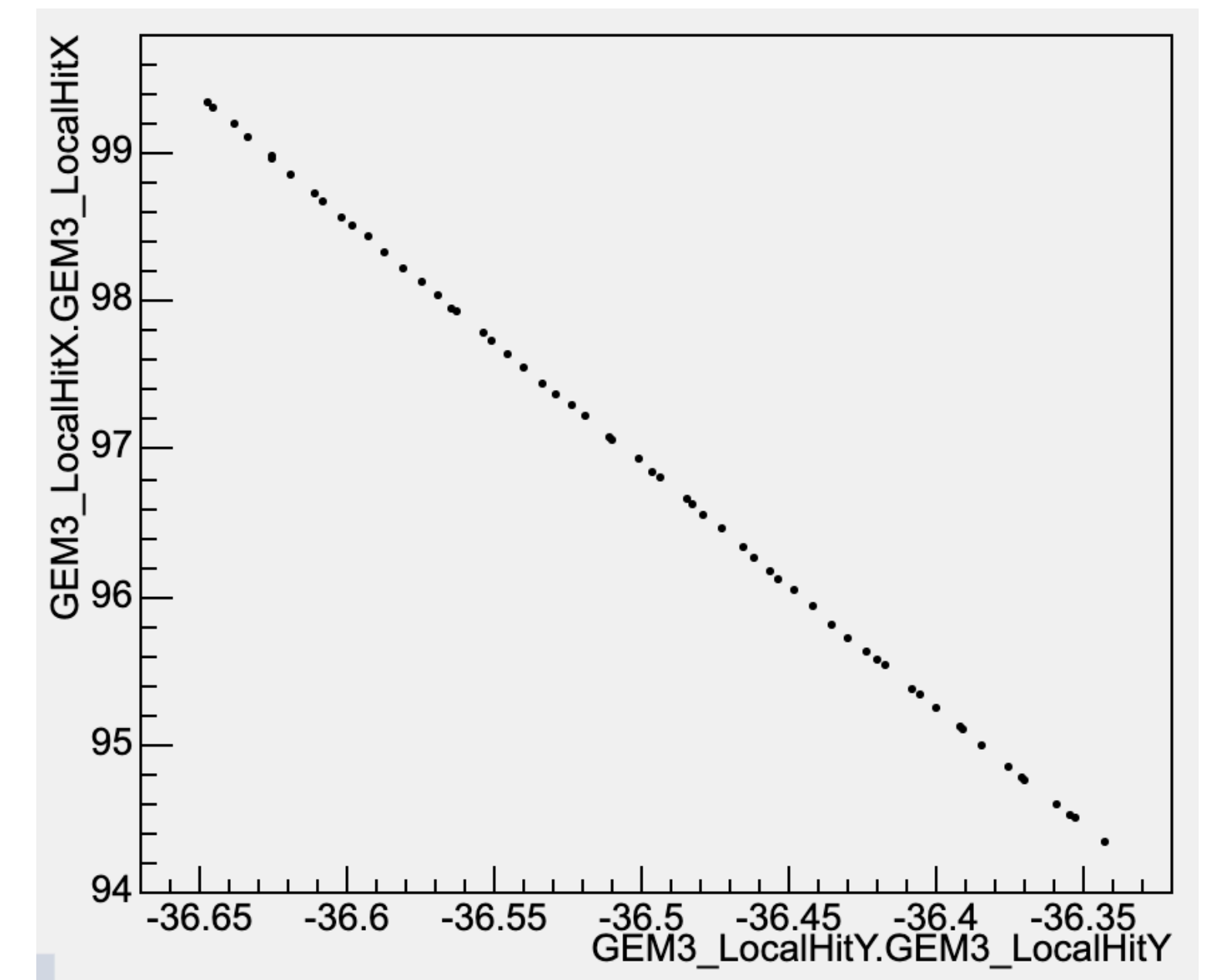
Method (Previously Implemented) continued

A peak finding algorithm then finds local peaks in the gaussian quality using a threshold value

However, this may result in misidentifying the same cluster as multiple clusters

This is because there can be multiple gaussian side by side in a single cluster if the electron enters at a high angles

The algorithm thinks there are multiple tracks despite only having one



Cluster Identification

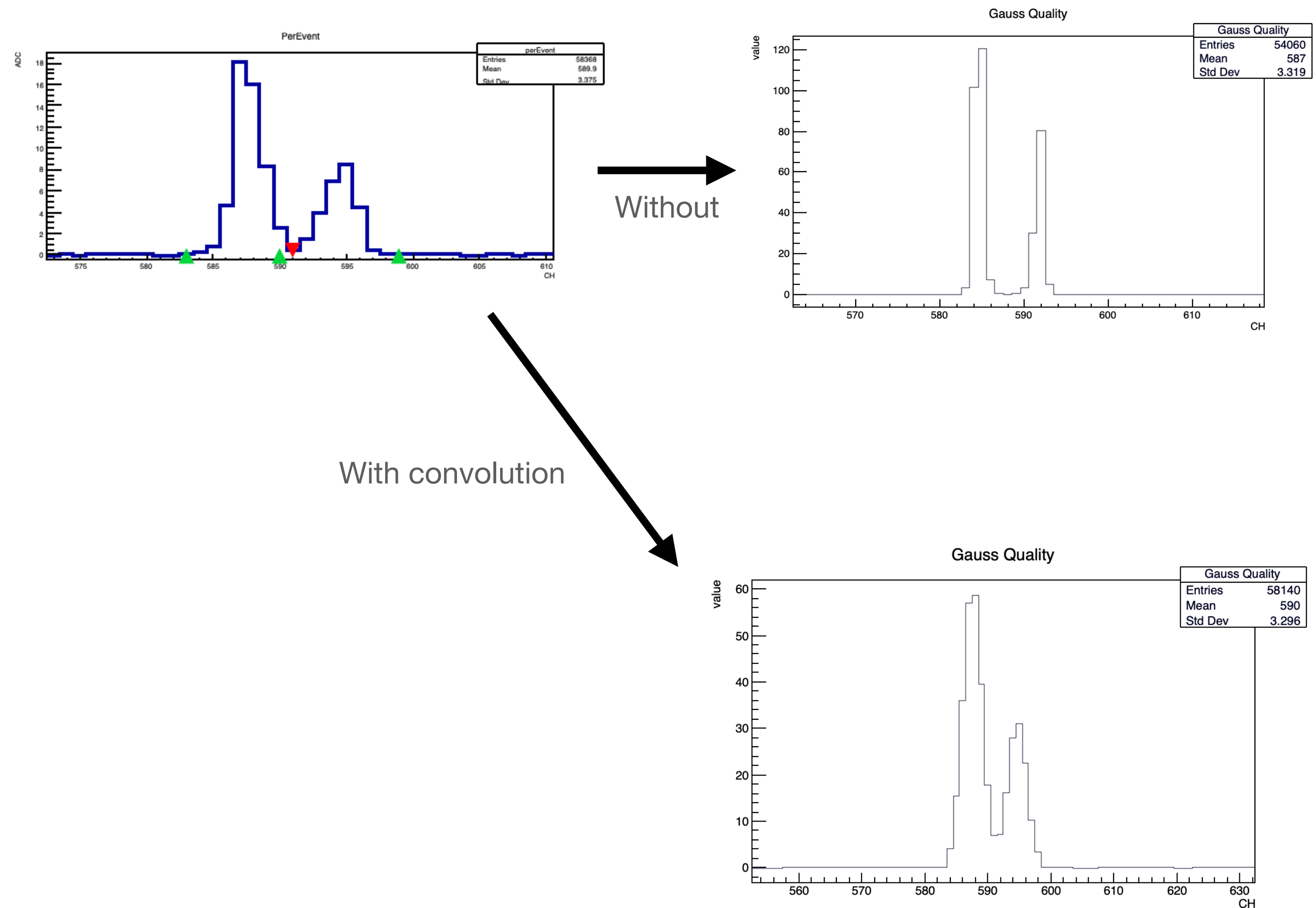
Method (improved)

Convolute the “quality” factors with a pulse function so that the dip between nearby peaks dont go below the threshold

The width of the pulse should be characteristic to the inter-event timing

For now, set to gaussian of $1.5 * 400\mu\text{m}$ sigma (from observation)

Will do more in-depth simulation of finding out what width of gaussian works best



Position Reconstruction

Using Averaging

Take weighted average of histograms

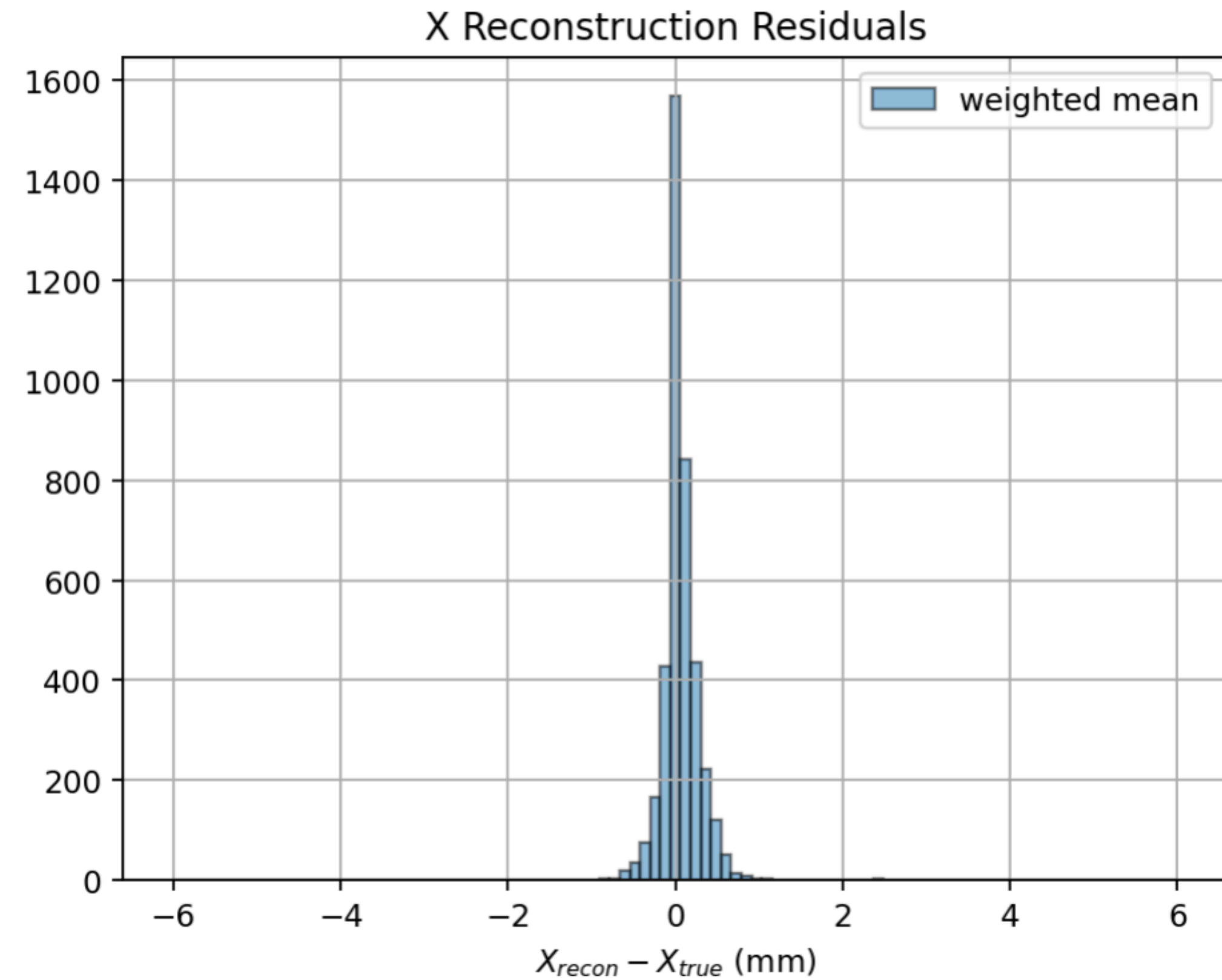
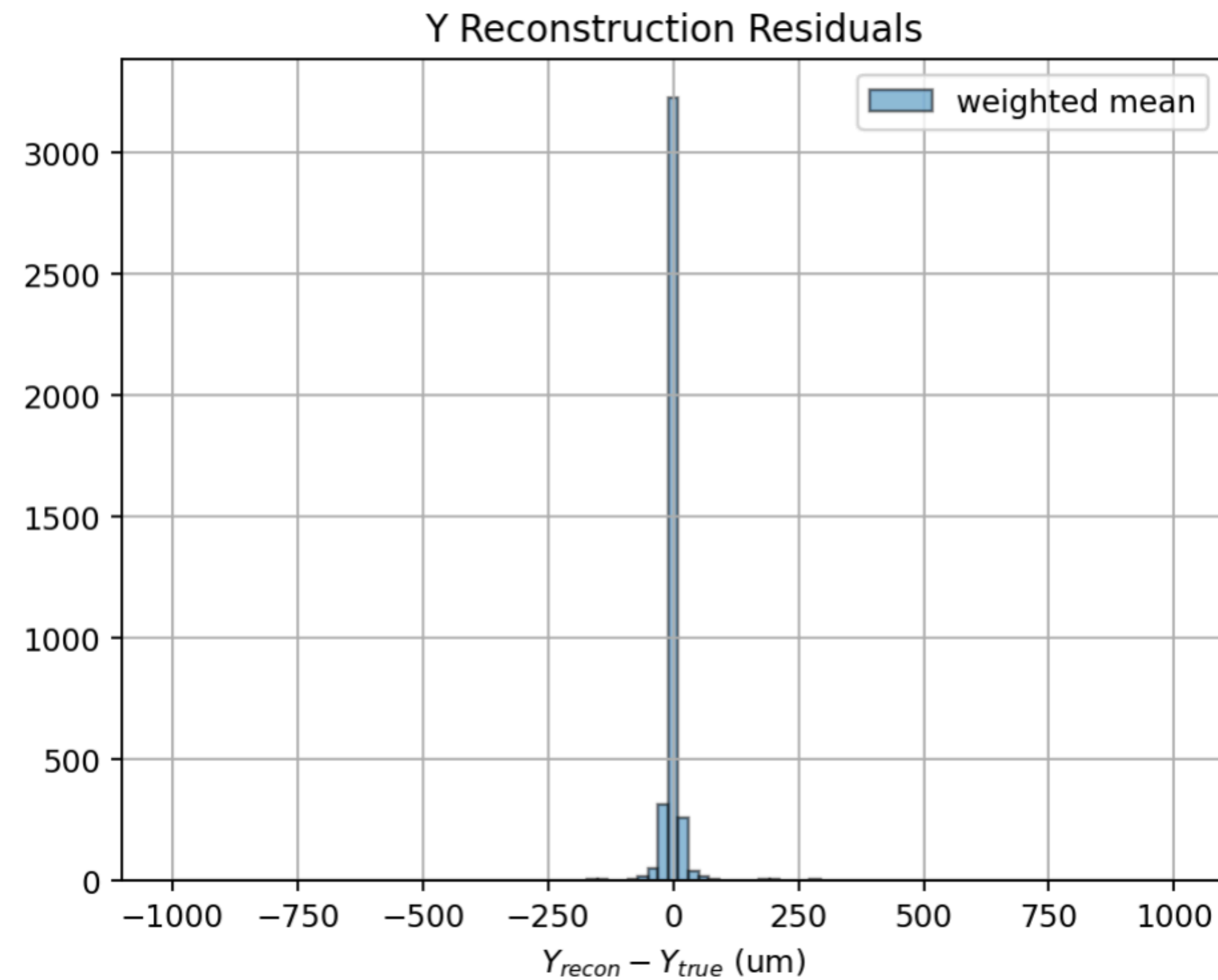
We see better resolution in X direction

Very simple and easy to do

However, it performs worse at high angles

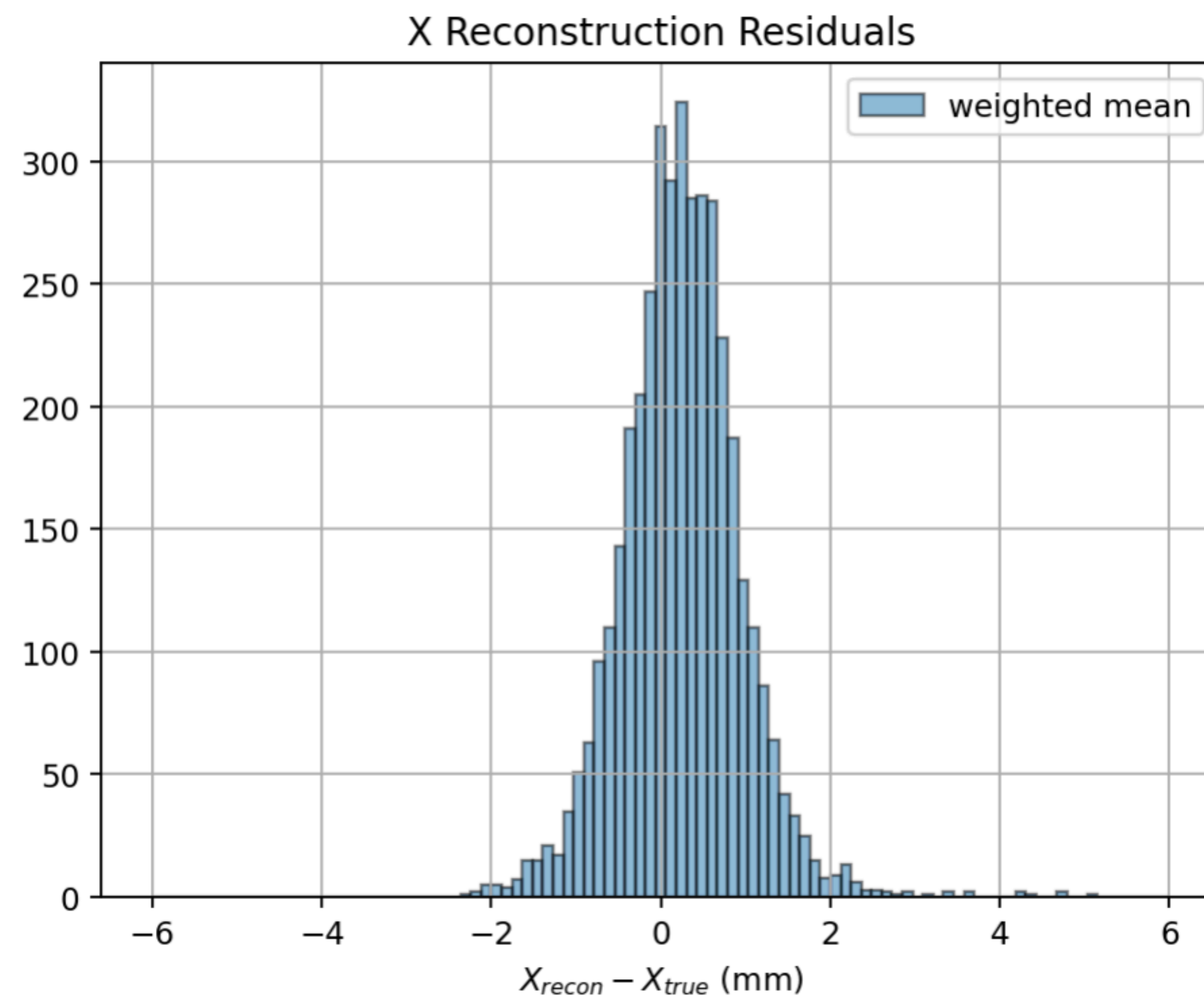
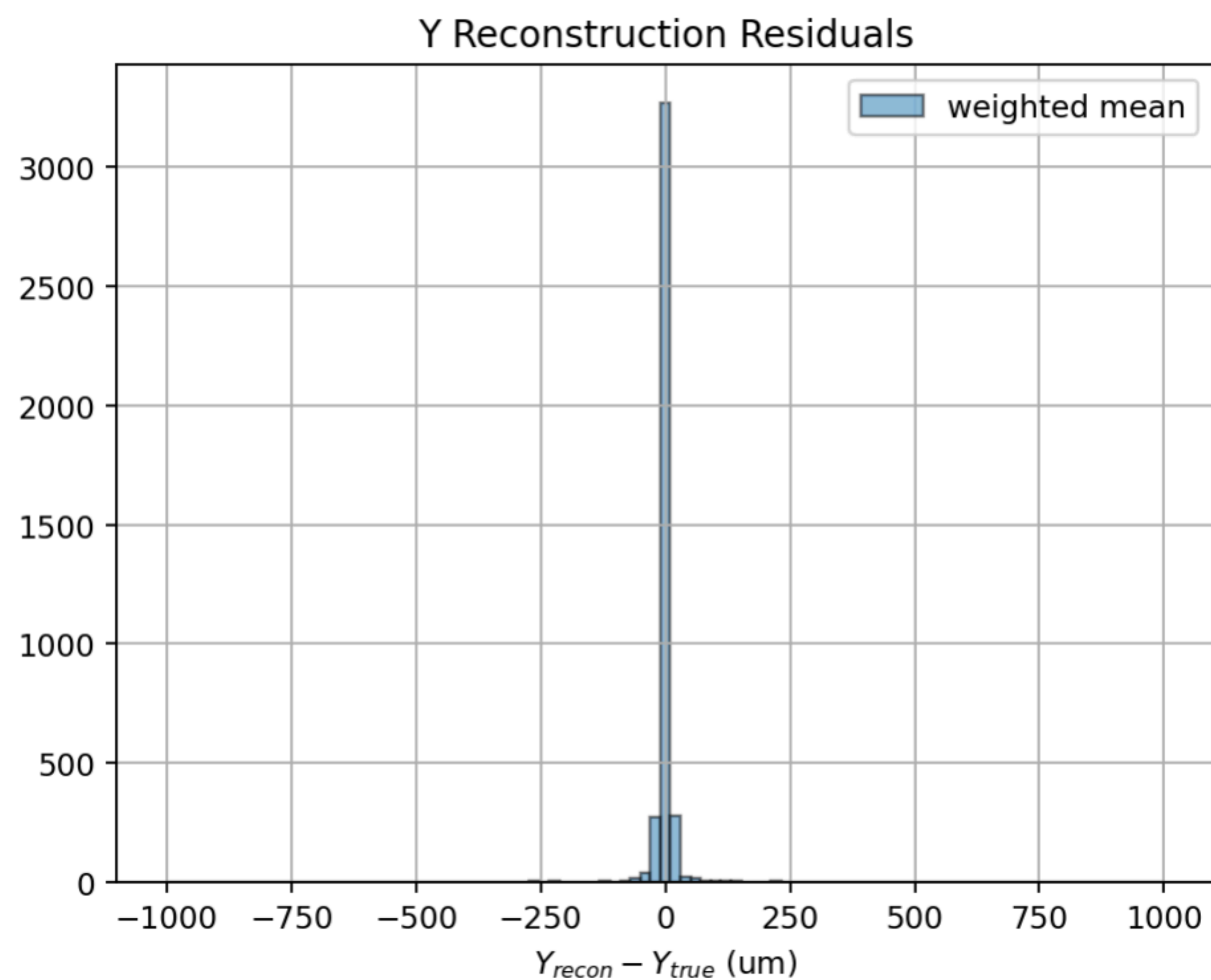
Position Reconstruction

Low Angles (0-40 deg)



Position Reconstruction

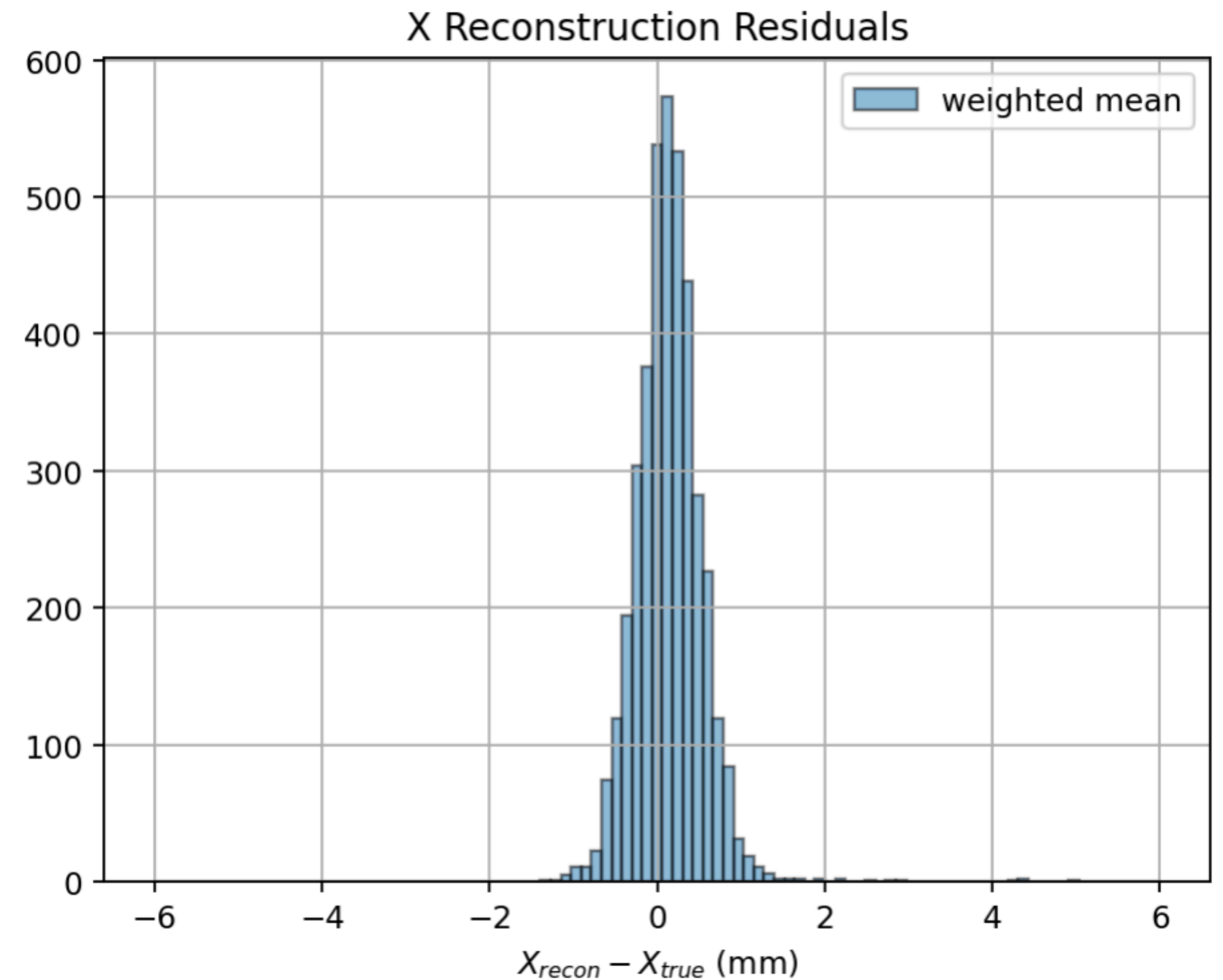
High Angles (50-70 deg)



Position Reconstruction

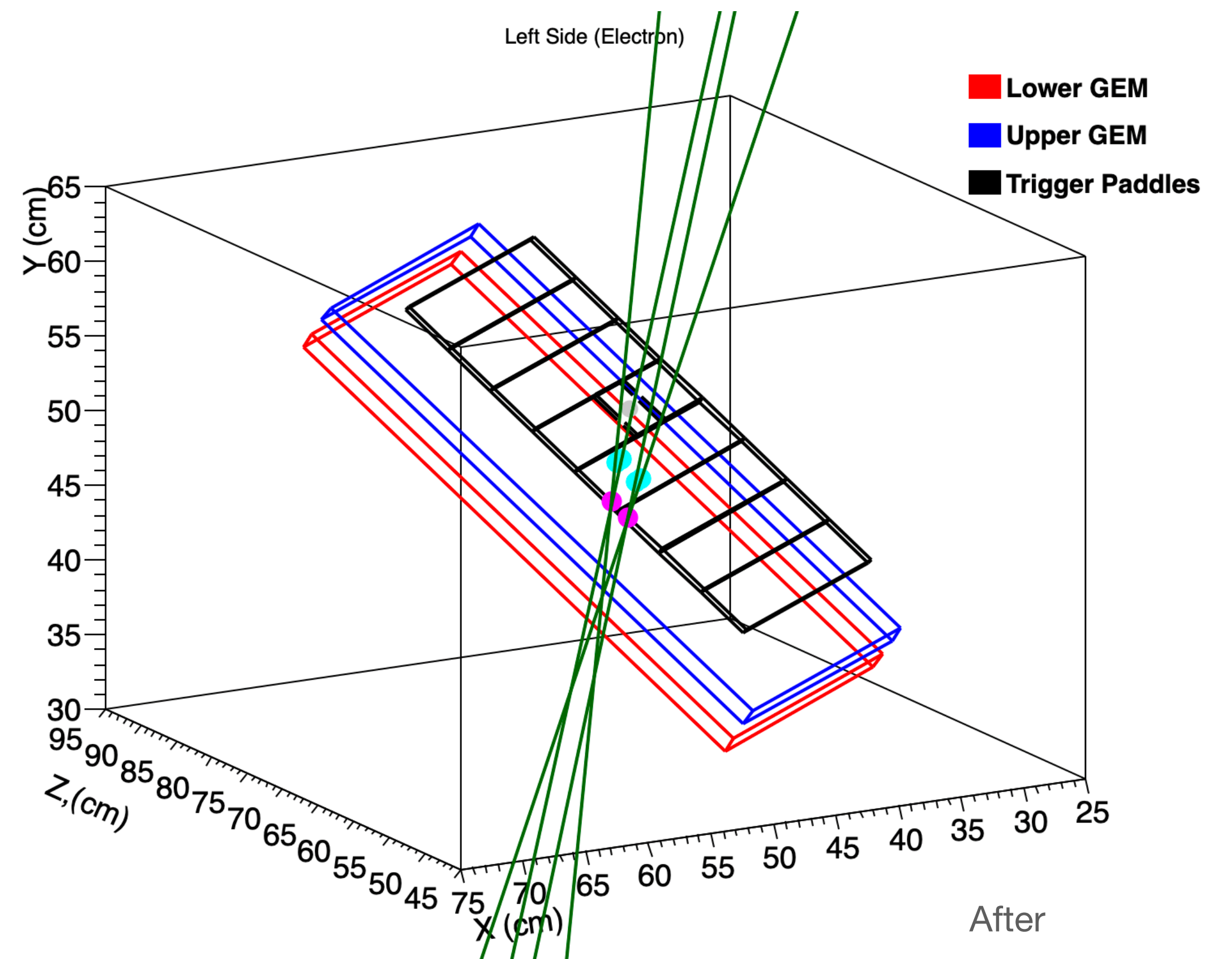
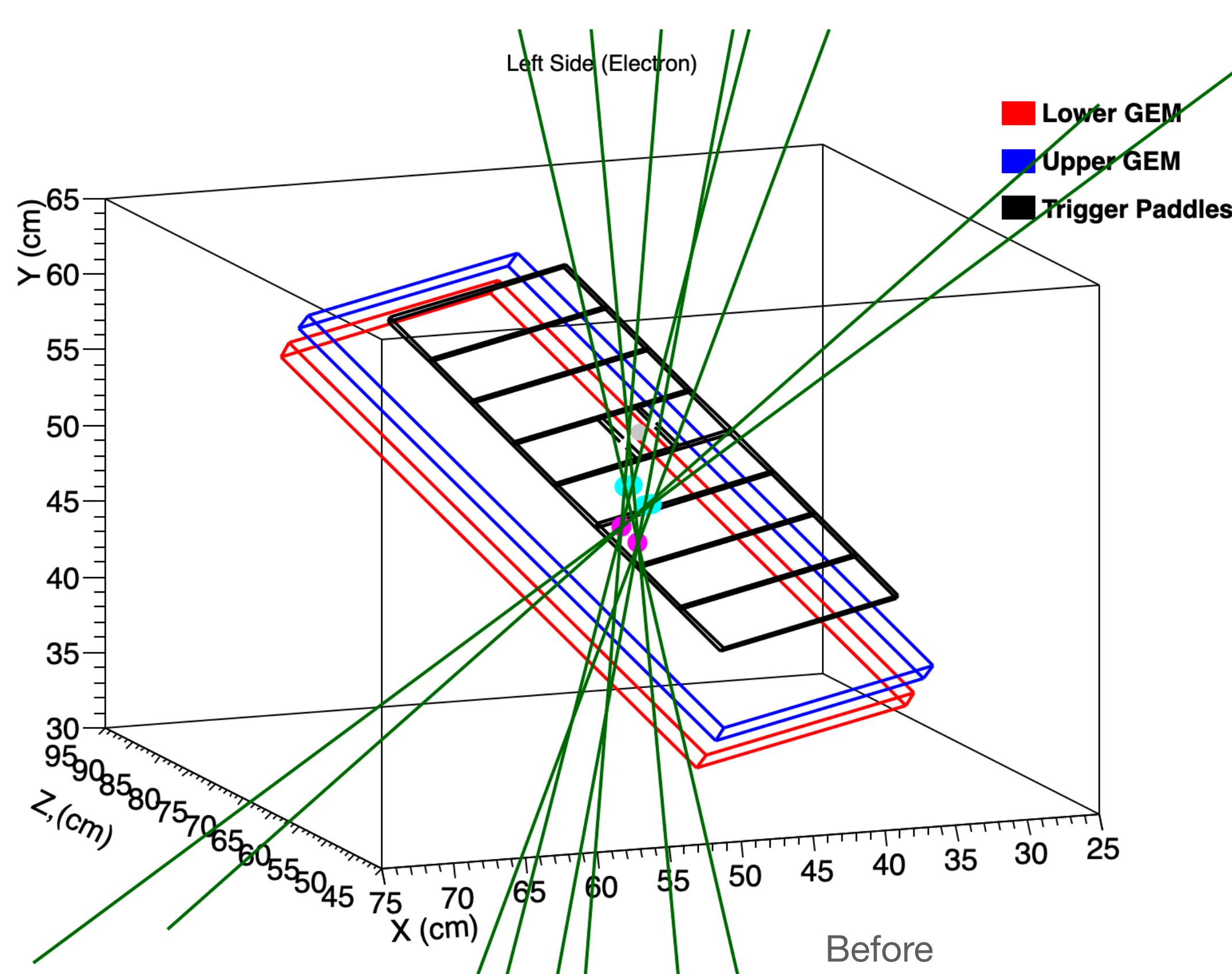
Near 40deg (what we expect)

Near 30-50 deg, using the mean
can get us to <1mm accuracy



GEM Tracking Improvements

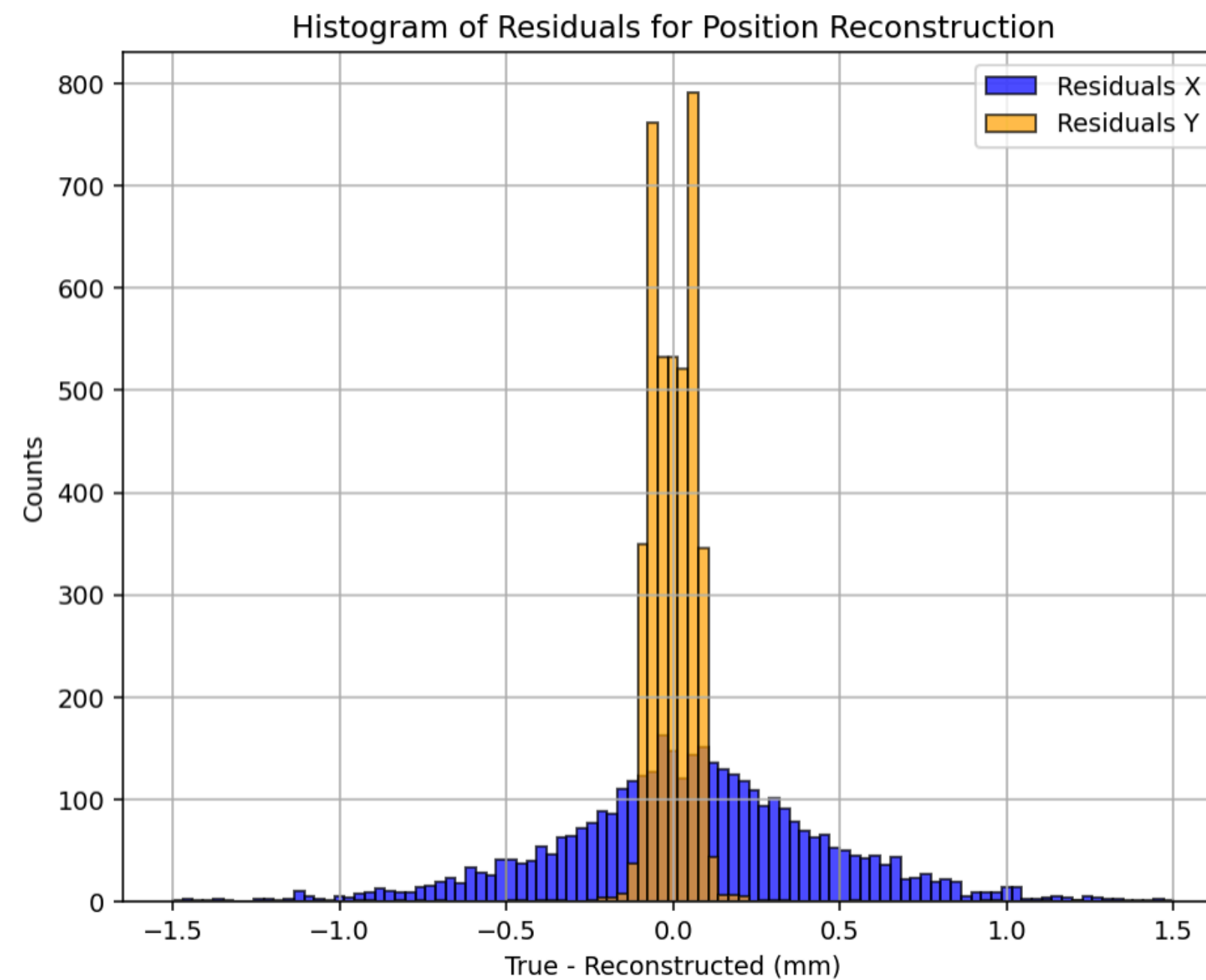
The algorithm now only uses tracks that passes through the correct trigger paddles



Reconstruction Residuals

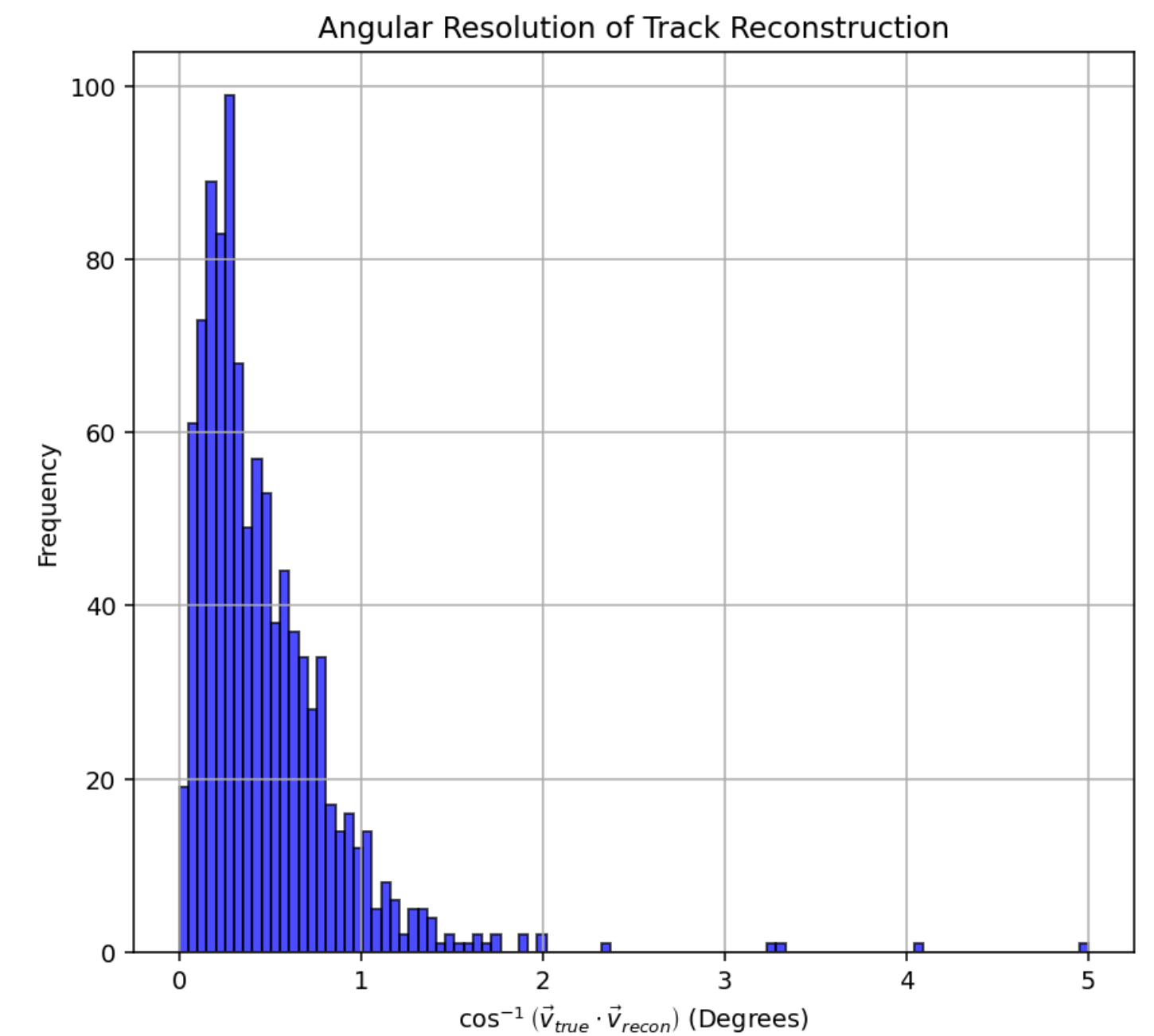
We look at the residuals of track+clustering reconstruction

Both track positions and track angles are analyzed



$\sim 0.4\text{mm } \sigma$ on X Recon

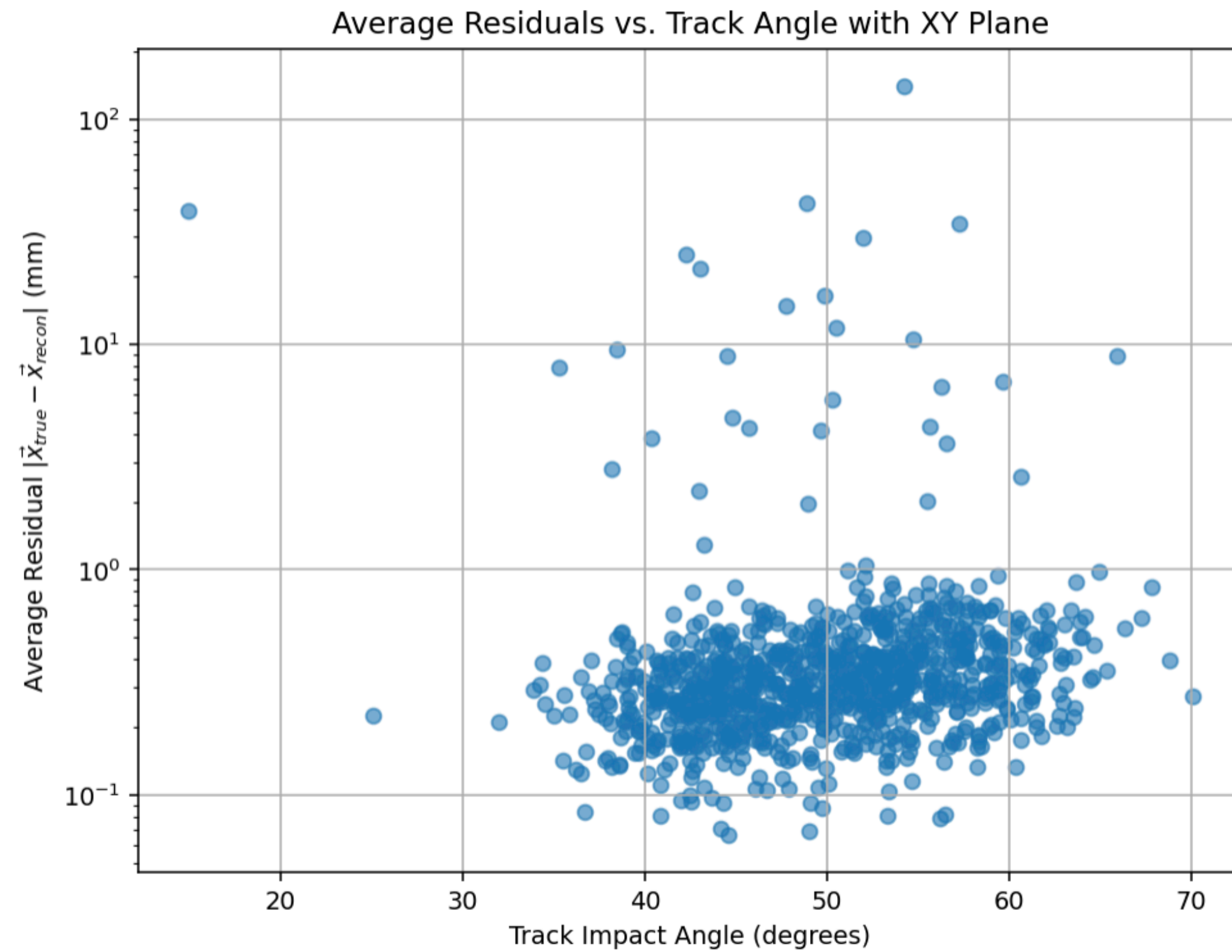
$\sim 0.2\text{mm}$ width on Y Recon



Relatively small of $\sim 0.5\text{deg}$

Reconstruction Residuals

Angle Dependence



Average Residual is avg
of distance between
reconstructed and true
positions of all four gem
planes