Analysis talk follow up

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- Beam momentum resolution is already accounted for in the MC simulation → reduce resolution to 1.2% or remove.

- Secondary pion KE limit → it is possible to enforce this cut in reco by looking at the reconstructed track lengths? (need more explanation by Richie).

- Toy MC method:
    1. adjust number of throws to 1000
    2. can evaluate the systematics at once to account for correlations between effects.

- Energy slice method → "slice incompleteness" or KE_{init} - KE_{int} < slice width is not ideal. Might be good to use same slicing method as Kang. This is likely the reason large migrations in the unfolding matrix occur.

- Fit inaccuracy → vary cross sections by 50% rather than 20%, to see if fit is not causing the discrepancy in the single pion production cross section.

- Final xs plots → instead of Geant4 cross section curves, use same binning as measurement.

- Most comments were geared towards the analysis being approved for publication, for thesis submissions, there is no real procedure or approval.

- So I can proceed, but need to put "DUNE work in progress" on my final plots.

▶ Beam momentum resolution is already accounted for in the MC simulation → reduce resolution from 2.5% to 1.2% or remove.

– Remove, systematic is already negligible at 2.5%

► Secondary pion KE limit → it is possible to enforce this cut in reco by looking at the reconstructed track lengths? (need more explanation by Richie).

– Will try to look into, not clear how track length could be used so will discuss with Richie.

– Alternate apporach is to exclude $\pi^{\pm}$ which deposit less than 100 MeV (still doesn't account for $\pi^{\pm}$ which undergo inelastic interactions).

- ▶ Toy MC method:
    1. can evaluate the systematics at once to account for correlations between effects.
    2. adjust number of throws to 1000 (currently 50).

- – Evaluating a combined systematic is fine, but this method would not allow a comparison between the different systematics like I have done.

- – Takes 1 minute to generate a toy with 1 millon events, and then another minute to run the analysis, toy with 10 million events takes around 10 minutes. 1000 throws would take too long but I could increase the number of throws to 200.
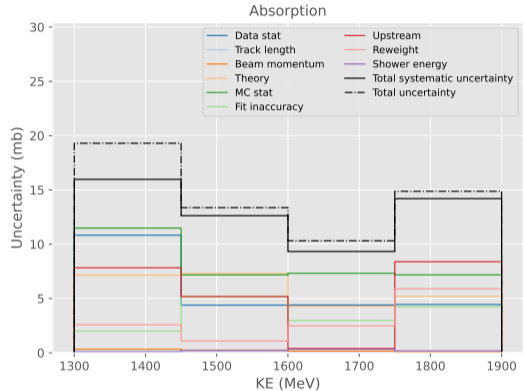
Absorption

- ▶ Energy slice method → "slice incompleteness" or KE_{init} - KE_{int} < slice width is not ideal. Might be good to use same slicing method as Kang. This is the reason large migrations in the unfolding matrix occur.

- – "Slice incompleteness" is a feature of the energy slice method others have presented on [1], so unclear why this was a surprise.

- – I performed a closure test to ensure the energy method works, so I won't change the slicing method (would also take too long).

- – Might be worth updating in the future (Dennis).

- – If the unfolding matrices are a problem, then I could drop the overflow and underflow bins in the analysis entirely (unsure how this would impact the results)

N_{int} unfolded matrix
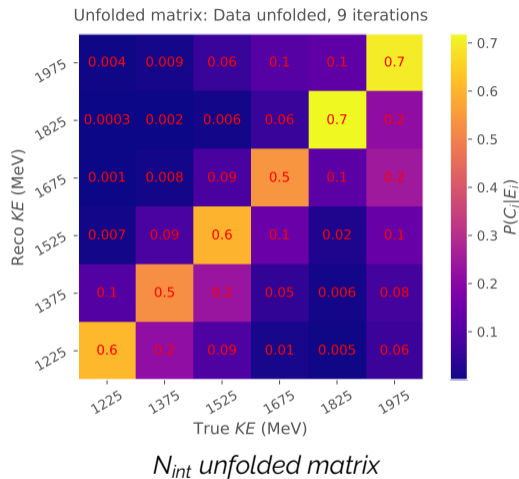
- ▶ Fit inaccuracy → vary cross sections by 50% rather than 20%, to see if the fit is not causing the discrepancy in the single pion production cross section.

- – Simple to test and already verified.

- – Top plot is μ_{spip}^{exp} vs μ_{spip}^{fit} for normalisations between 0.5-1.5.

- – Bottom plot shows the analysis chain ran using the toy for 0.5 and 1.5 normalisation.

- – Note that range of μ_{spip}^{exp} is not exactly 0.5 and 1.5, because in the toy the total cross section is unchanged.

process : single pion production

Single pion production
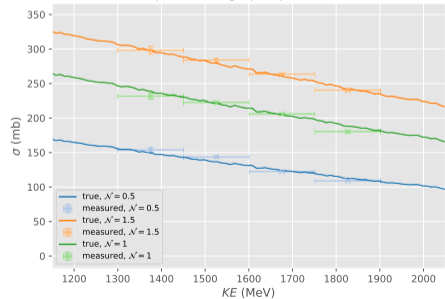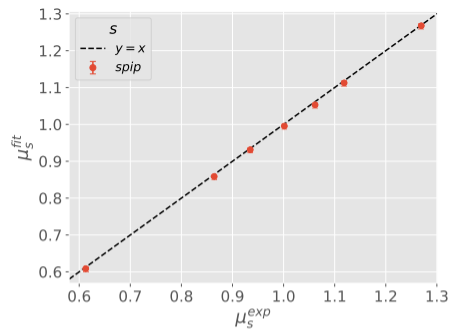
▶ Final xs plots → instead of Geant4 cross section curves, use same binning as measurement.

– Can do, show both histogram and distribution of Geant4?