

Acceptance and Scattering angle Study

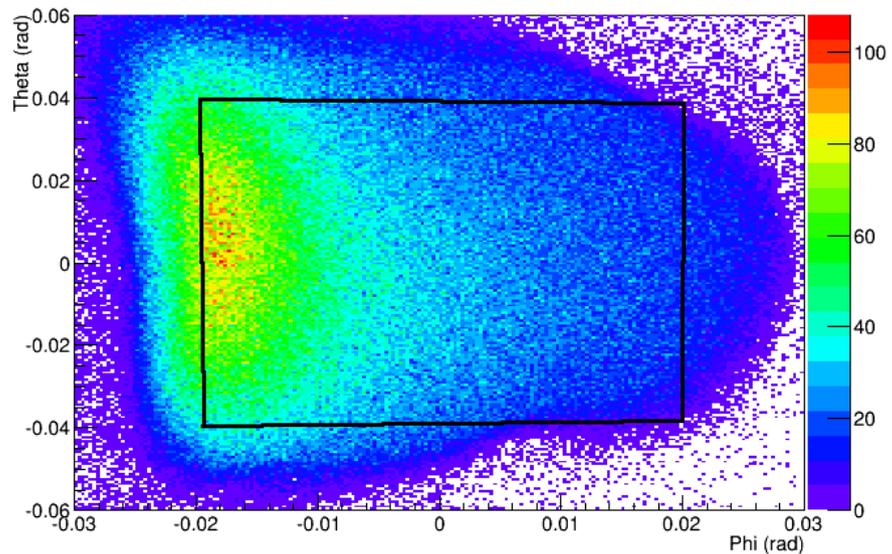
Goal:

- Perform several cuts on reconstructed theta and phi at the target, with varying levels of strictness.
- For each cut (loose, medium, strict, extreme) calculate the real scattering angle using theta/phi before and after scattering (from BPM and optics, respectively).
- Run P.Bosted XS model using the resulting scattering angles from each cut (using a bin weighting method).
- Compare the resulting XS model to yield data.
- *The idea is to find a region that will eliminate acceptance effects in the yield, so that the generated model (using the real scattering angle) best represents our data and can be used in the dilution.*

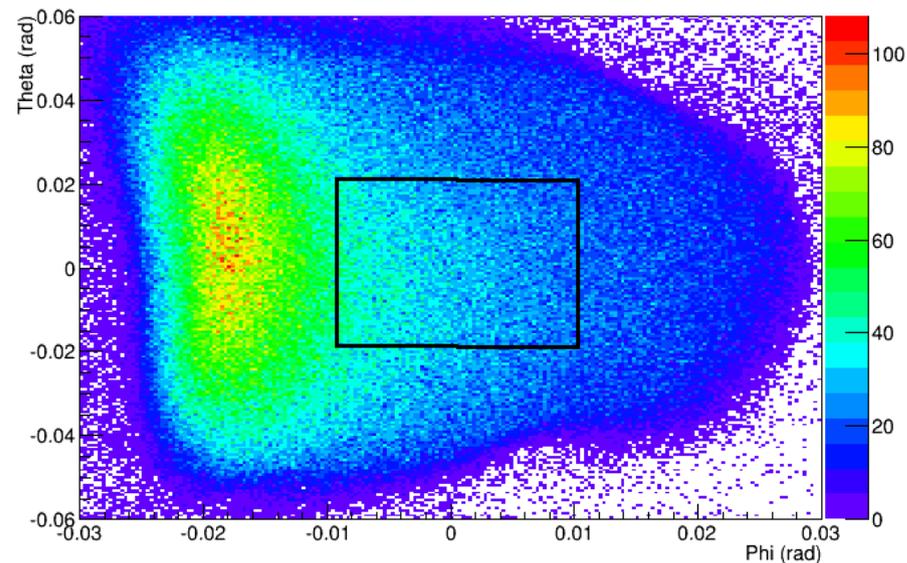
2.254GeV 5T Longitudinal / Left arm / Empty dilution

Cut on reconstructed theta vs phi at the target.

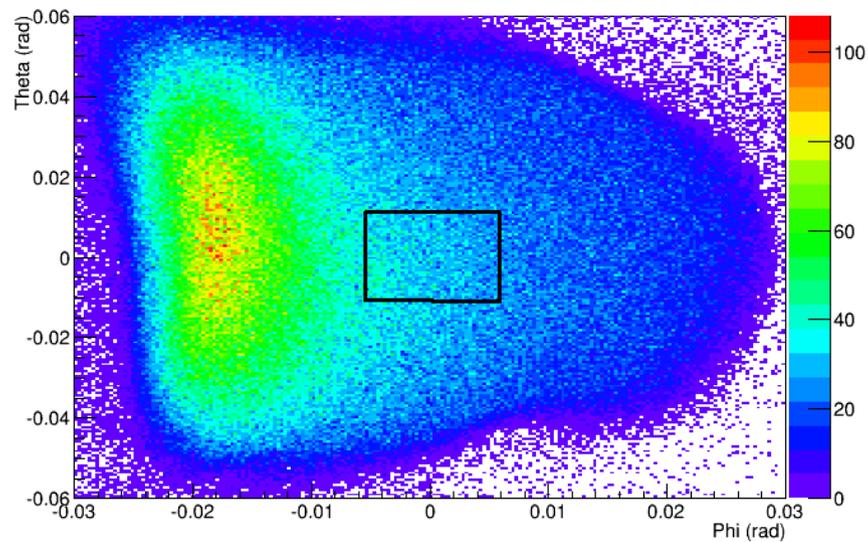
Loose Acceptance Cut



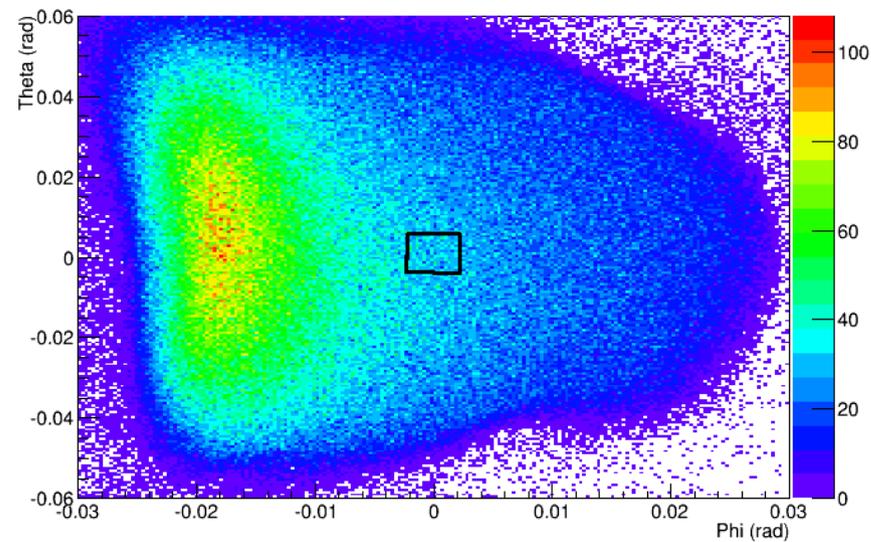
Medium Acceptance Cut



Strict Acceptance Cut



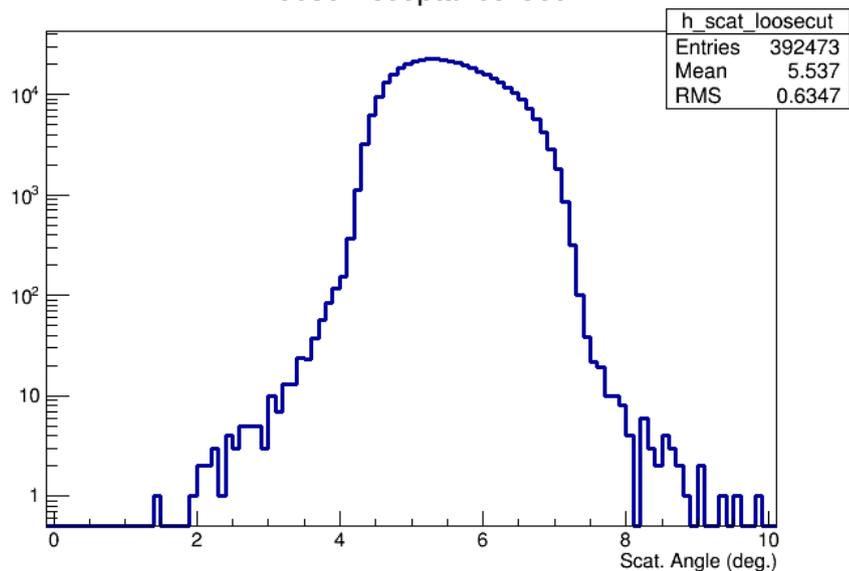
Extreme Acceptance Cut



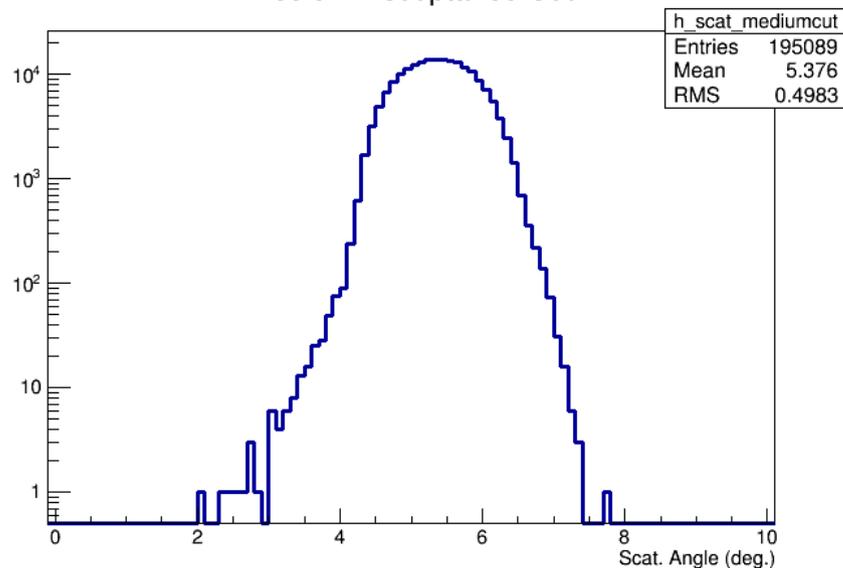
2.254GeV 5T Longitudinal / Left arm / Empty dilution

Calculated scattering angle (using acceptance cuts on previous slide)

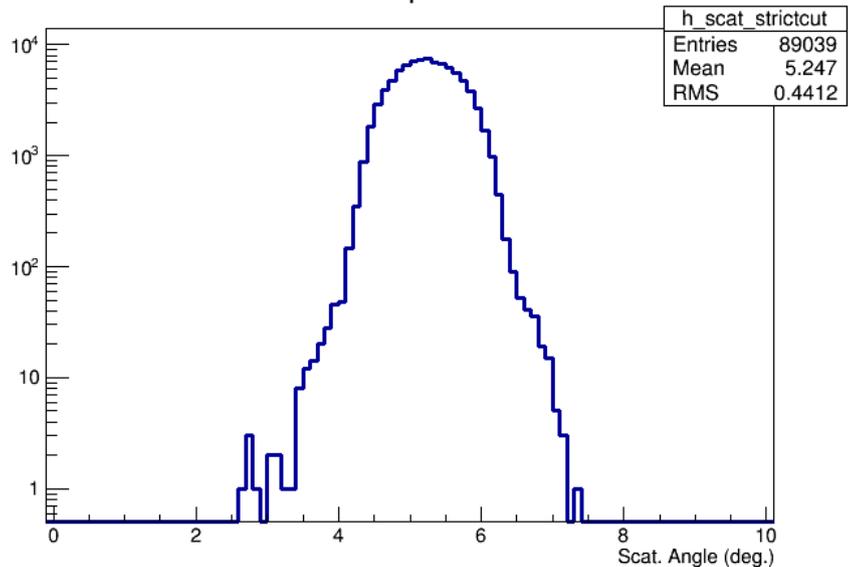
Loose Acceptance Cut



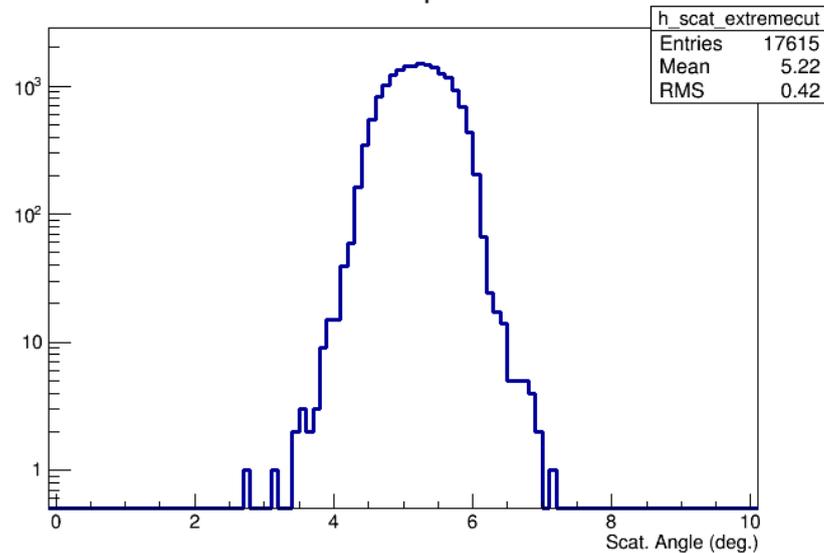
Medium Acceptance Cut



Strict Acceptance Cut

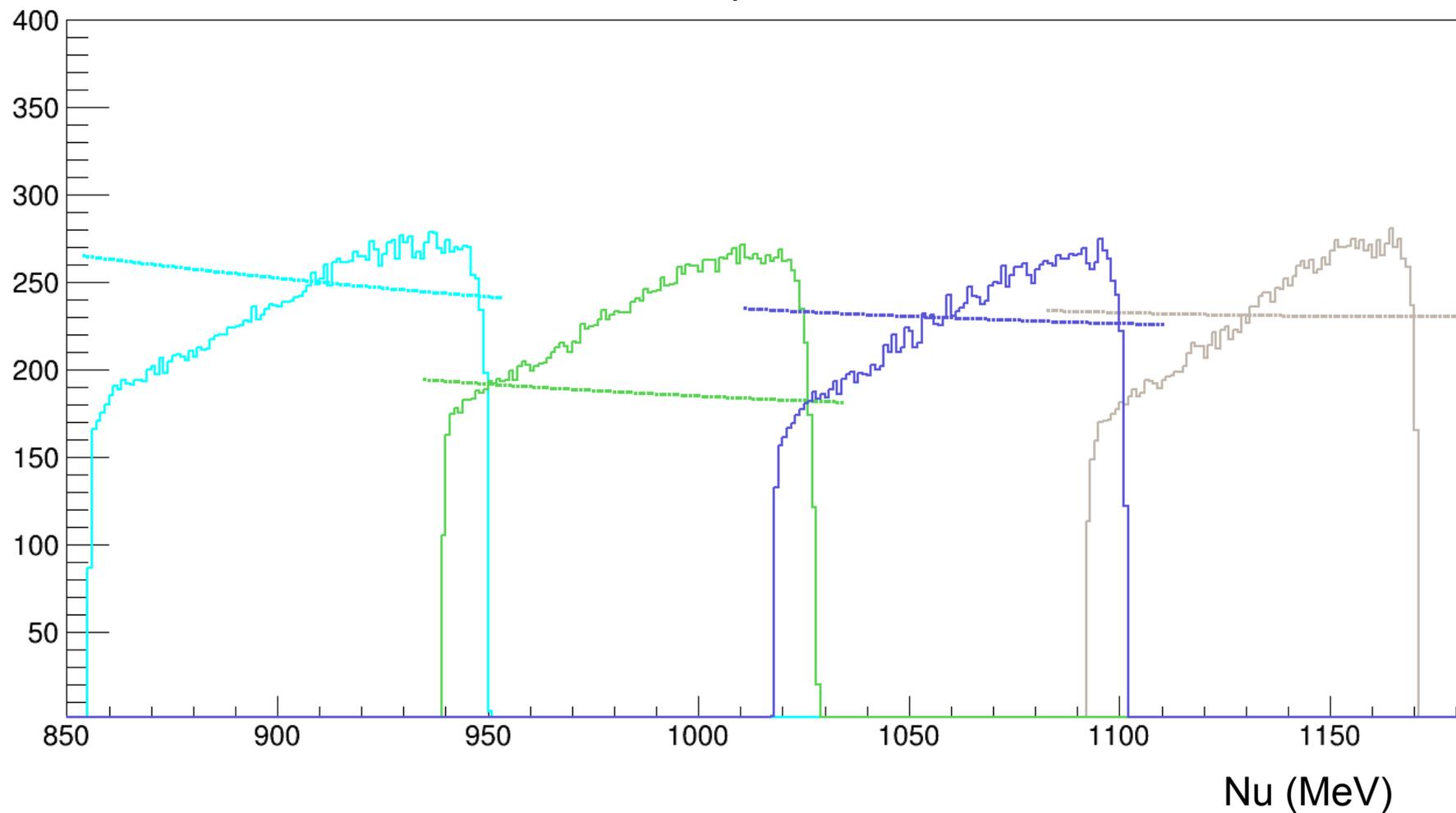


Extreme Acceptance Cut



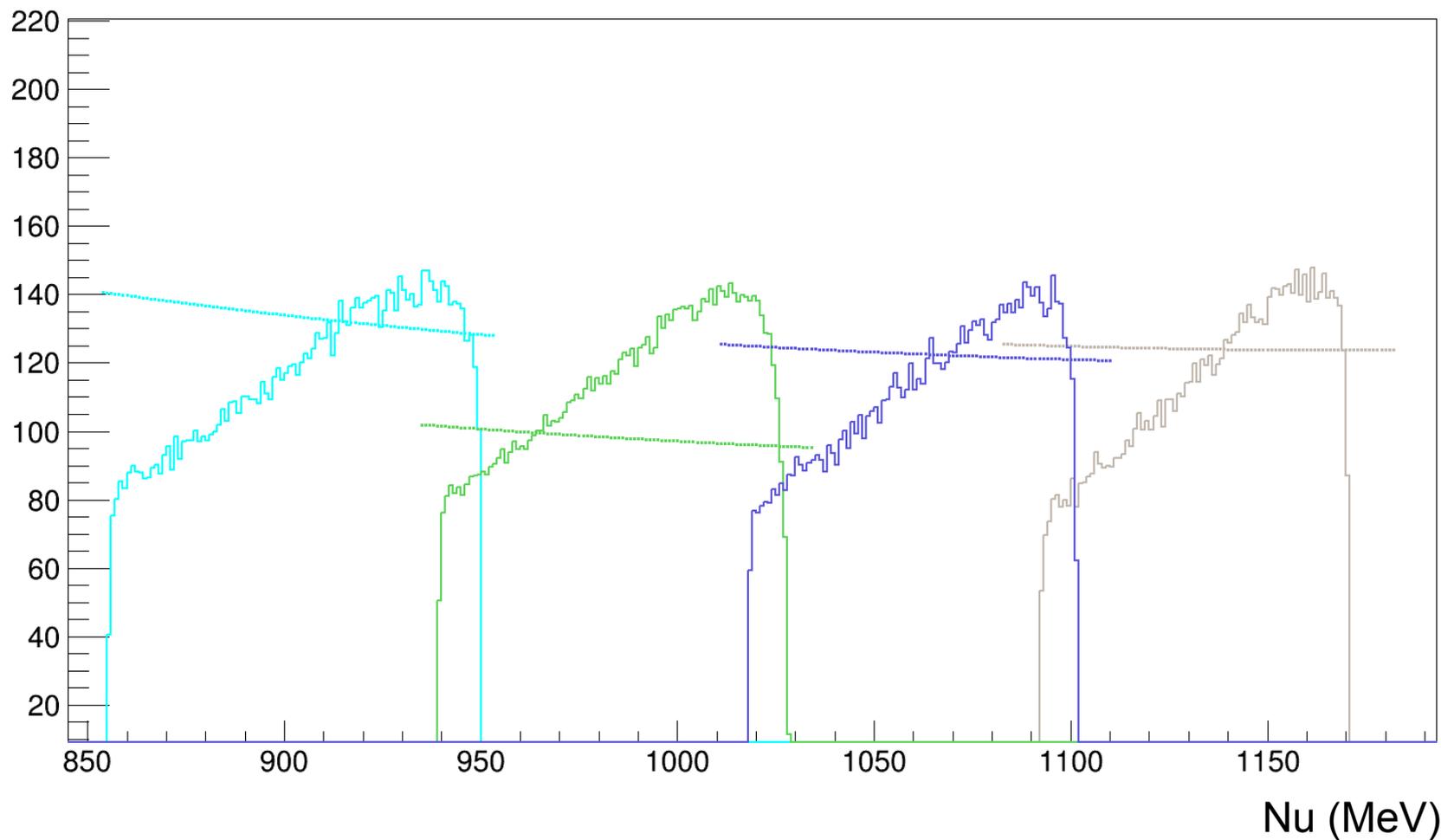
2.254GeV 5T Normalized Yield w/ P.Bosted model comparison

Loose Acceptance Cut



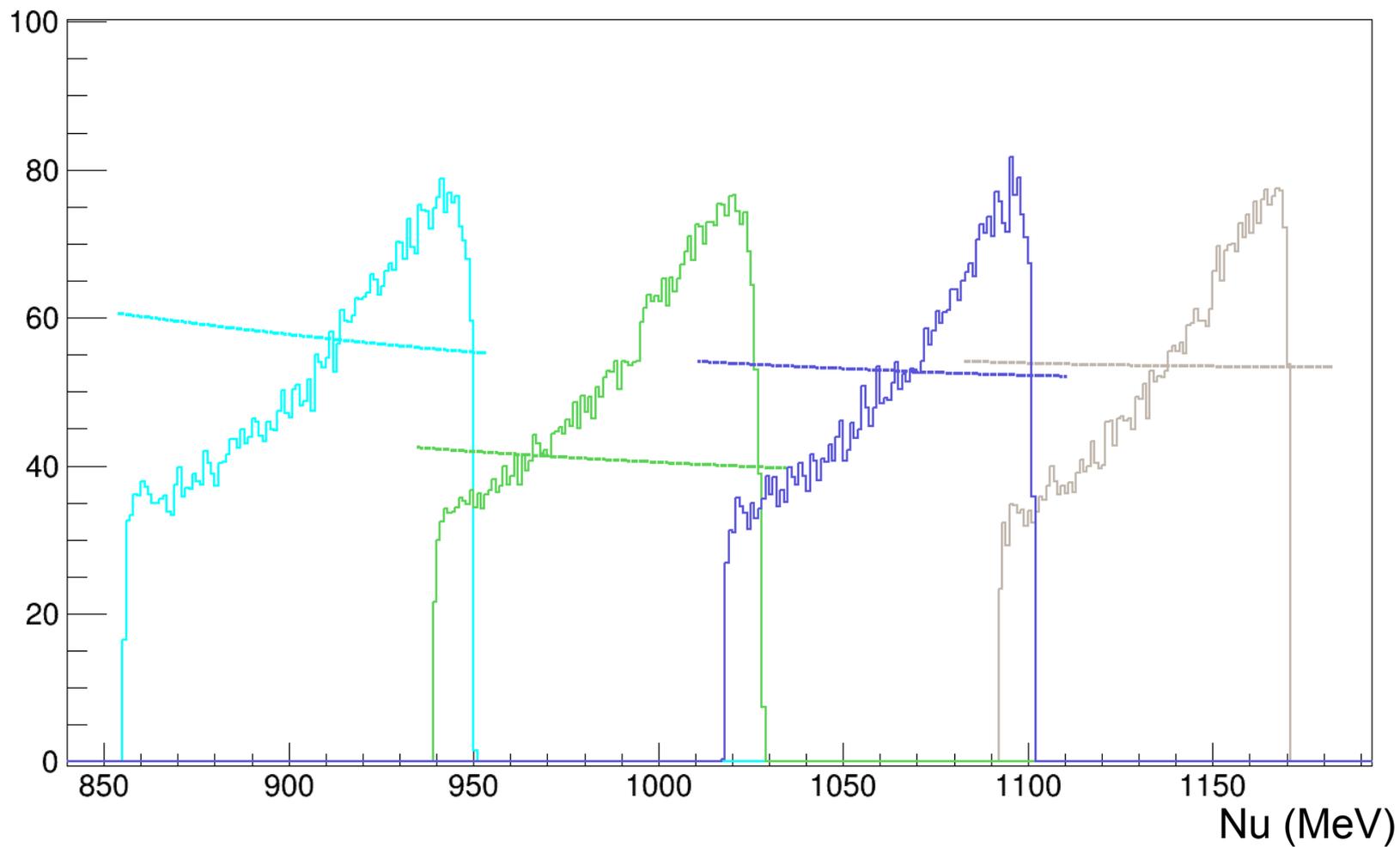
2.254GeV 5T Normalized Yield w/ P.Bosted model comparison

Medium Acceptance Cut



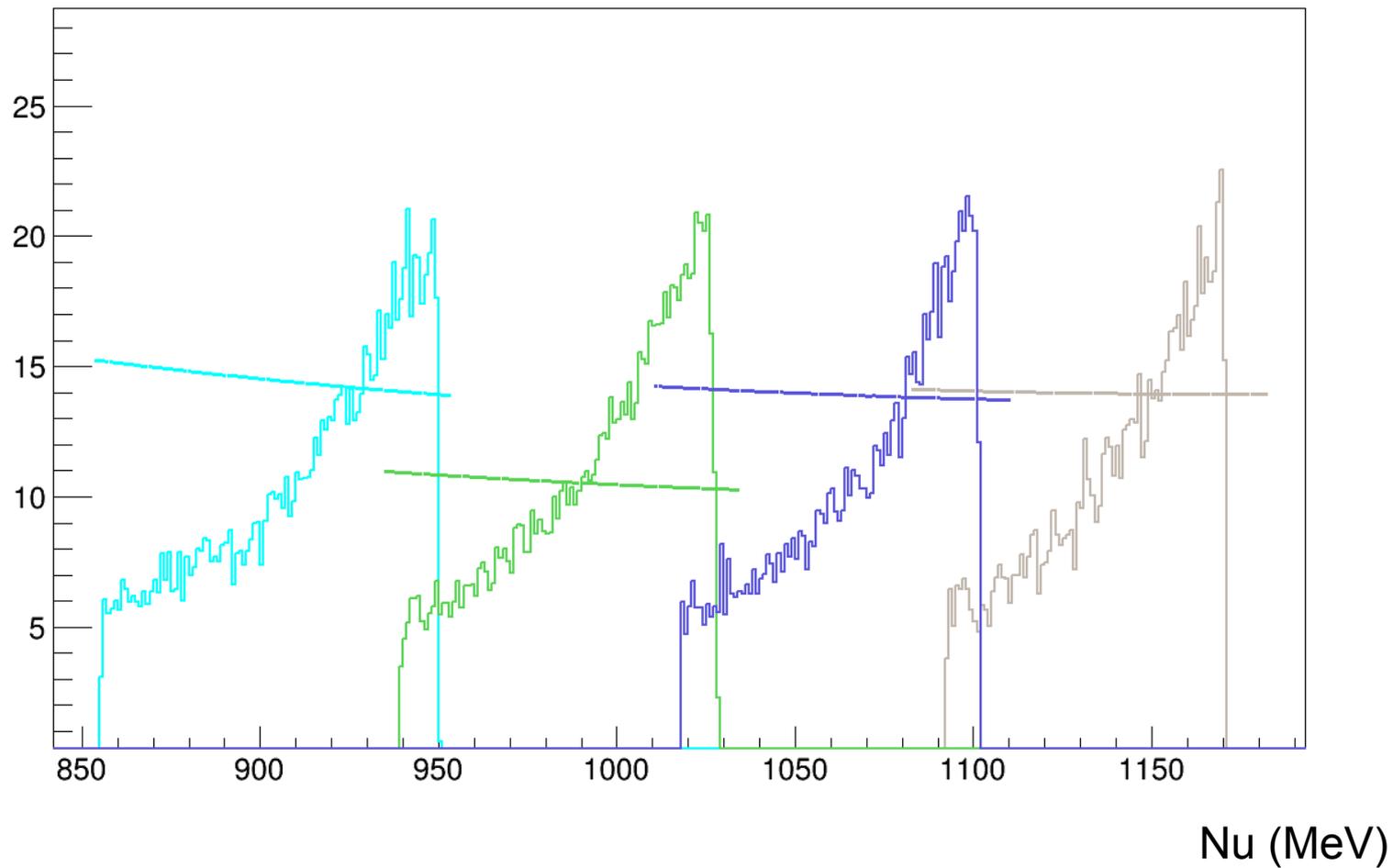
2.254GeV 5T Normalized Yield w/ P.Bosted model comparison

Strict Acceptance Cut



2.254GeV 5T Normalized Yield w/ P.Bosted model comparison

Extreme Acceptance Cut



- All data shown is of Empty dilution runs (so just helium).
- Fully radiated. I've experimented with changing the R.T. of the target, has little effect on the model.
- No matter what cuts I make on reconstructed variables, I can't reproduce data with Bosted model! (I have experimented with graphical cuts of other various shapes and sizes in the acceptance that I didn't show)
- Would really like to get this finished so dilution can be finalized, currently don't have a reliable way to scale C to N without being able to reproduce our data/acceptance.
- Idea: divide acceptance (target theta vs. phi) up into a grid (e.g. 8x8 square). Find scattering angle in each square and search for region with no acceptance effects. Time consuming!
- Suggestions from meeting?