CROSS SECTION IN SHOE

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7/04/2021

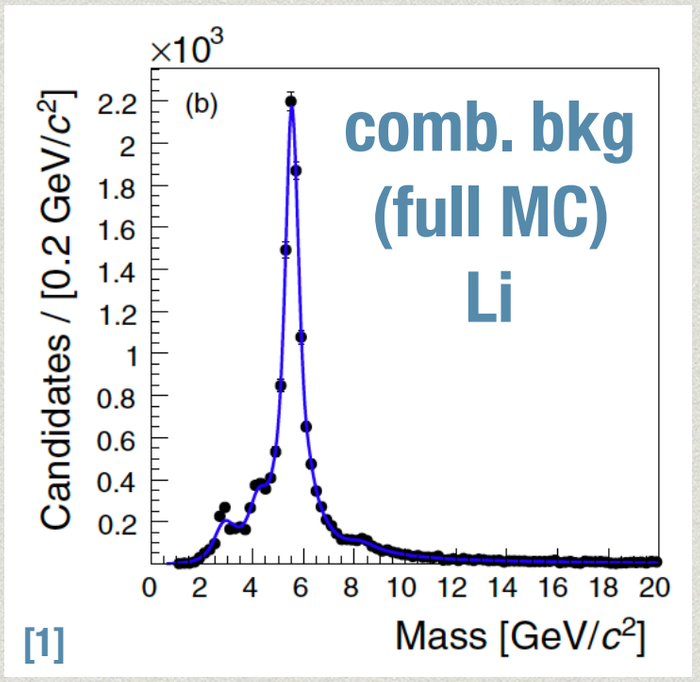
FOOT Global Reconstruction Analysis

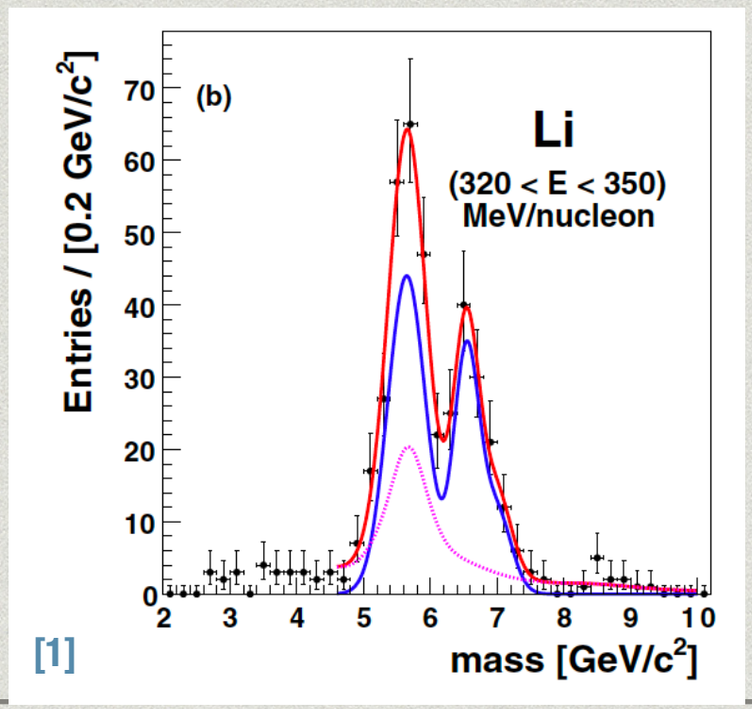
- **Compute the cross section**

$$\frac{d\sigma_i}{d\Omega}(\theta) = \frac{Y_i(\theta)}{N_C \times N_{TG} \times \Delta\Omega \times \epsilon^i_{trk}(\theta)}$$

$$\frac{d\sigma_i}{dE_{kin}}(E_{kin}) = \frac{Y_i(E_{kin})}{N_C \times N_{TG} \times \Delta E_{kin} \times \epsilon^i_{trk}(E_{kin})}$$

1. ALM/Chi2 fit: performance evaluation of glb tracking
2. Y_i^{raw} from **mass spectrum** in i-th bin of Ekin (Theta) reco, given a Z reco: fit with signal (gauss) + bkg (comb)





[1] Toppi et al,"Measurement of fragmentation cross sections of 12C ions on a thin gold target with the FIRST apparatus", PHYSICAL REVIEW C 93, 064601 (2016)

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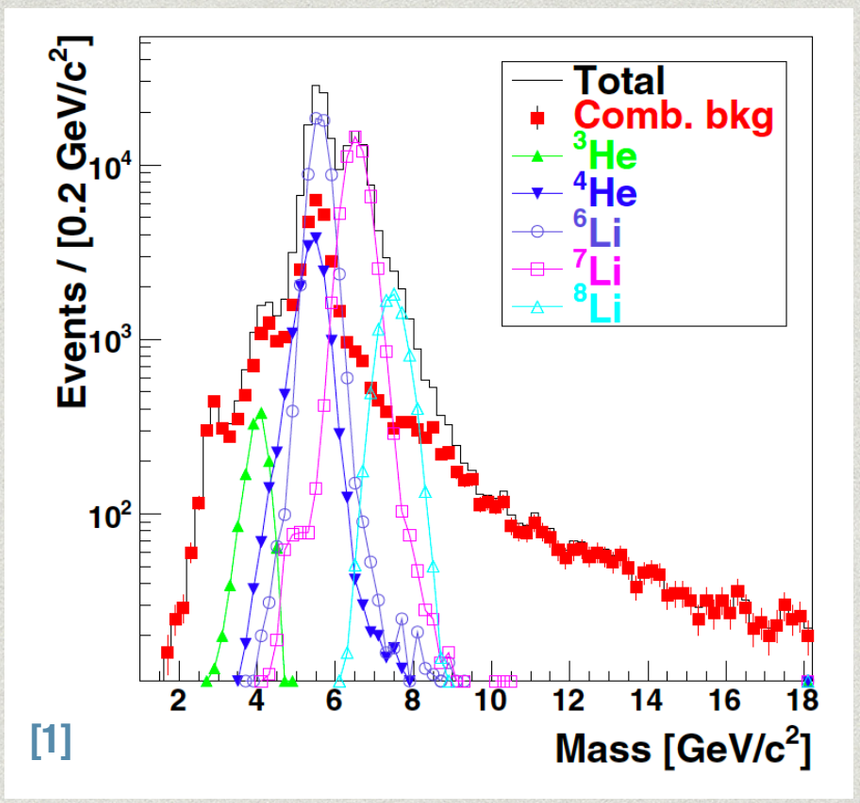
3. $Y_i = Y_i^{raw}$ with **cross feed** correction in i-th bin of Ekin reco (FULL MC)

$$Y_i = \frac{Y_A}{Y_A + Y_B} \times Y_i^{raw} = \varepsilon_i^{xf} \times Y_i^{raw}$$



[1]

→ systematics

FOOT Global Reconstruction Analysis

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4. **Unfolding** (FLAT MC): Ekin true vs Ekin reco (Z reco; Zreco+Mreco) => $Y_i^{true} = Y_i$ in i-th bin of Ekin true

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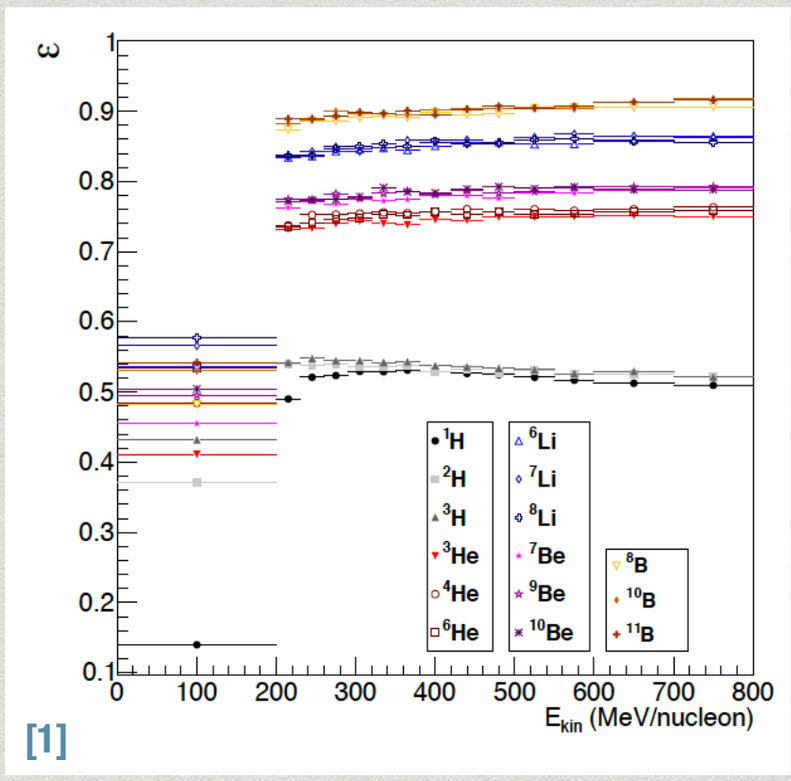
5. Correction of Y_i^{true} for the **tracking efficiency** (FLAT MC)

$$\varepsilon_{\mathrm{trk}} = \frac{\mathrm{n_{REC}}}{\mathrm{n_{PROD}}}$$



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FOOT Global Reconstruction Analysis

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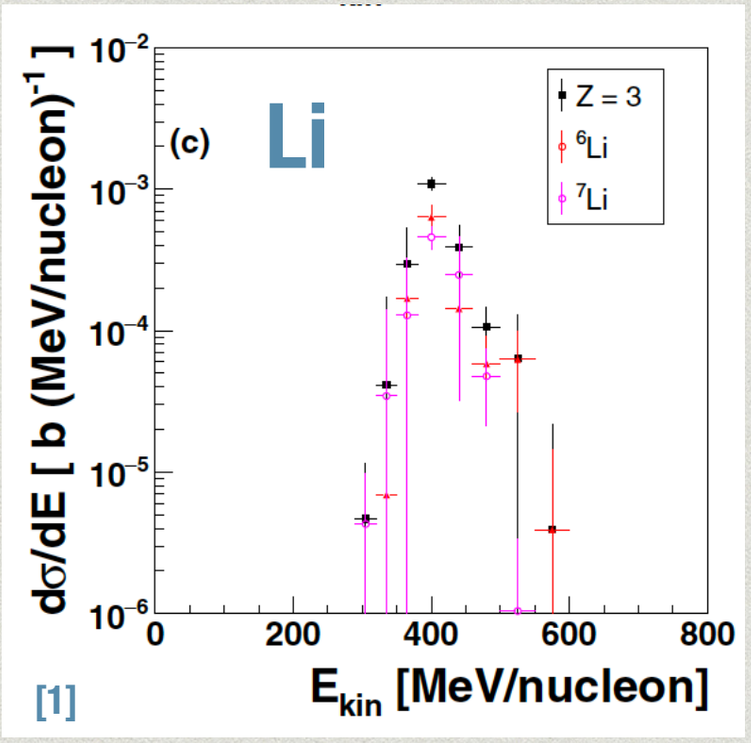
Single Differential Cross Section



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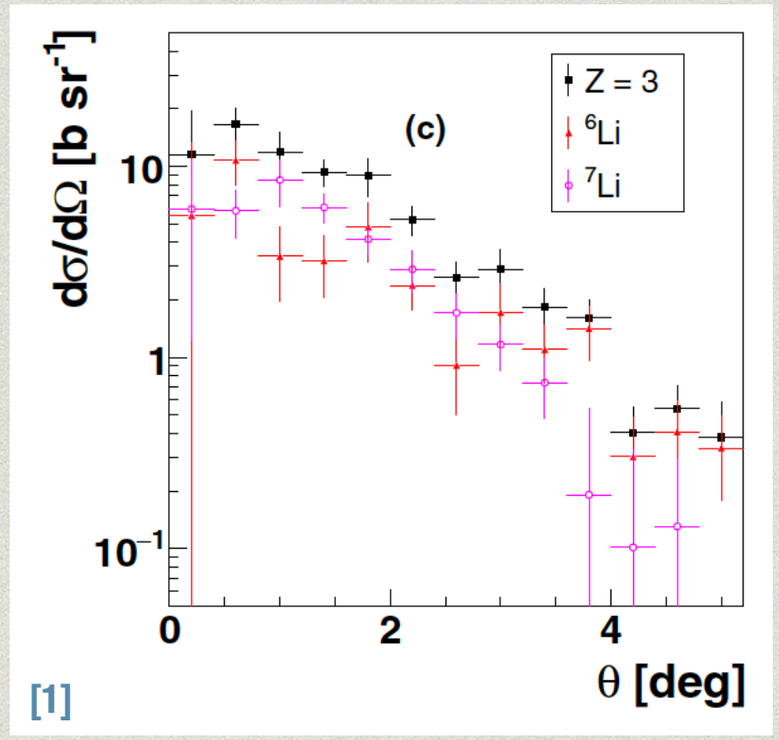


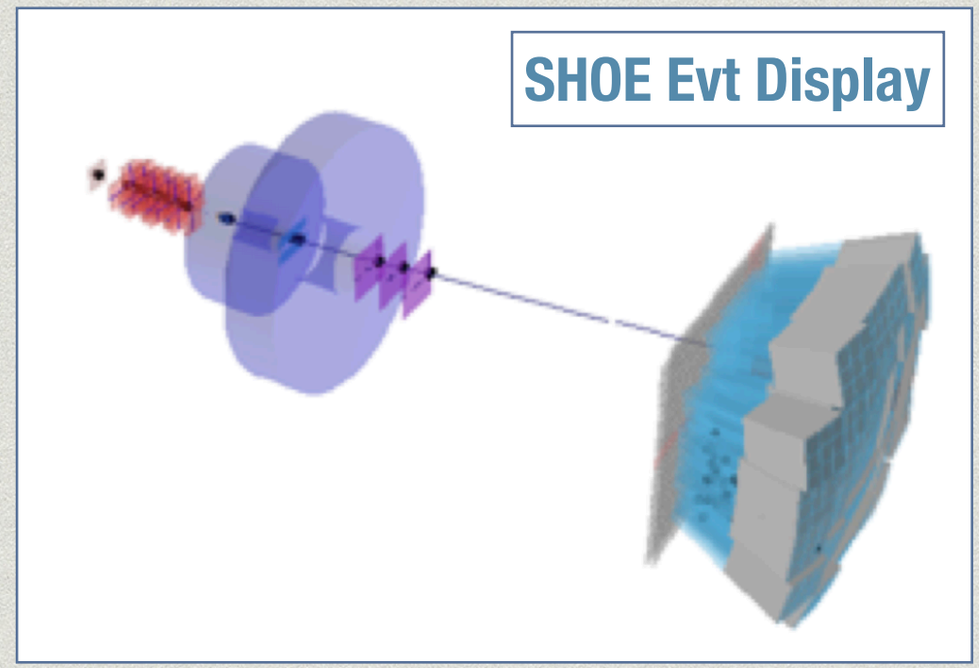
[1]

inversion

FOOT Global Reconstruction Analysis

INGREDIENTS

- **Get the measured quantities**
  - p from glb tracking
  - Z & TOF from TW
  - Ekin from CALO (+ TW + MSD)
  - Theta from VT track



- **Evaluation of the mass**
  1. p & TOF
  2. Ekin & TOF
  3. Ekin & p

$$p = mc\beta\gamma$$

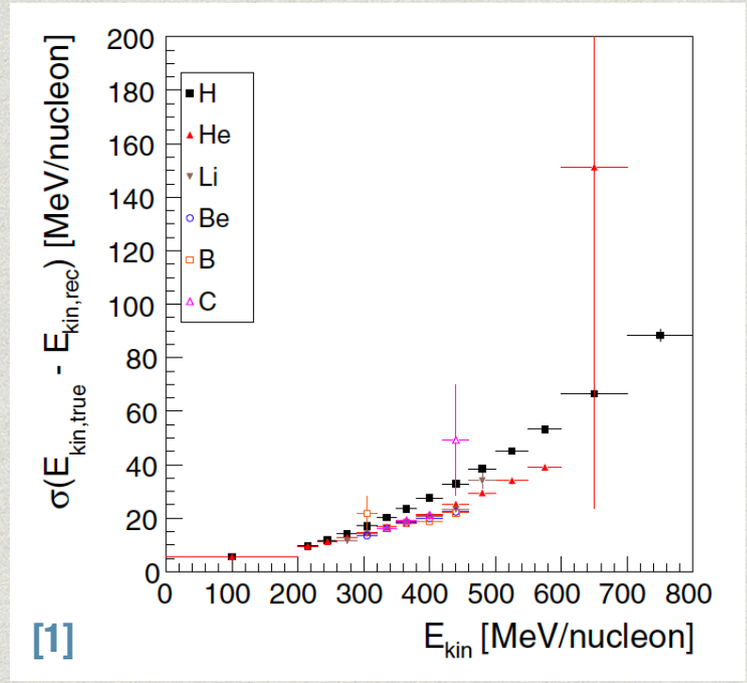
$$E_{\text{kin}} = mc^2(\gamma - 1)$$

$$E_{\text{kin}} = \sqrt{p^2c^2 + m^2c^4} - mc^2$$

FOOT Global Reconstruction Analysis

INGREDIENTS

- **Compute the resolutions** (Z reco selection):
  - Ekin
  - Theta (wrt TGT exit & production)
  - Mass (in bins of Ekin & Theta)



[1]

- **Find the best binning for Ekin/Theta**
- **Compute the tracking efficiency** as a function of true quantities => FLAT MC

SHOE: DecodeGlbAna HOW TO

1. Run Txt2NtuRoot w/ -reg flag **from build/Simulation**

```
../bin/Txt2NtuRoot -in simfile_TXT.dat -out outsim_shoereg.root -reg
```

2. Run DecodeMC on *shoereg.root output of Txt2NtuRoot
   EnableRootObject: y
   EnableRegionMc: y
   from build/Reconstruction/level0

```
../../bin/DecodeMC -in outsim_shoereg.root -out Out_DecodeMC.root -exp 12C_200 -run 1 -mc
```

3. Run DecodeGlbToe on DecodeMC output
   IncludeTOE: y
   EnableLocalReco: y
   from build/Reconstruction/fullrec

```
../../bin/DecodeGlbToe -in ../level0/Out_DecodeMC.root -exp 12C_200 -run 1 -mc -out Out_DecodeToe.root
```

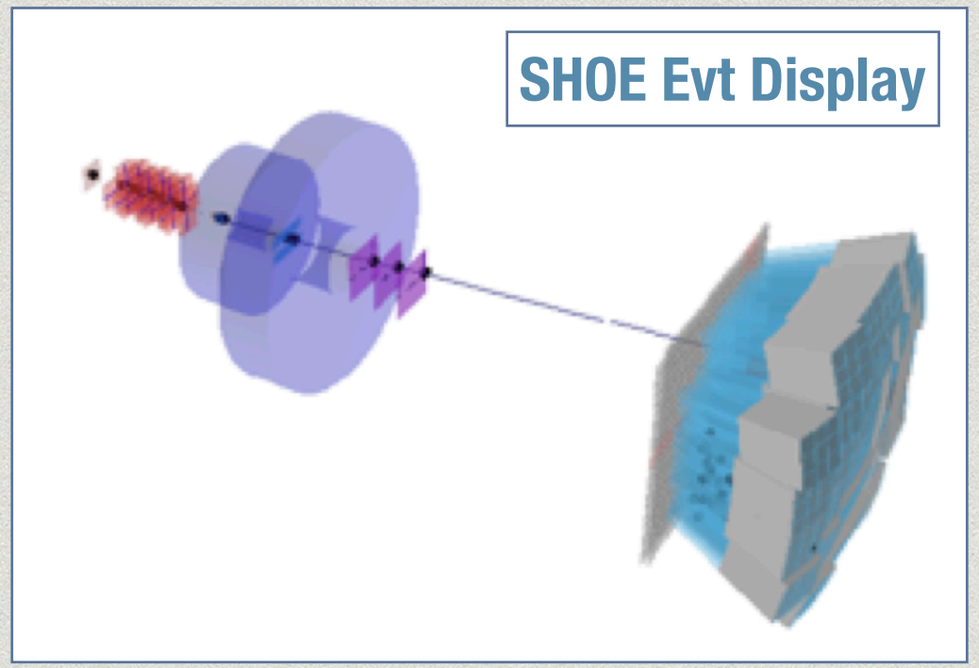
4. Run DecodeGlbAna on DecodeGlbToe output

```
../../bin/DecodeGlbAna -in Out_DecodeToe.root -out Out_Ana.root -exp 12C_200 -run 1 -mc
```

NB: the MC regions are needed to the global analysis

DecodeGlbToe

- Input: clusters/points of each detector
- Conversion of detectors clusters/points to glb track points
- Fit with mass hypotheses exploiting the charge Z reconstructed by the TW
- Able to retrieve detectors clusters/points from glb track points



DecodeGlbAna: the Analysis (1)

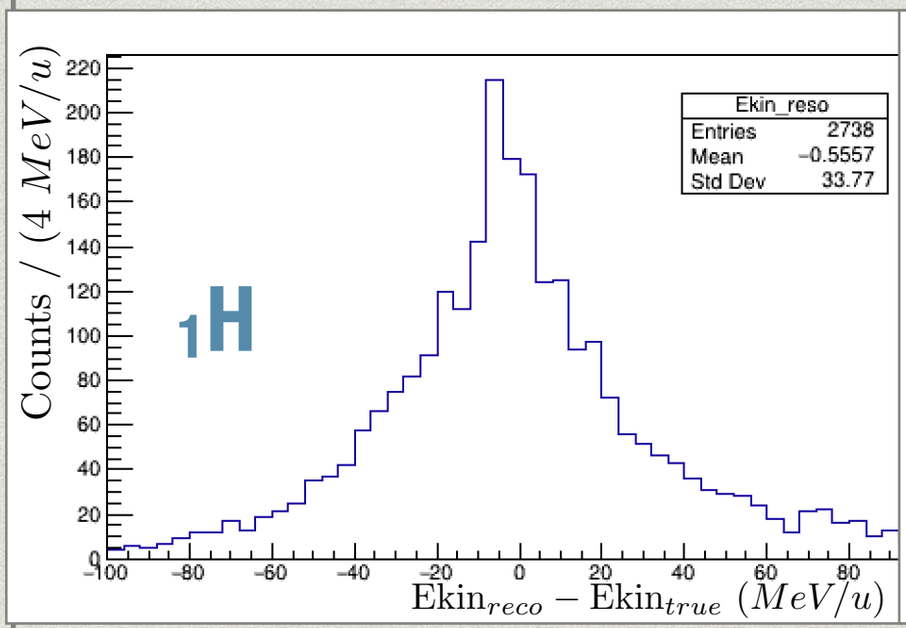
- **Assign a glb track particle index to retrieve the true MC info**
  - Retrieve clusters/point of each detector from global track measured points (VT tracks > 1 => fragmentation events)
  - Assign a true MC particle index to each cluster/point
    => the purity of clusters (which may be composed by different particles) is ~ 98-100%* for each detector (100% by definition in TW)
  - Assign a glb track particle index
    => the track purity (same particle for all track point) is ~ 86%*

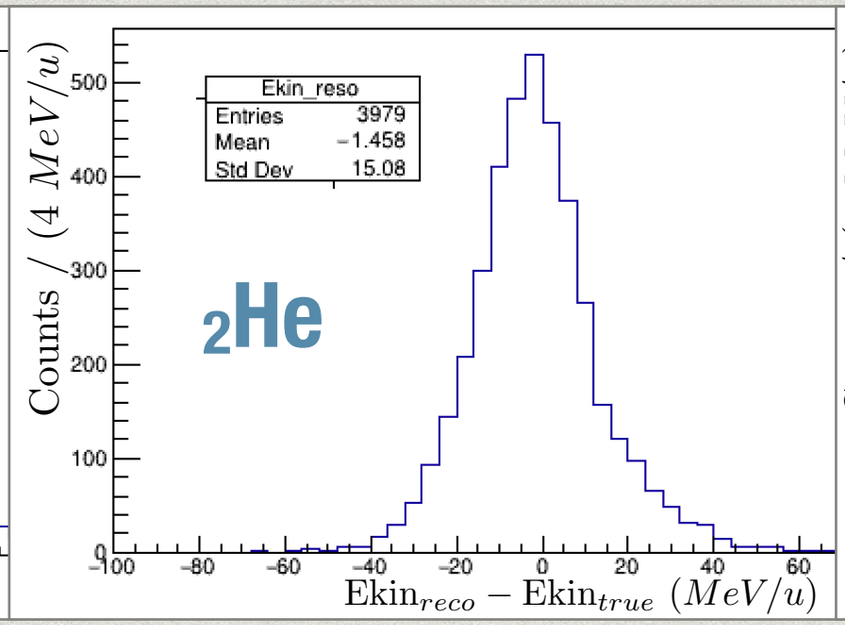
preliminary

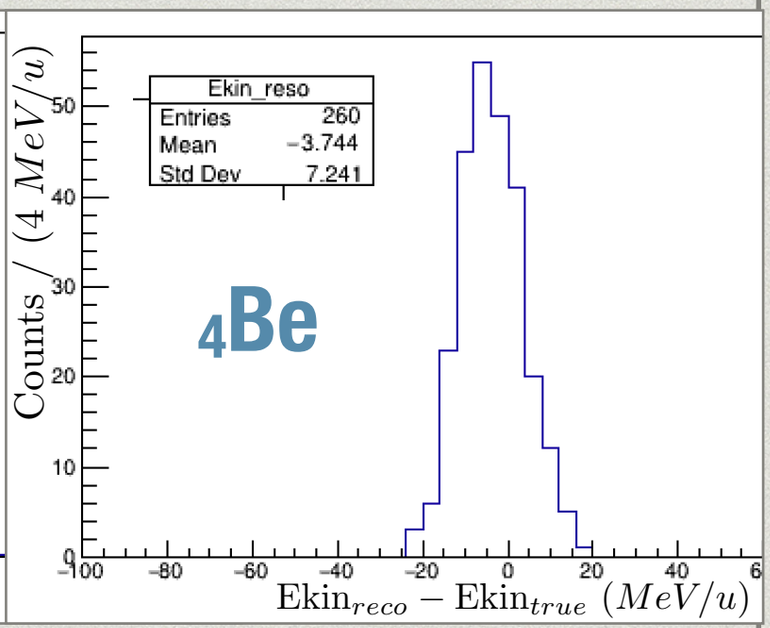
***no PileUP events**

DecodeGlbAna: the Analysis (2)

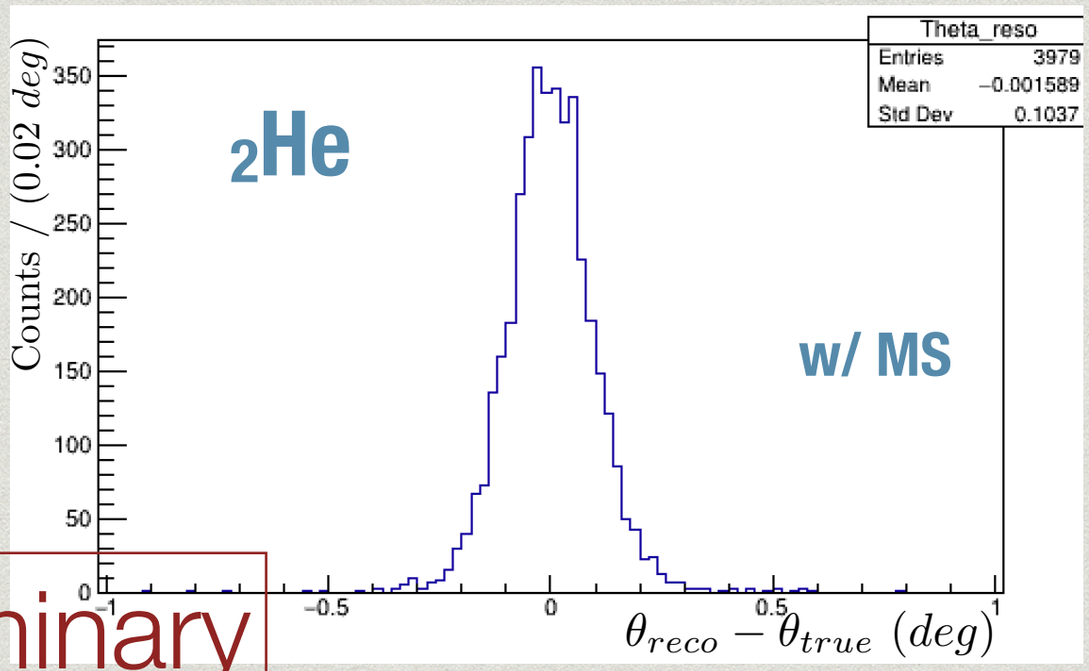
- Ekin reso

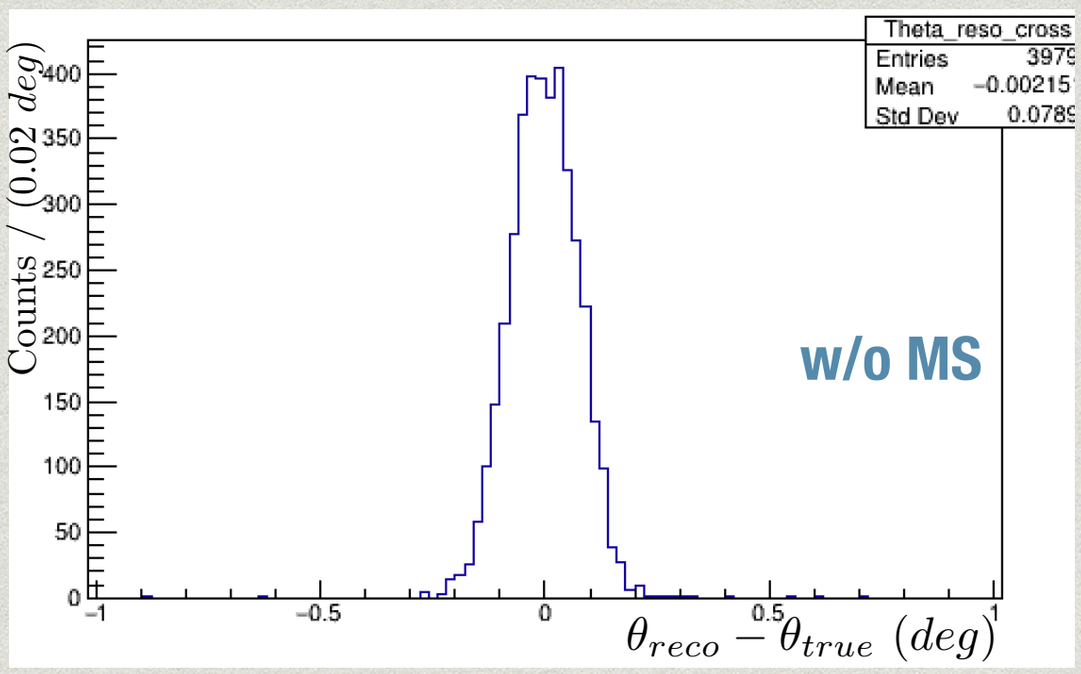






- Theta reso





preliminary

TO DO (a lot of stuff…):

- Ekin/Theta reso study to set the cross section binning
- Combinatorial Bkg evaluation
- Cross Feed correction
- Efficiency
- Unfolding
- …

…but we have almost everything in there