Bin optimization and cross-section studies

Monaco Vincenzo
Abdul Haneefa K
University & INFN of Torino

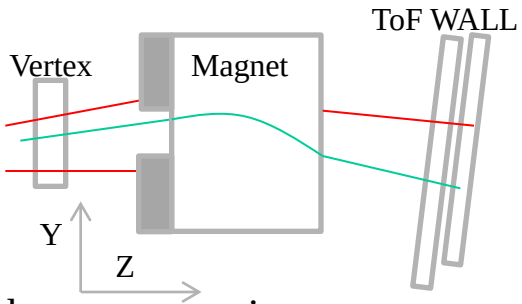
Look Up

- Fraction of wrong tracks
- Use of Vtx Chg for track match
- Optimization of bin sizes
- DATA/MC comparisons
- Cross-section studies

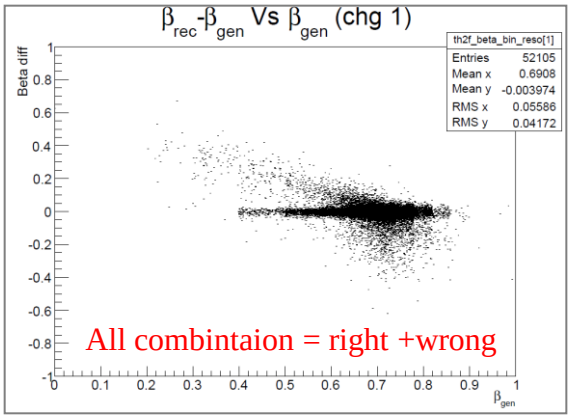
Fraction of wrong tracks

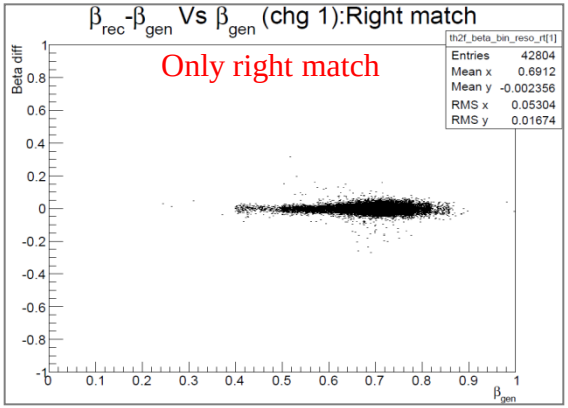
Navigation in the MC particle chain to check if the match of VTX track with the TOF hits made in the reconstruction is right or wrong.

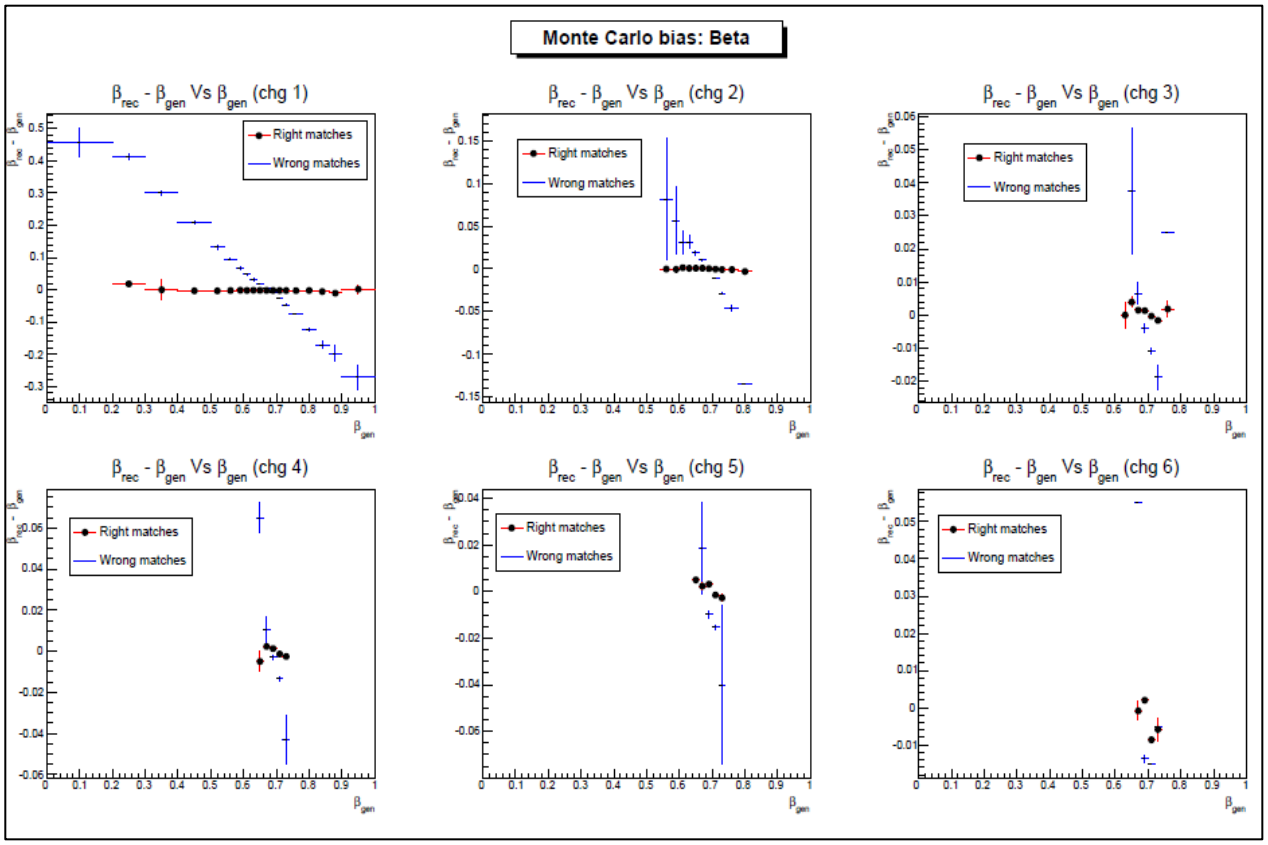
$$\%\ \text{of wrong matches} = \frac{N_{reco}^{Wrong}}{N_{reco}}$$



The study using only VTX tracks from a vertex matching the BM track in the reconstruction.







Only right matched tracks are considered for further studies

Optimization of the TOF/VTX matching criteria in the reconstruction

Selection of best match:

- tracking performed on all combinations of VTX tracks and TOF hits

The final track selection can be done by using:

- Delta(y): difference between the Y at the TOF and the Y extrapolated from the VTX track
- Delta(ch): difference of VTX and TOF charges

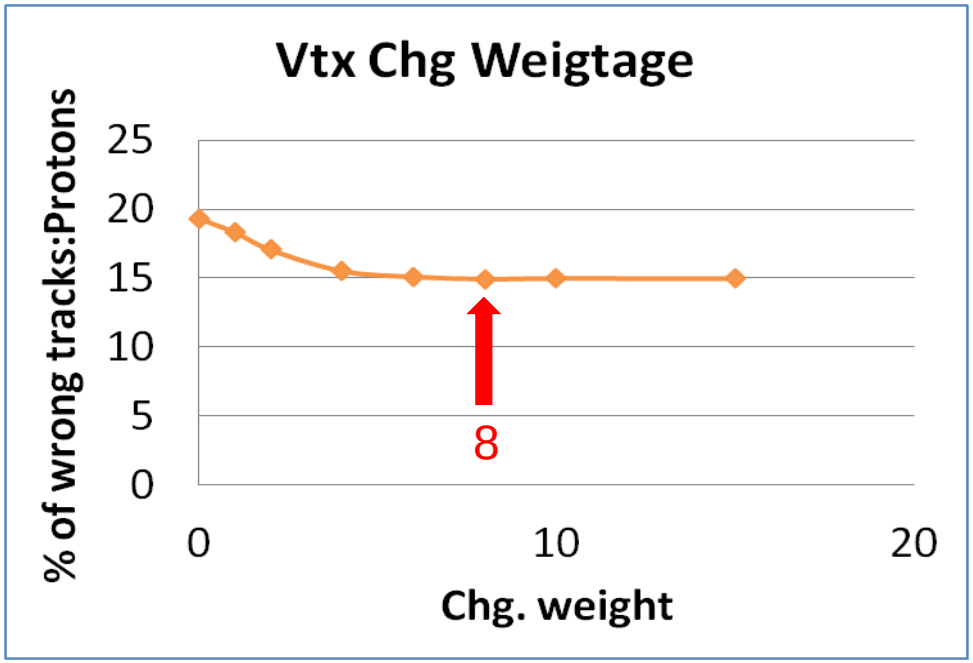
Minimum difference in Diff $_{tot}$ to select best track (scoring function):

$$Diff_{tot} = \sqrt{Diff_{y}^{2} \cdot y_{w}^{2} + Diff_{ch}^{2} \cdot C_{w}^{2}}$$

Final values of scoring functions are:

y_w=1.

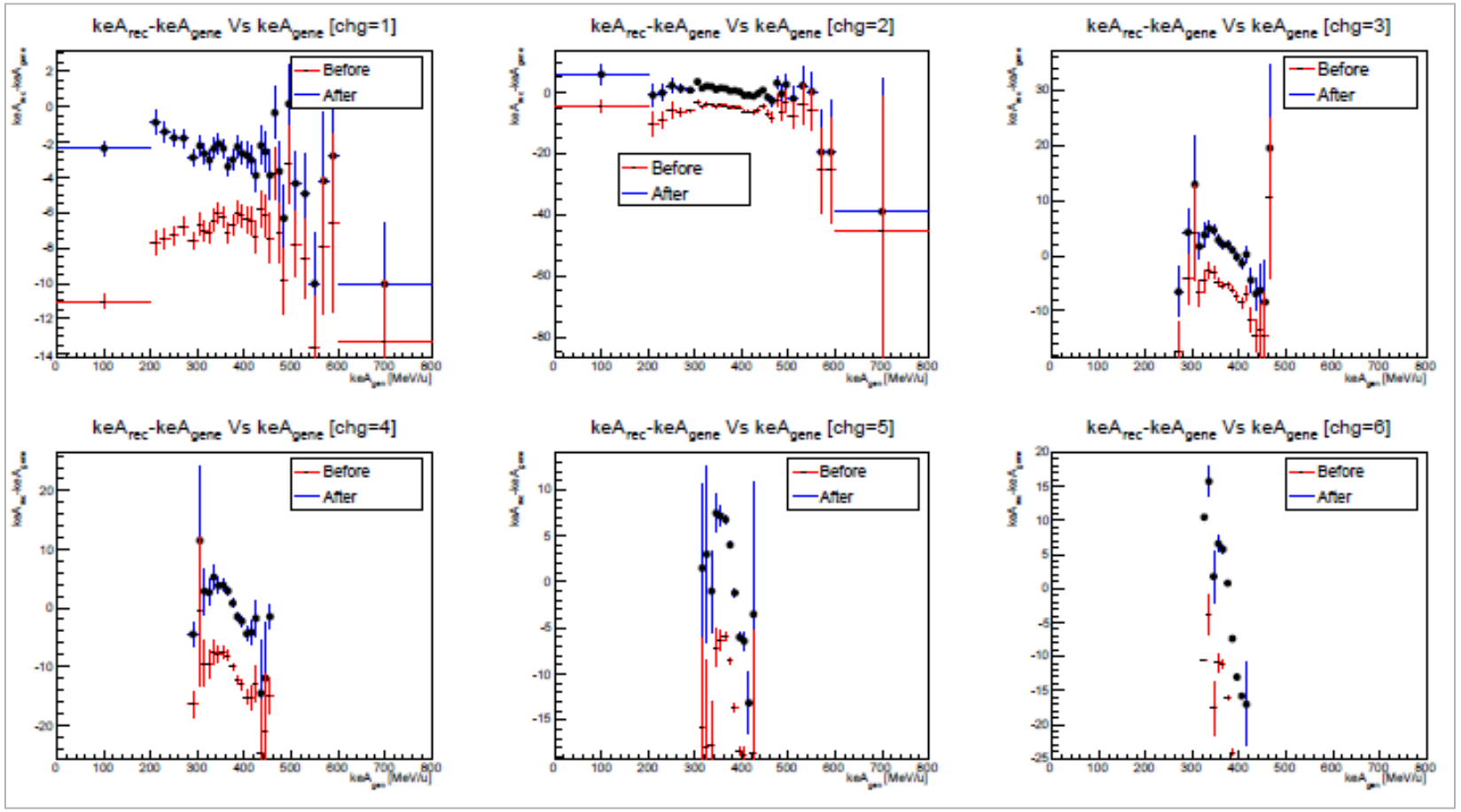
c_w=8.



Correction for energy loss in half thickness of the target

8 mm carbon high density of 4.48 g/cm^3

- An offset in resolution fits remains even for right matched events .
- It is corrected by considering the expected energy loss in half thickness of the target.
- Energy loss at target is corrected (using the bethe bloch with the chg, beta information from the reconstruction) for different reconstructed quantities : ke/A, β, mom/Z.

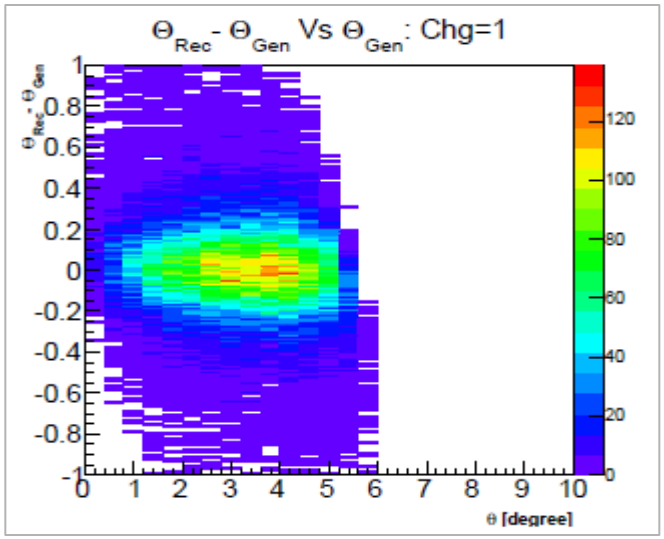


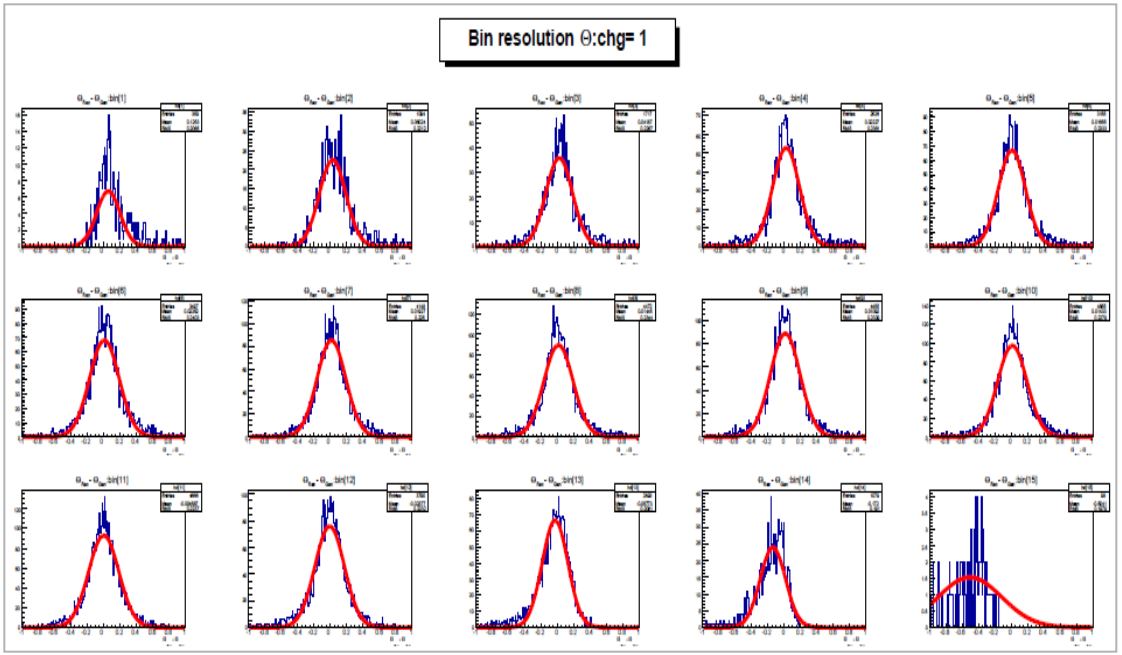
Bin definition

- To limit the migration between different bins, reasonbale bin definitions are needed.
- Bin sizes are chosen to compact with the offset and resolutions between reconstructed and generated quantities
- Only right TOF/VTX matches used in the following plots.
- $\Theta_{reco} - \theta_{gene}$ plotted with respect to $\theta_{generated}$ to give the resolution of theta for different charges.
- Bins are chosen to maximize efficiency and purity.

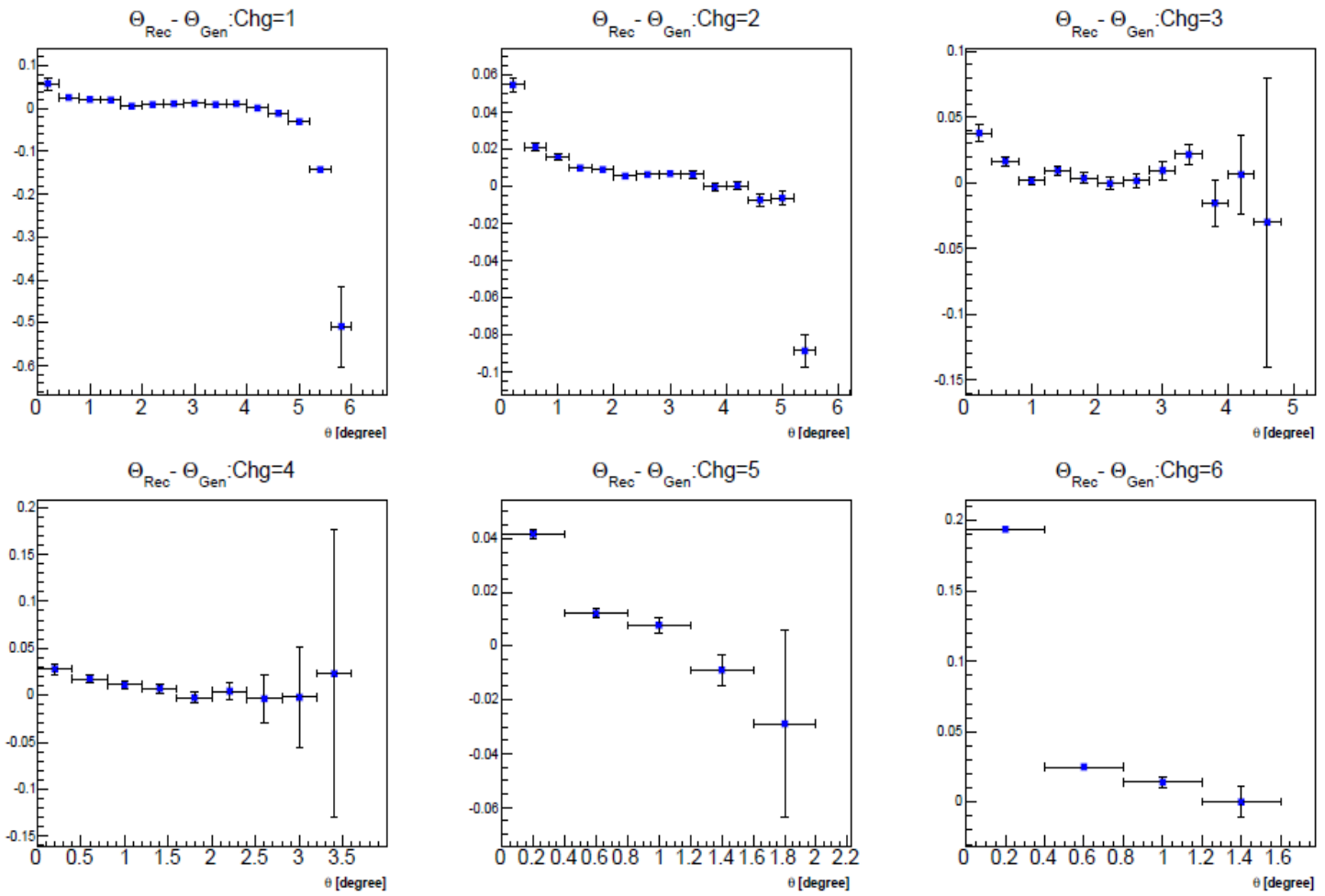
$$Efficiency\ (Z,B) = \frac{reco + gene(Z,B)}{gene(Z,B)}$$

$$Purity(Z,B) = \frac{reco + gene(Z,B)}{reco(Z,B)}$$





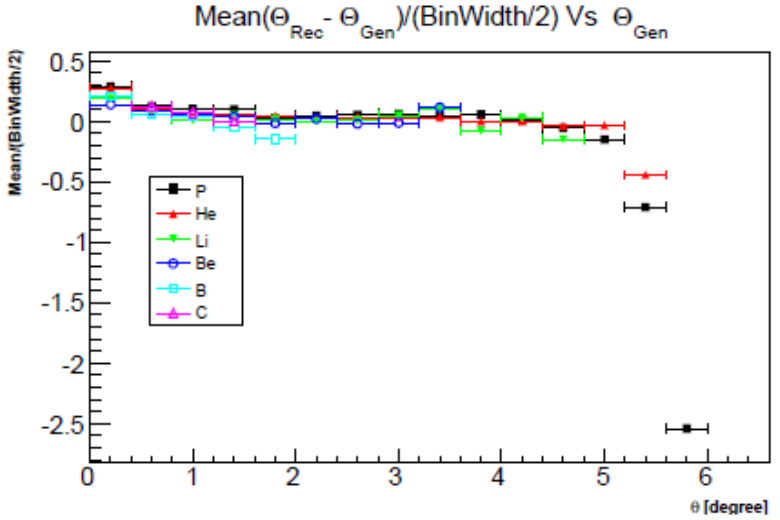
➢Resolution offsets from mean of previous fits (θ_{reco} - θ_{gene}) ; after the corrections.

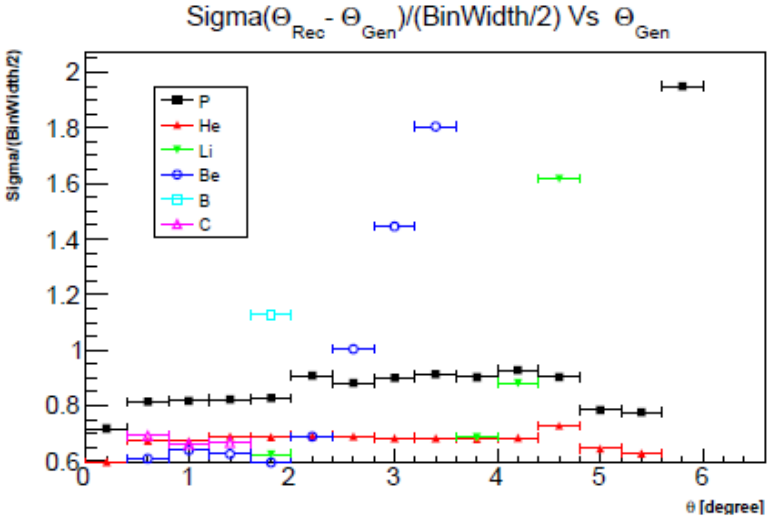


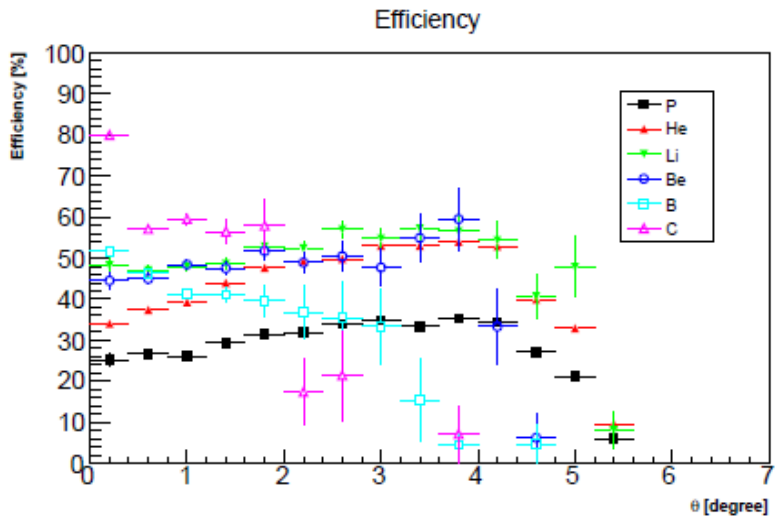
The offset are less than the bin sizes

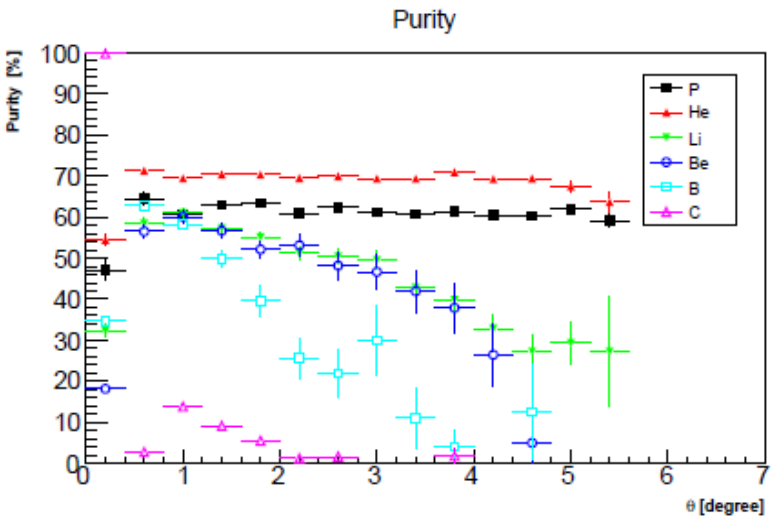
- Mean and sigma of the fits compared with the bin sizes.
- Efficiencies and purities for each bin

Bin resolution study



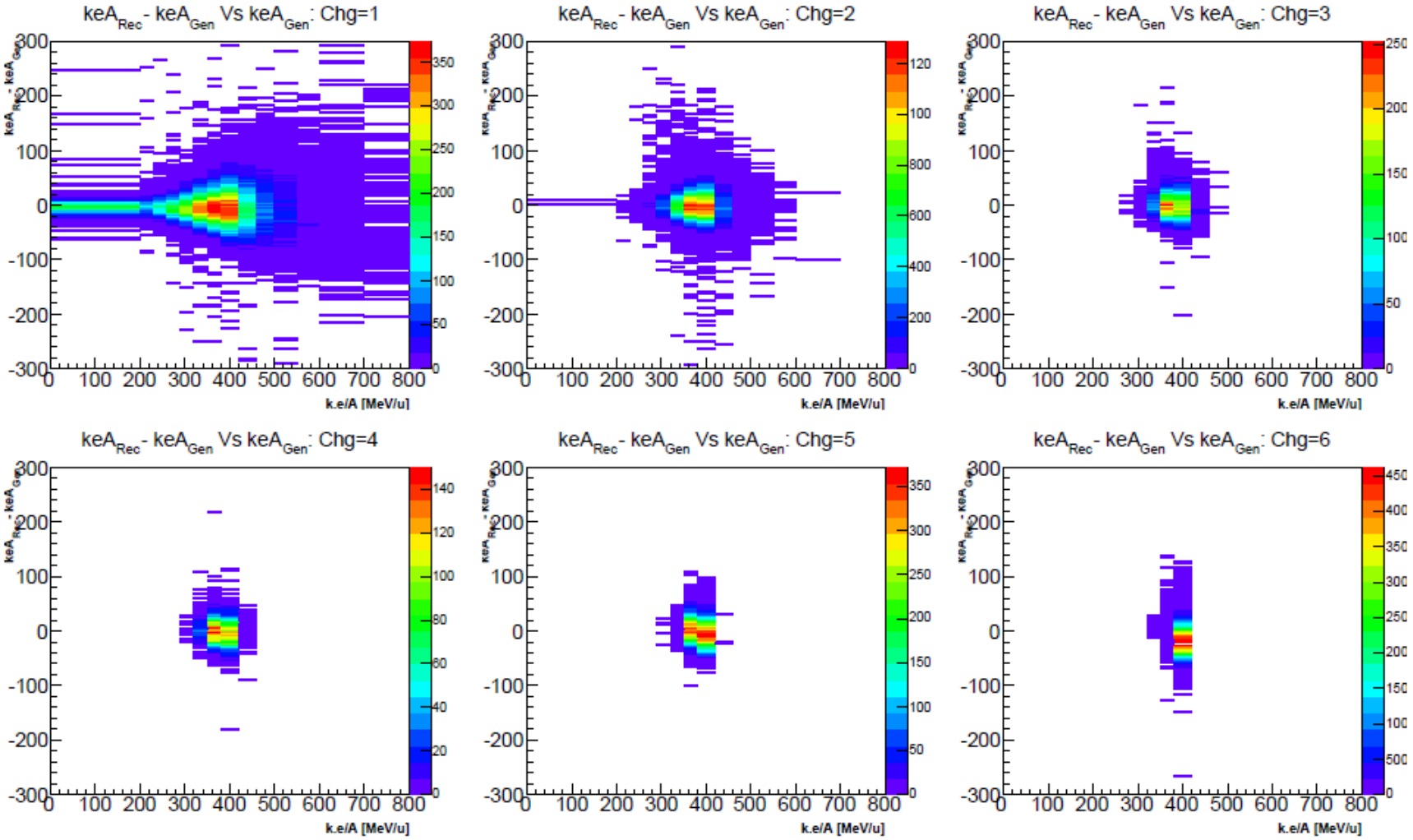






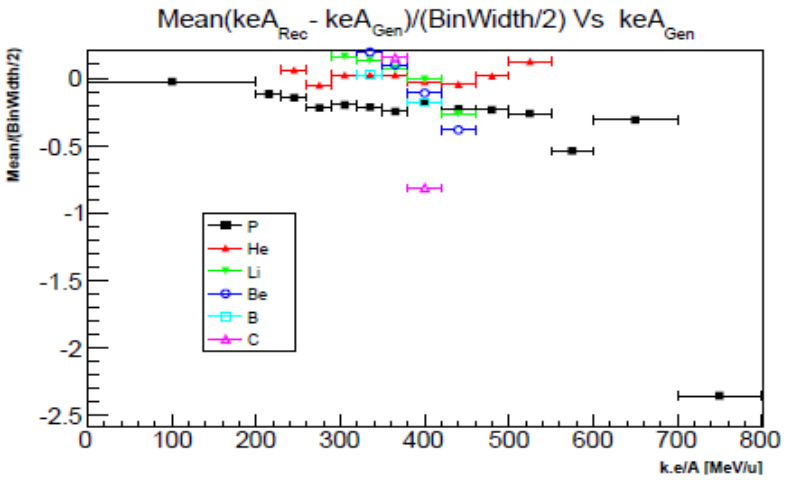
Kinteic energy per atomic mass : ke/A

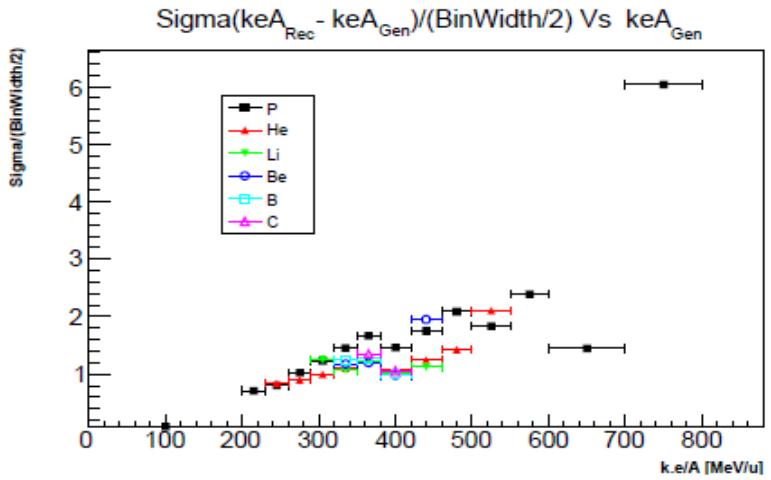
Bin resolution:keA

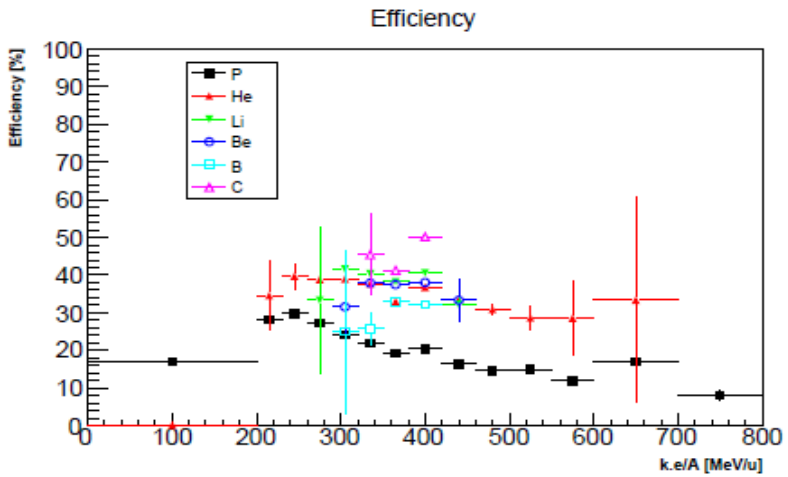


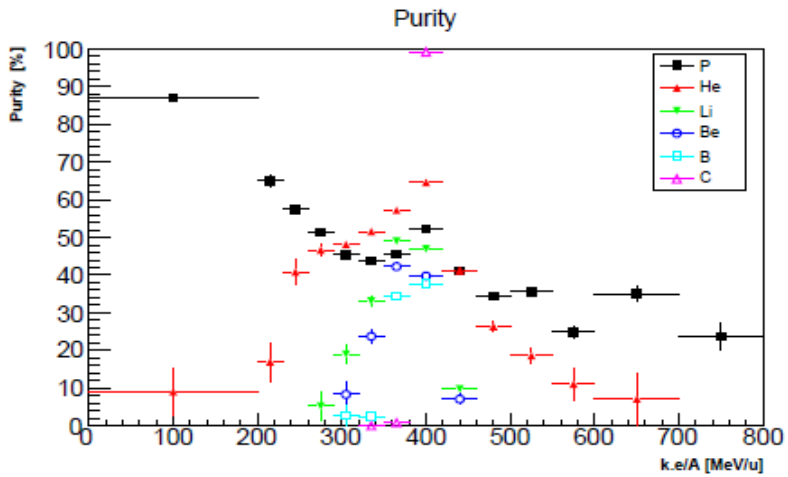
- Mean and sigma of the fits compared with the bin sizes.
- Efficiencies and purities for each bin

Bin resolution study

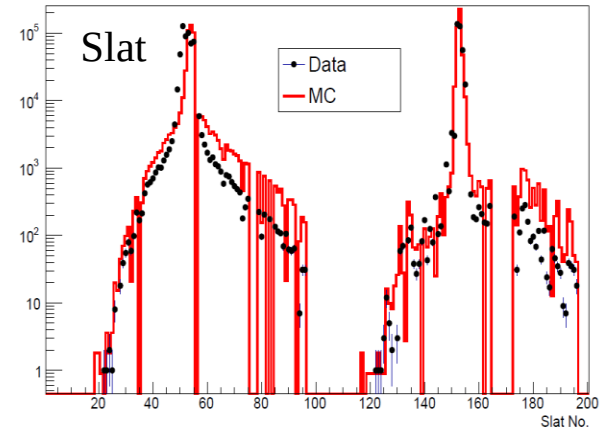


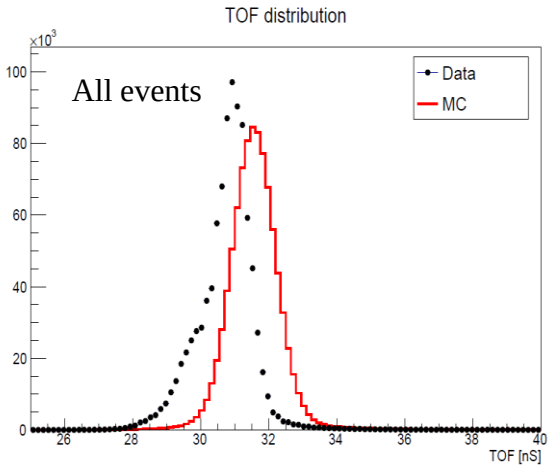


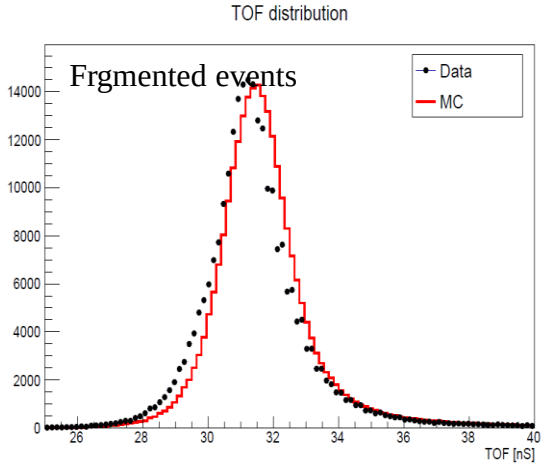


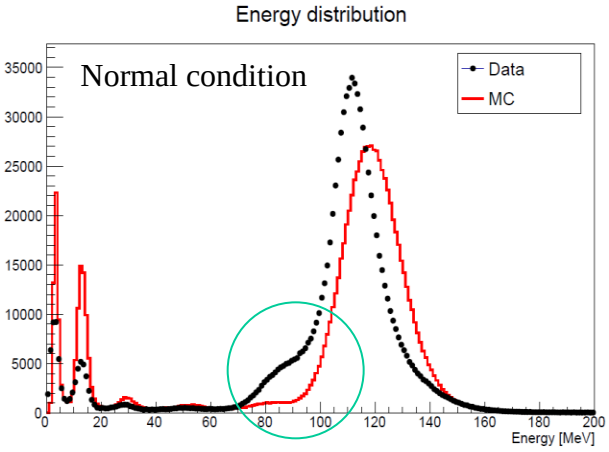


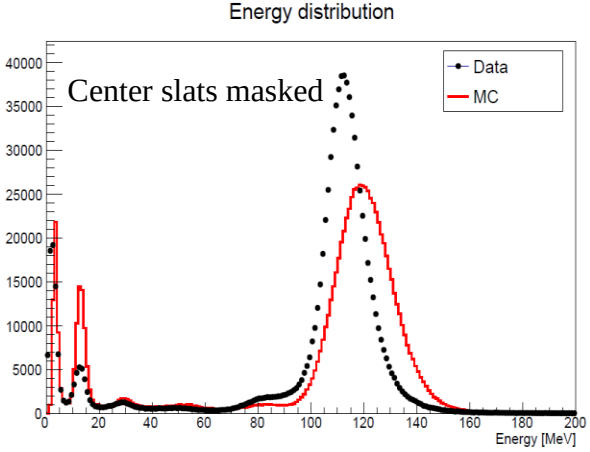
Data/MC comparison:ToF WALL quantities

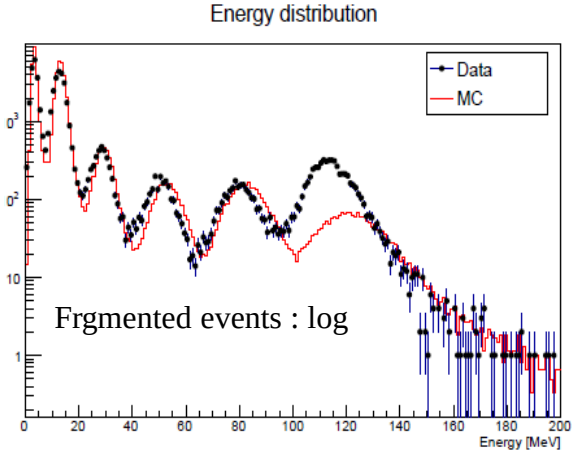








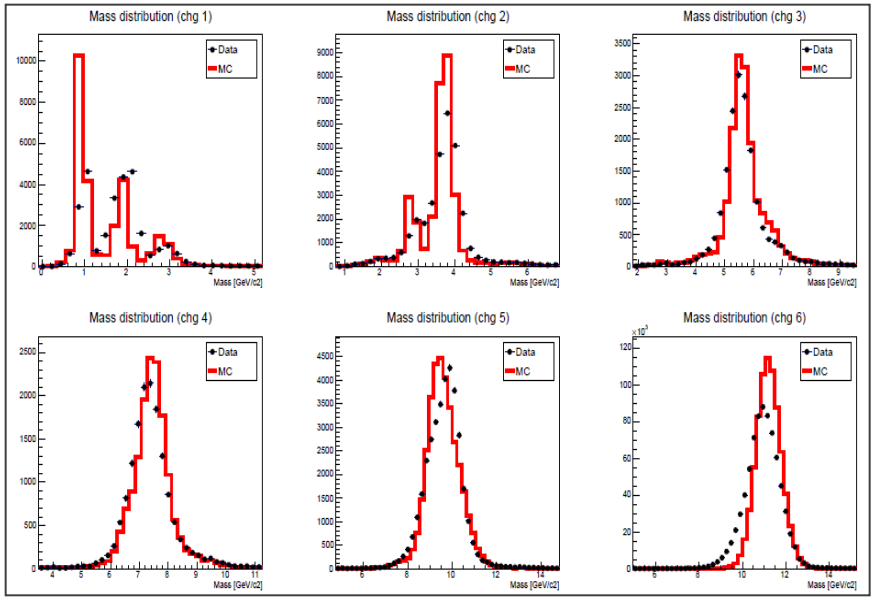




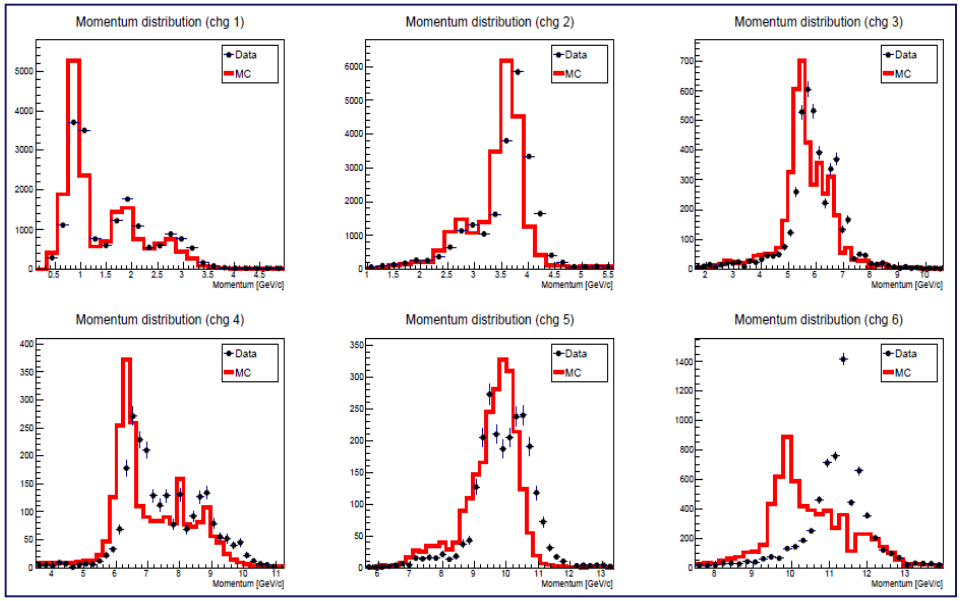
- Slat occupancy having good match with DATA and MC
- Disagreement in TOF and Y (not shown here) alomost disappears by requiring fragmentation at the VTX
- Excess peak at charge =5, disappears by masking problematic central slats
- Calibration problems in the central slats
- Good agreement in eloss at low energies, offset at the C peak

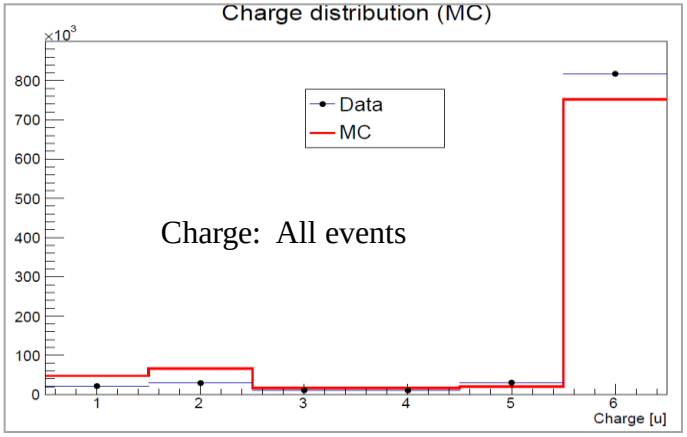
Data/MC comparison: mass

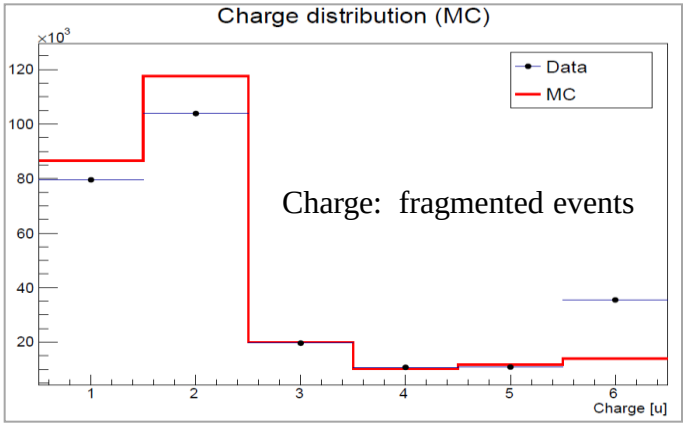
Mass: All events



Mass: Fragmented events

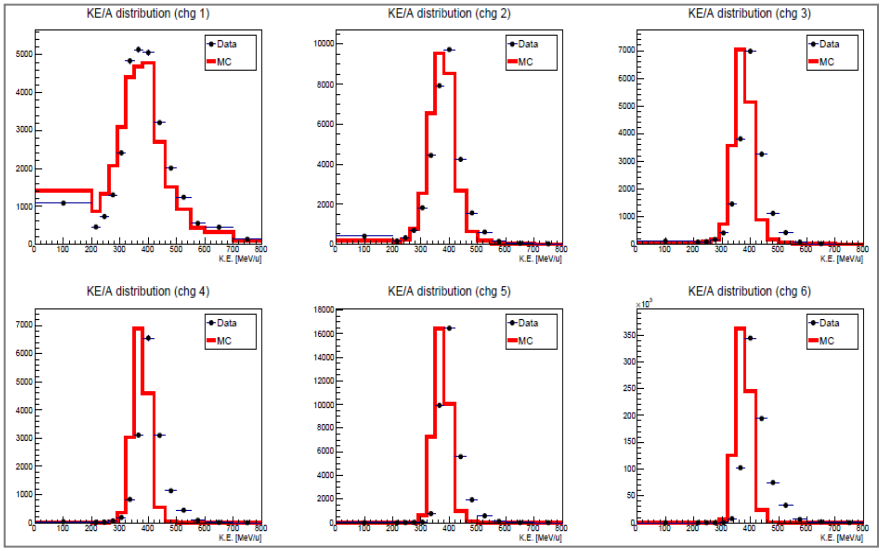




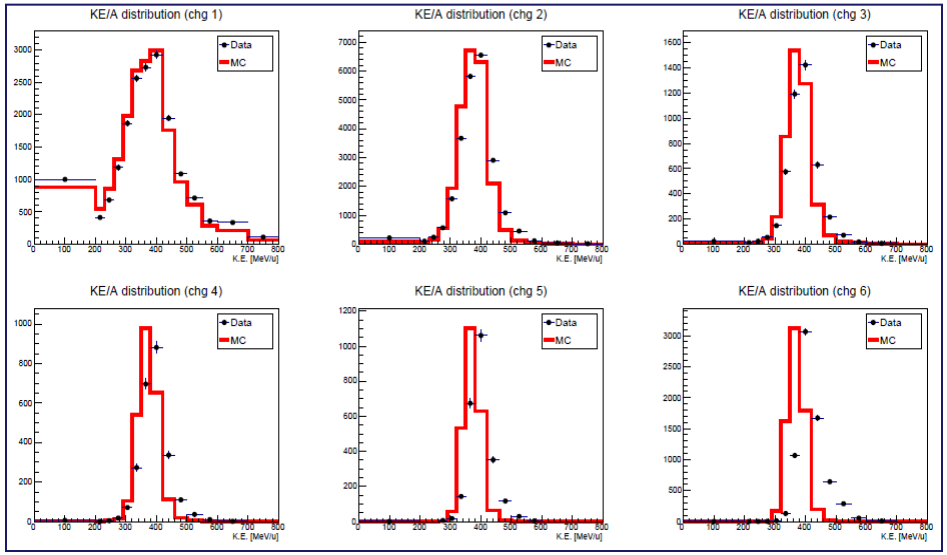


Data/MC comparison: ke/A, Theta

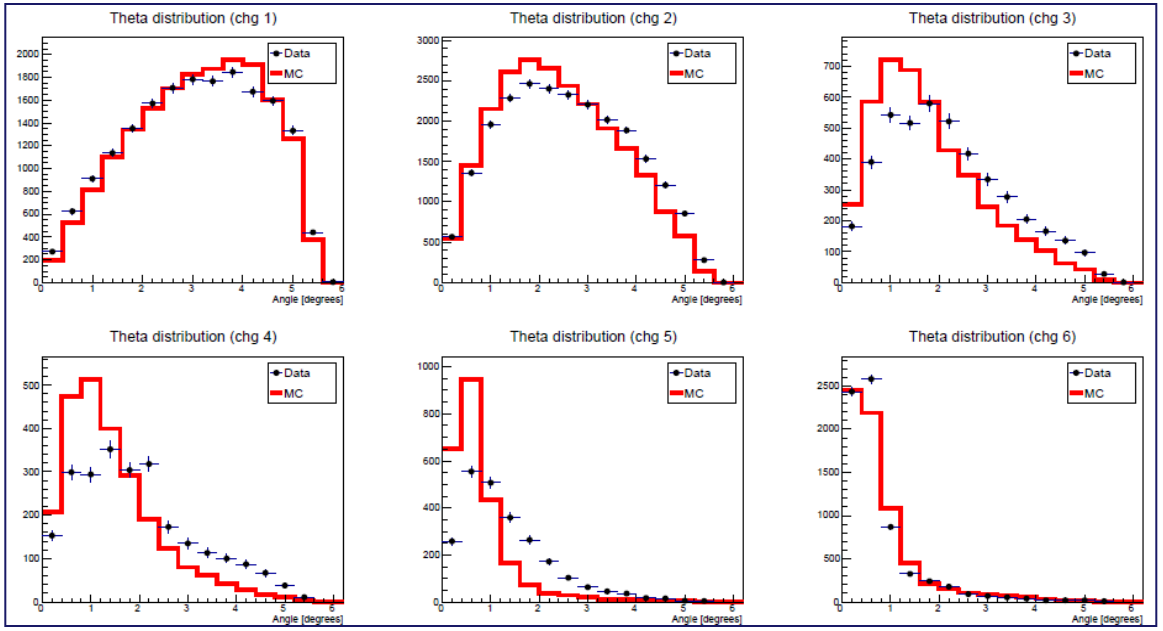
Ke/A: All events



Ke/A: Fragmented events



Theta: Fragmented events



Definition of cross section

➢Preliminary cross sections (vs θ , β or KE/A) evaluated using purities and efficiencies from Monte Carlo for each θ, β or ke bin.

$$N_{corr}(Z,B) = \frac{pur(Z,B)}{eff\,(Z,B)} \cdot (1 - w(Z,B)) \cdot N(Z,B)$$

Were;

w = fraction of wrong matches estimated using MC

$$Efficiency\,(Z,B) = \frac{reco + gene(Z,B)}{gene(Z,B)}$$

$$Purity(Z,B) = \frac{reco + gene(Z,B)}{reco(Z,B)}$$

$$\frac{d\sigma}{d\Omega} \text{ or } \frac{d\sigma}{dke} \text{ or } \frac{d\sigma}{d\beta} = \frac{N_{corr}(Z,B)}{N_C^{12} \cdot N_{ts} \cdot sp_{phase}}$$

Where;

N_c^{12} = No. of triggers

N_{ts} = No. of target nuclei for unit surface

= $TGT_{thickness}$. $TGT_{density}$. 6,02 .10 ^{23} / $TGT_{atm.no}$

sp_{phase} = 2.π. ($\cos\theta_{min} - \cos\theta_{max}$) for theta

= bin width for beta and KeA

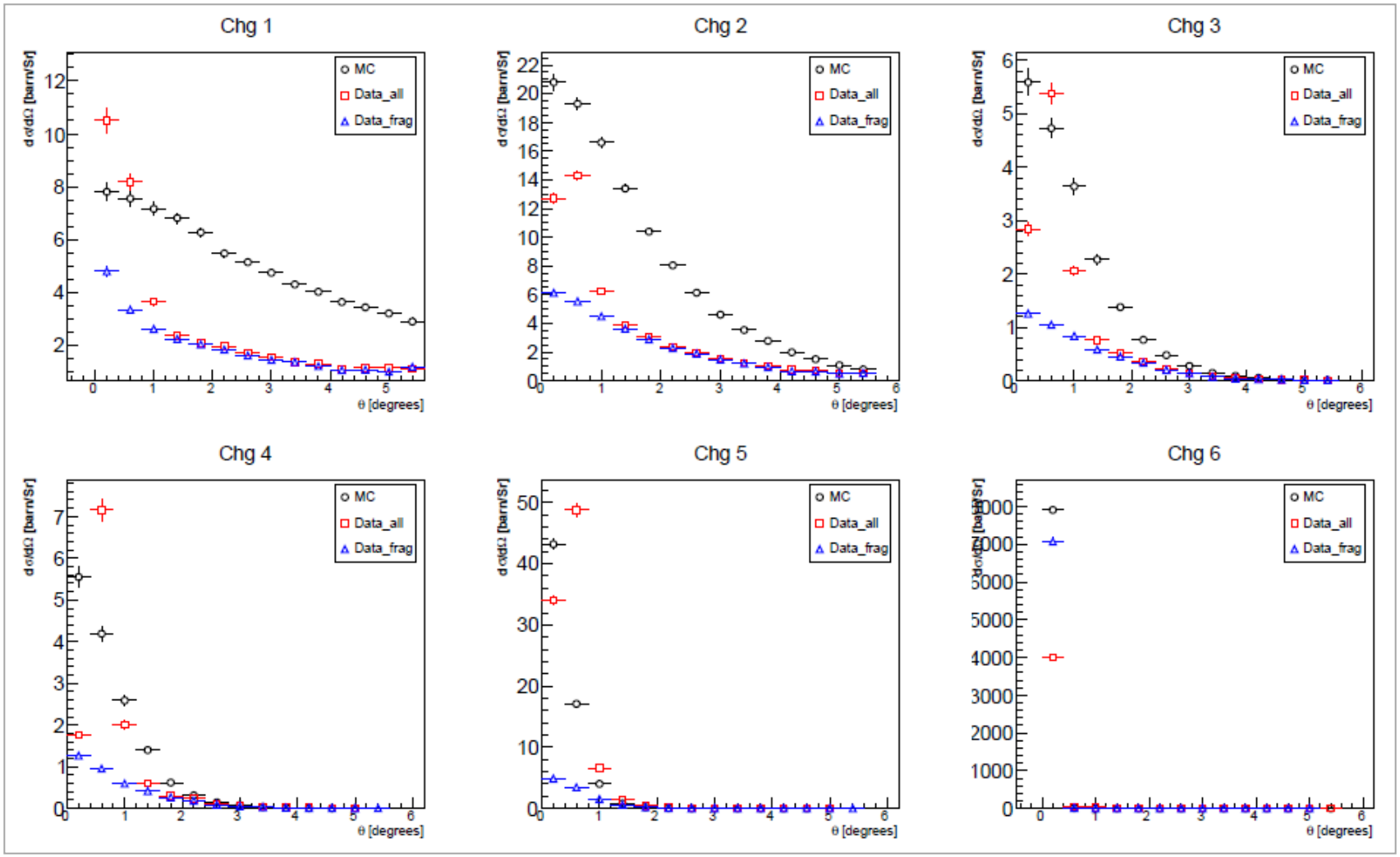
dσ/dθ x 10 $^{-24}$ to convert into barn

Different “hlreco” conditions

- BM: standard conditions, were the VTX tracks matches with the BM
- noBM: selected VTX tracks not restricted to the BM matched vertex
- noCntSlat: Problematic center slats (51,52,53,151) are masked
- noSinCh: Single channel calibration is disabled
- noClust: Clustering of ToF WALL hits is disabled

One million events used for this study in both DATA and MC , software version v1455

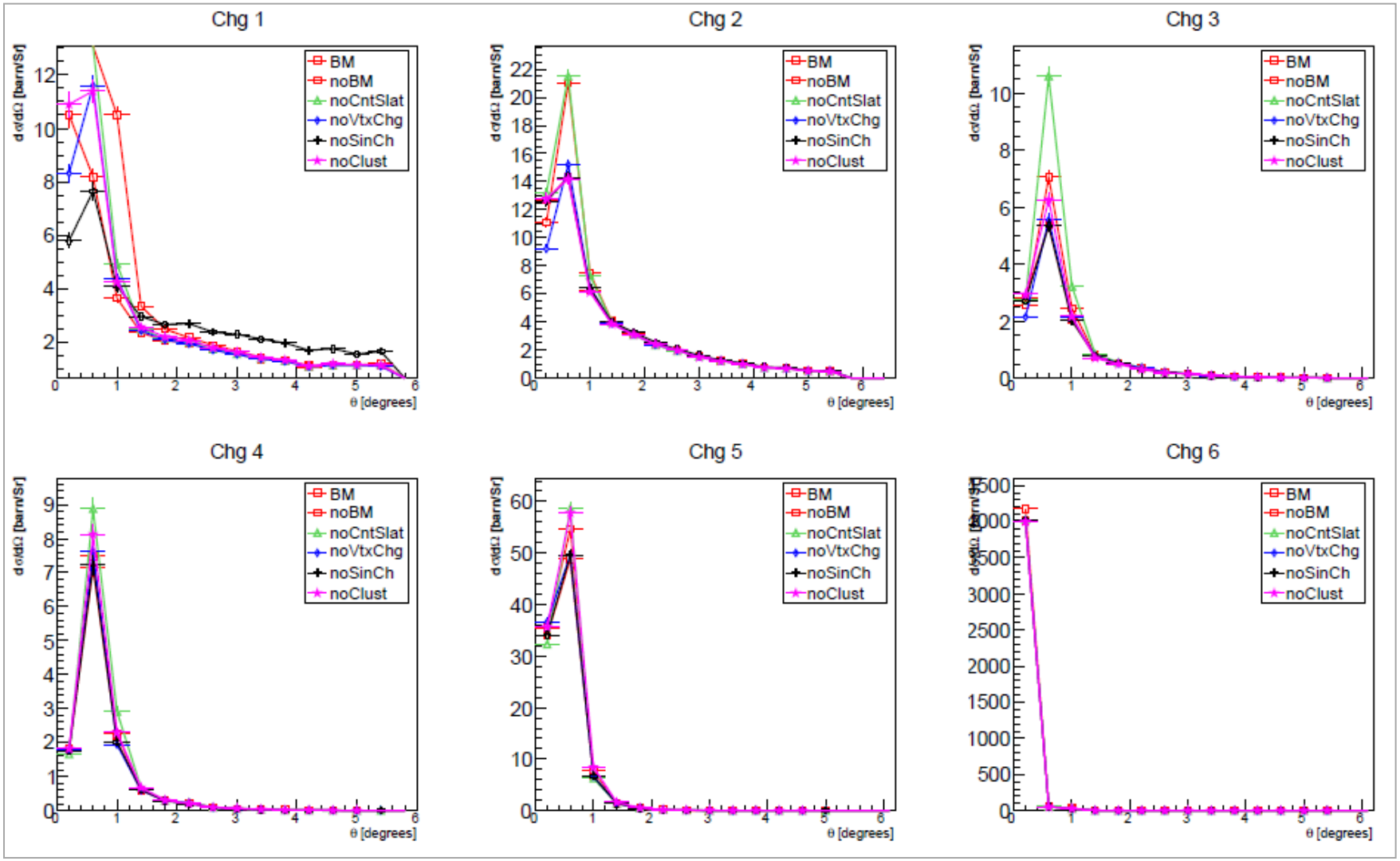
Cross-section studies : θ



- Reasonable agreement between cross sections evaluated with all events or fragmented events.
- Reasonable agreement for theta>1 degree

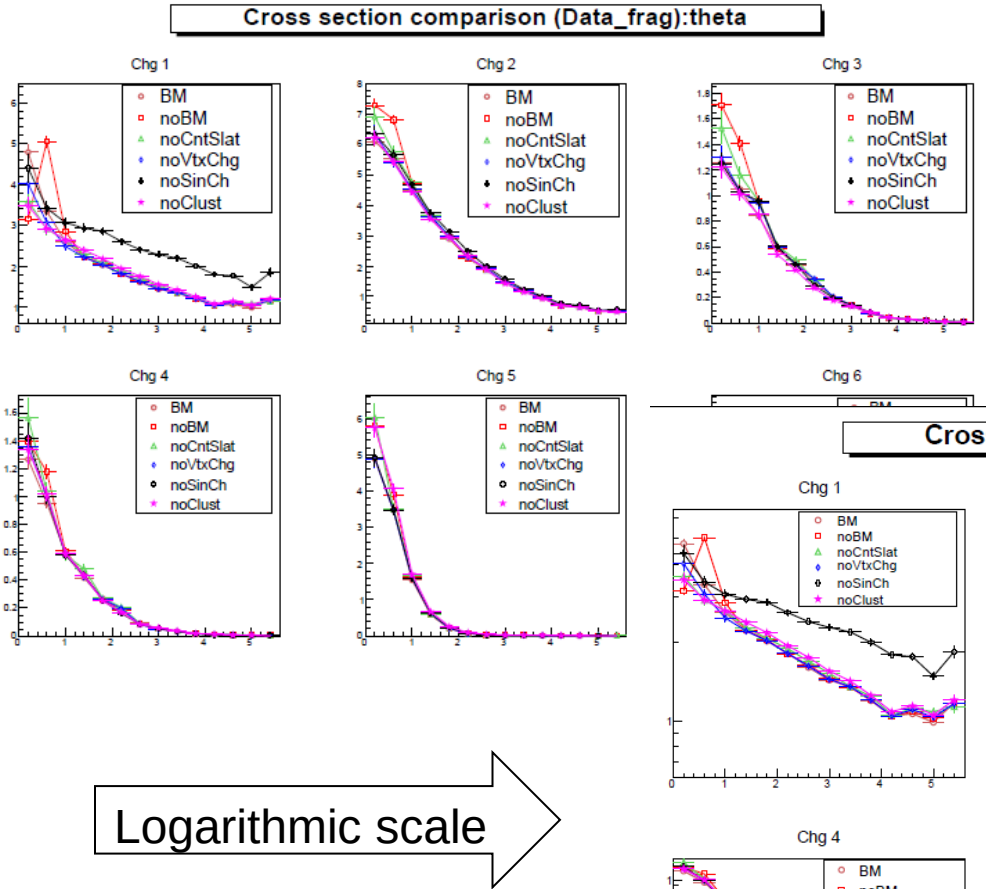
Differential cross section vs θ: for different "hlreco" conditions

Different "hlreco" conditions :- both data and MC to check the stability of the result.

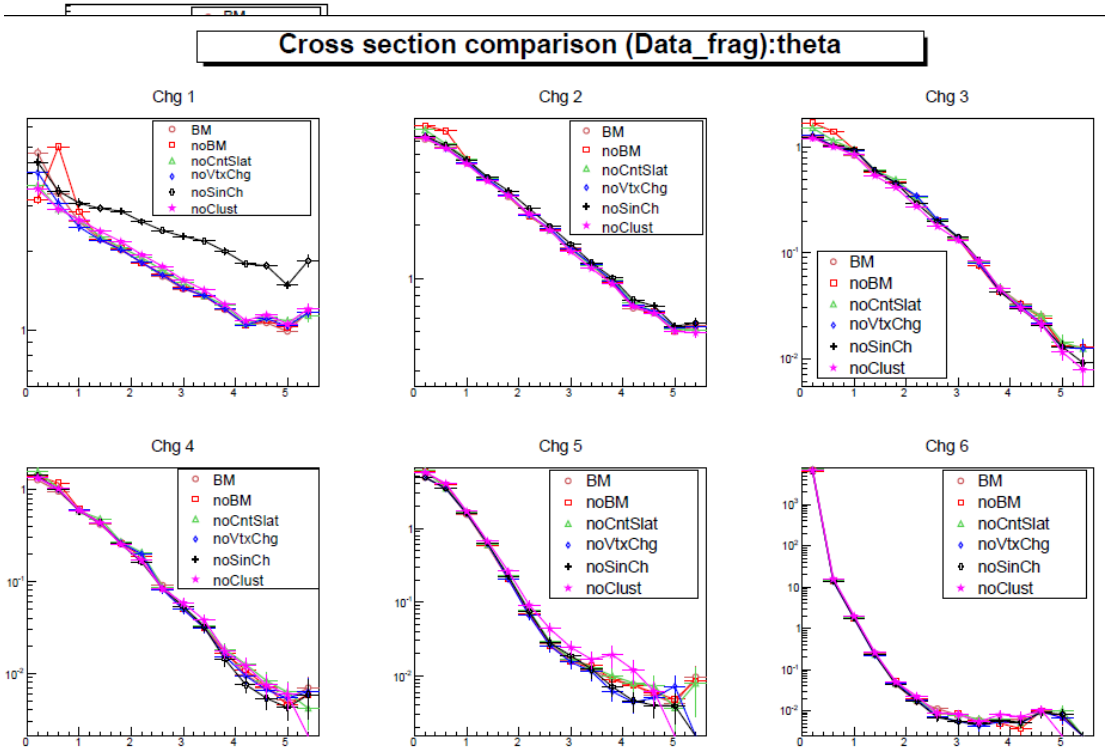


Differential cross section vs θ: for different "hlreco" conditions (2)

Fragmented events :



Normal scale

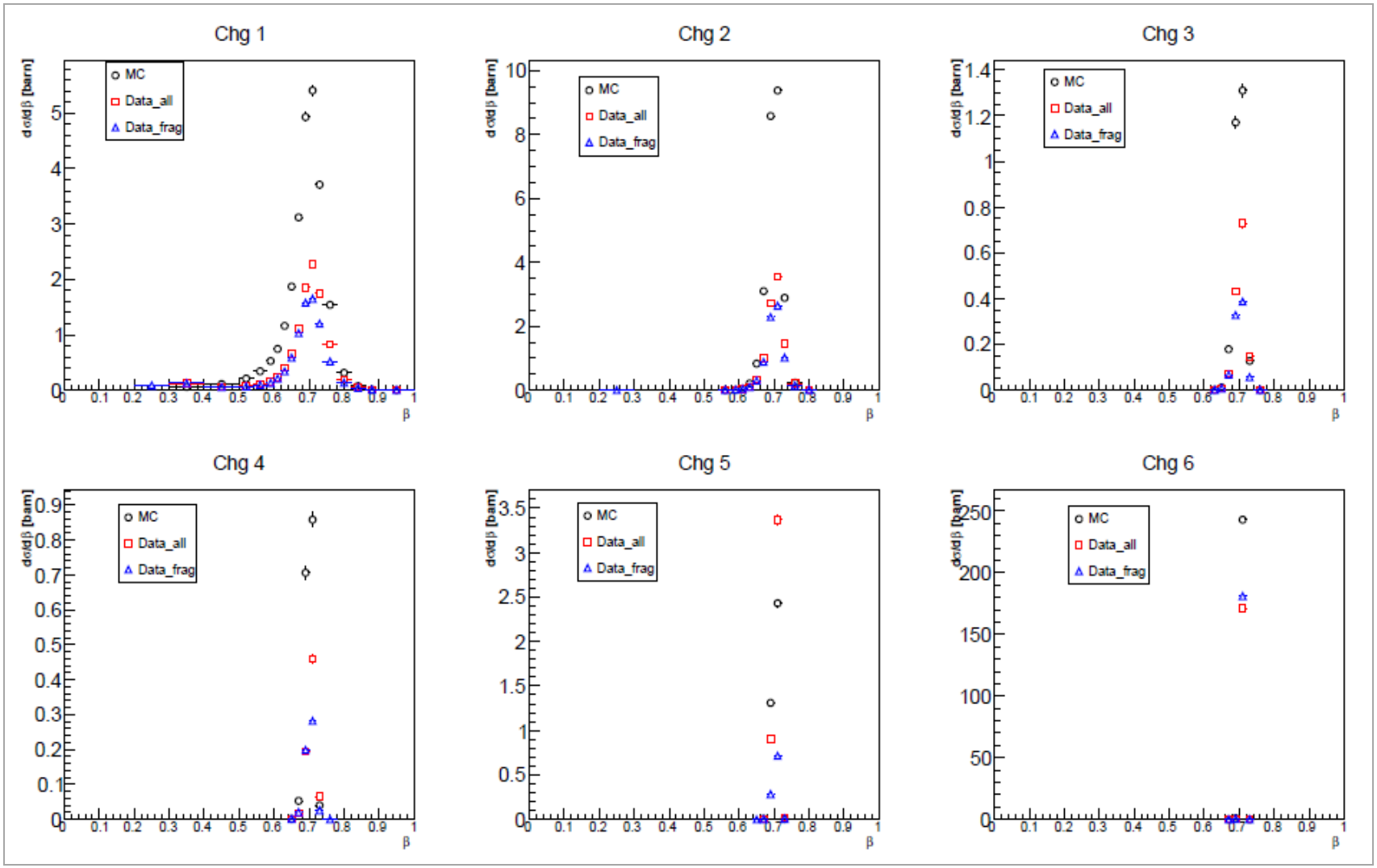


Logarithmic scale

Disagreement when the single channel calibration is disabled.

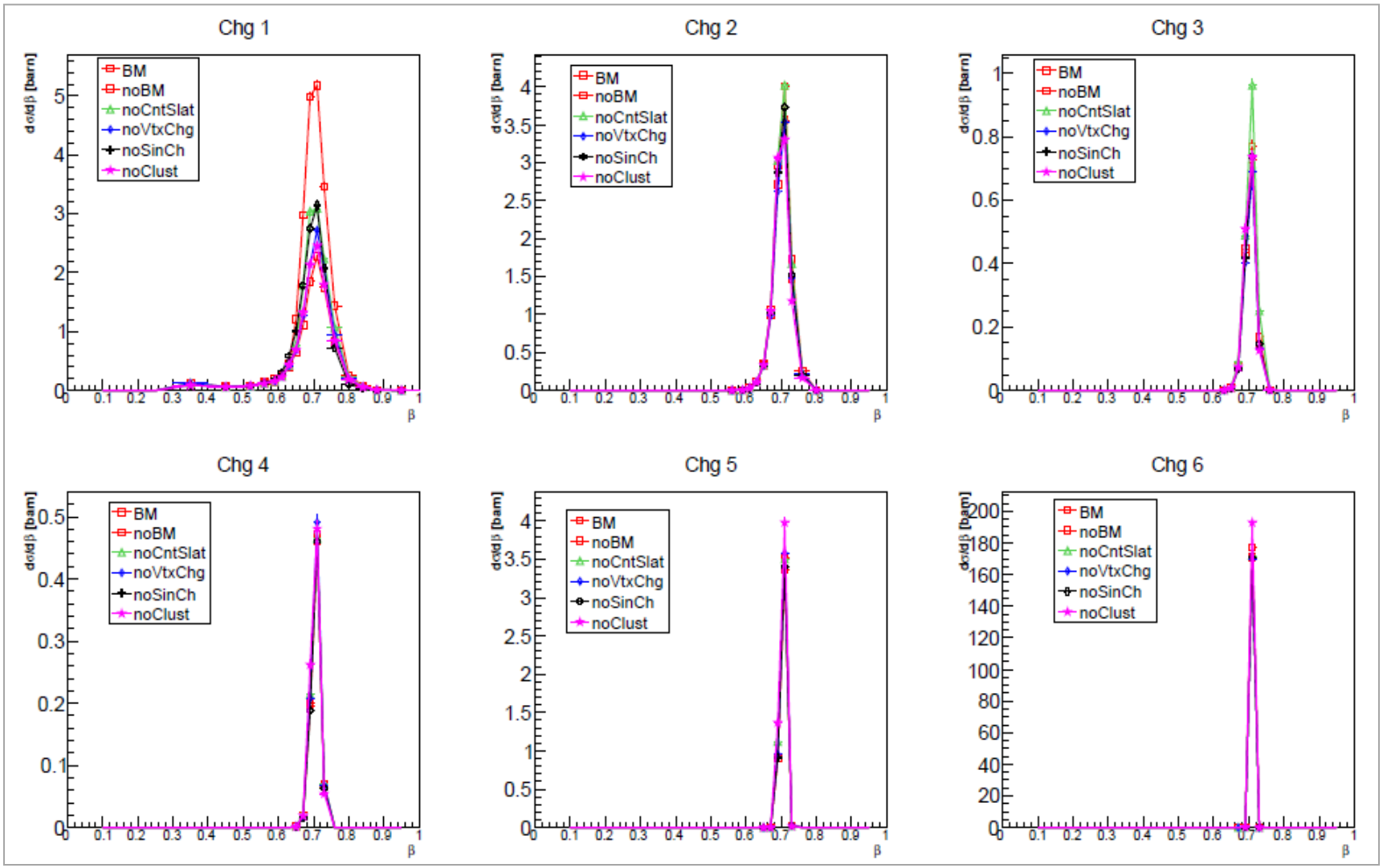
Cross-section studies : beta

We looked at beta because it does not depend on the charge assignment



Cross-section studies : beta (2)

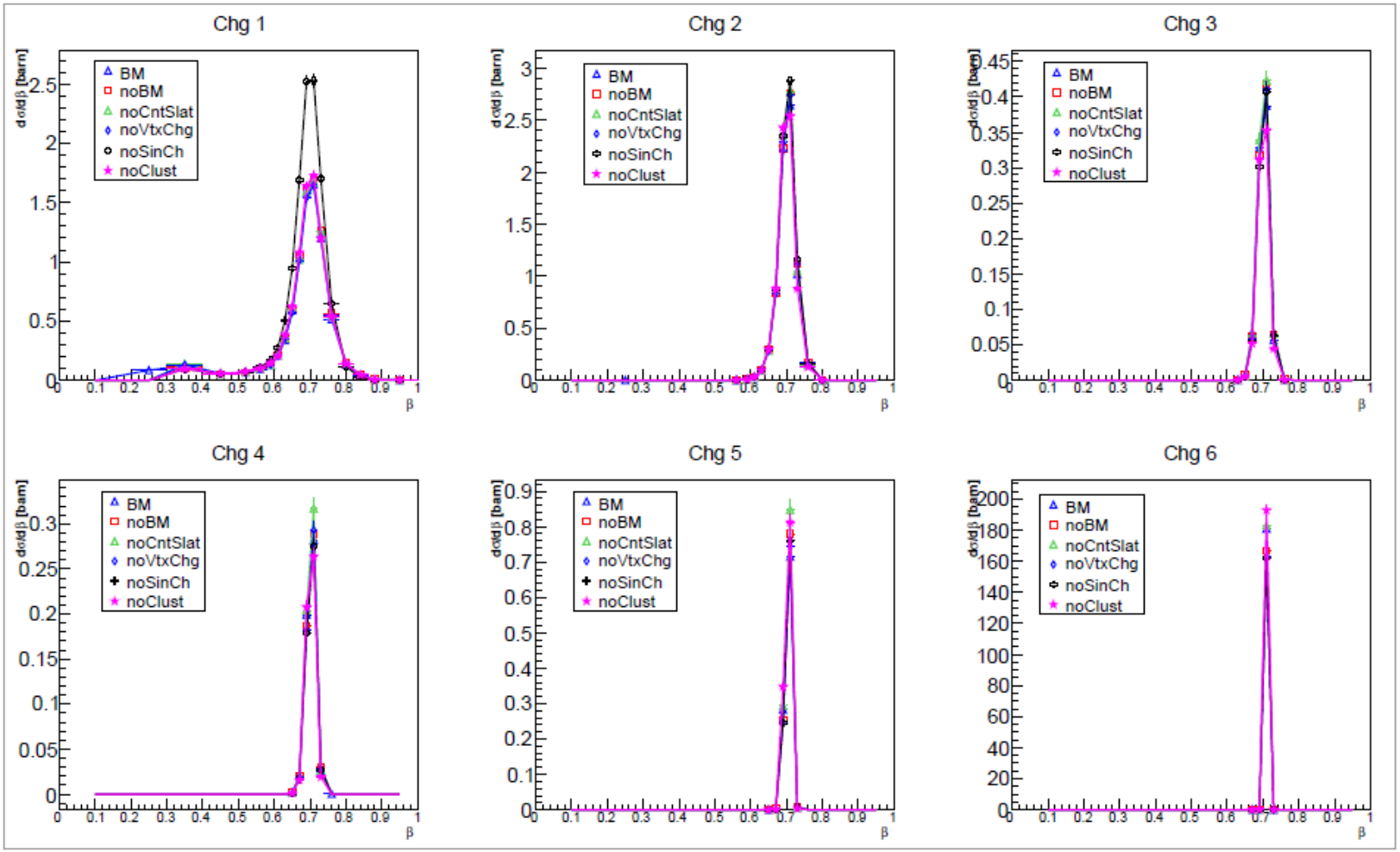
Different “hlreco” conditions :- both data and MC to check the stability of the result.



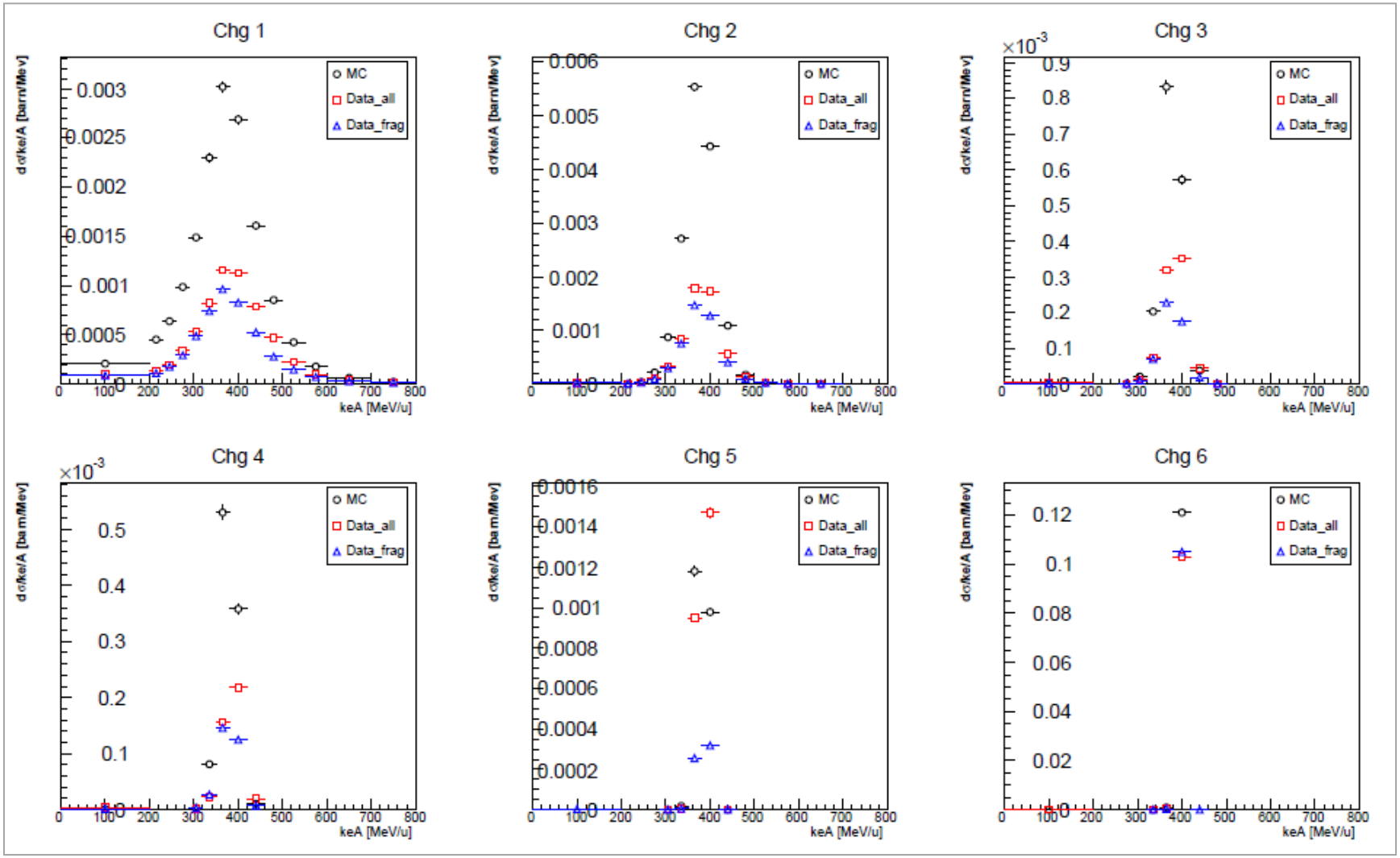
Cross-section studies : beta (3)

Different “hlreco” conditions :- both data and MC to check the stability of the result.

Fragmented events :

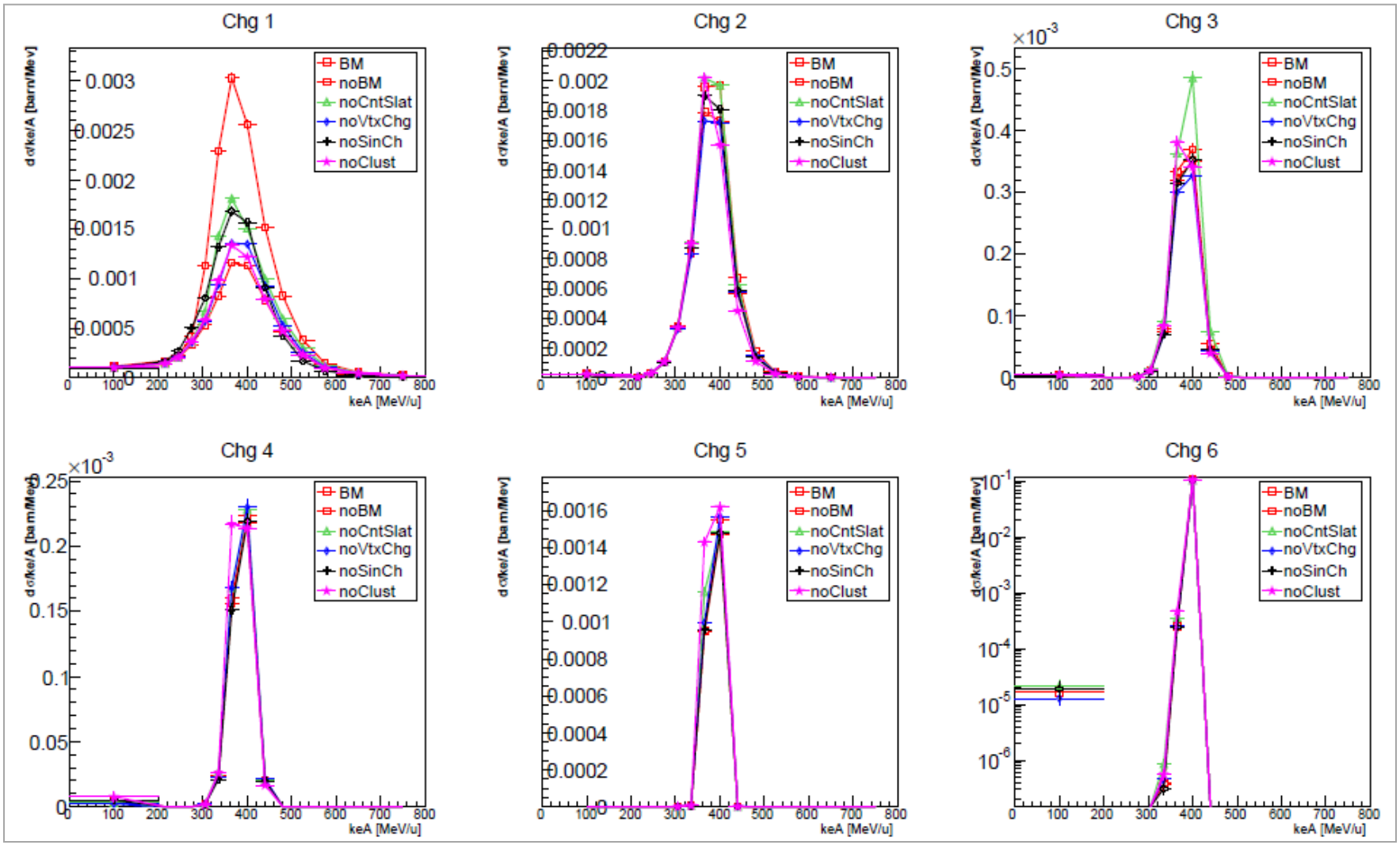


Cross-section studies : keA



Cross-section studies : keA (2)

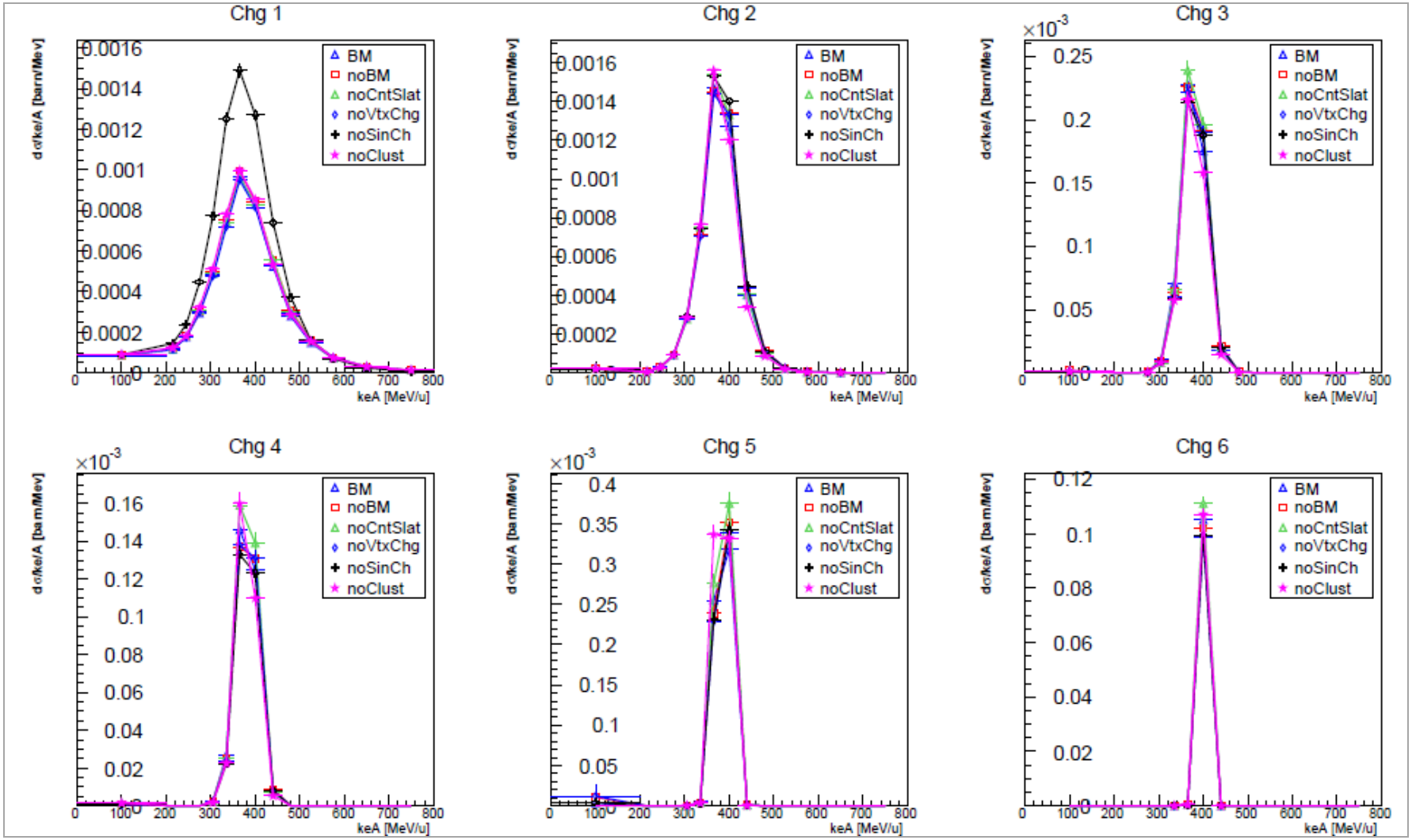
Different “hlreco” conditions :- both data and MC to check the stability of the result.



Cross-section studies : keA (3)

Different “hlreco” conditions :- both data and MC to check the stability of the result.

Fragmented events :



Conclusion

Changes in the reconstruction code to improve the VTX/TOF matches

- Vtx charge used
- Only VTX tracks matching the BM are used
- Bias in the MC reconstruction under control if only right matches are selected (wrong matches are considered as a background and estimated from MC for each bin)
- Attempt to define bins that minimize migrations
- DATA/MC comparison with issues related to the TOF calibration
- Preliminary single-differential cross section quite stable for theta>1 degree