

## **CSC Alignment**

- Closest hit approach
- All hits approach
- CSC case
- CSC hits cut
- New fit method
- New alignment results



## Closest hit approach

Aligned position

**Unaligned position** 



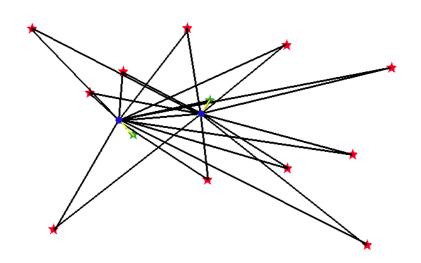
- ★ wrong hit, ★ right hit, - track extrapolation
- We can lose right residuals
- If we far away of aligned position, all residuals can be wrong

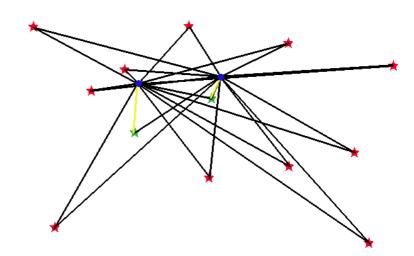


## All hits approach

Aligned position

**Unaligned position** 

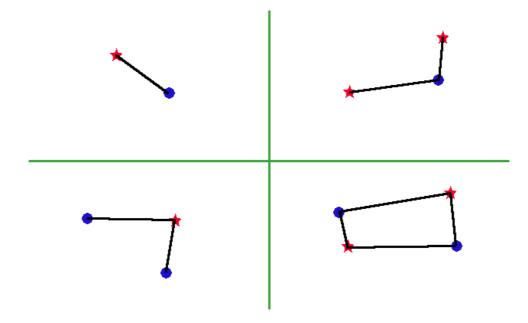




- ★ wrong hit, ★ right hit, - track extrapolation
- We do not lose right residuals
- If the number of wrong hits is large, we will have a large combinatorial background
- Due to large background we need to use more sophisticated fitting algorithms



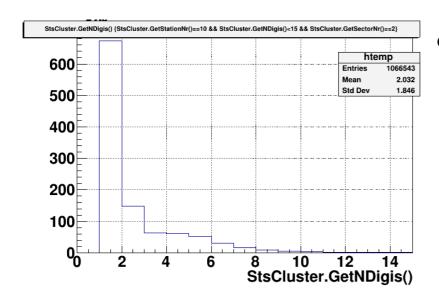
#### CSC case

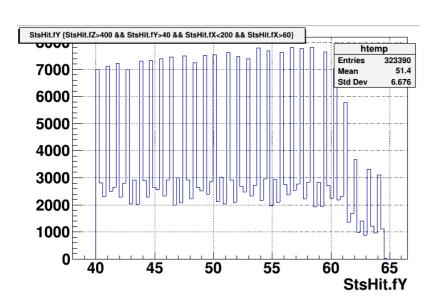


- ★ hit, - track extrapolation
- Average number of combination without 1-digit clusters in hits <3</li>
- Closest hit and all hits approaches in this case seem to be equal

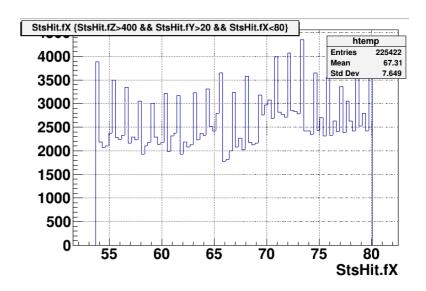


#### CSC Hits cut





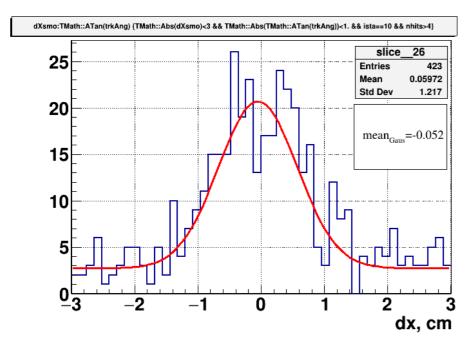
Average number of trackshits combination per event >8

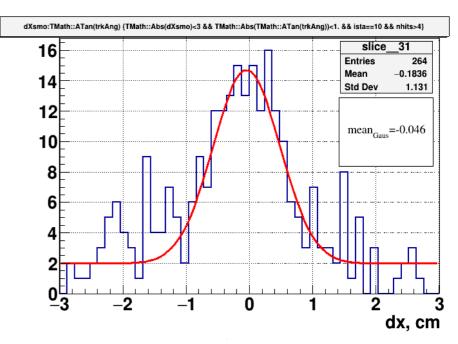


Remove hits with at least 1 cluster containing 1 digit



#### New fit method

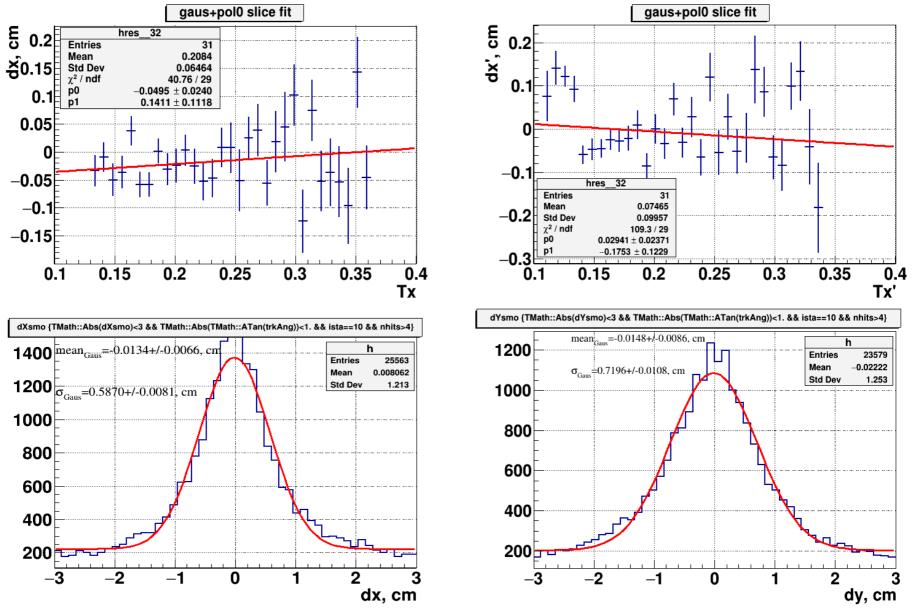




- Mean<sub>Distrib</sub>-Mean<sub>Gaus</sub> variates more than ±1 mm
- Use gaus+pol0 to fit slices by T<sub>x</sub>



## New alignment results





## New alignment results

 To get new aligned CSC position following shifts are implemented:

```
- Z_{AllHits}=Z_{GEM}-0.88, cm (Z_{ClosestHit}+0.13 cm)
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- X<sub>AllHits</sub>=X<sub>GEM</sub>-0.213, cm (X<sub>ClosestHit</sub>)
- Y<sub>AllHits</sub>=Y<sub>GEM</sub>+0.085, cm (Y<sub>ClosestHit</sub>)
- Residual misalignment by X and Y <200 μm</li>
- For the CSC Closest Hit approach, the alignment is simpler and gives the same results





## Backup



### Data without field

• Run 4648

Argon beam

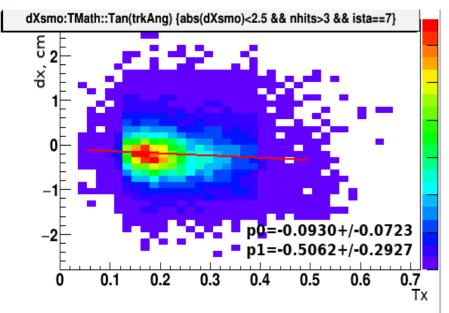
• Al target 3.3 mm wide

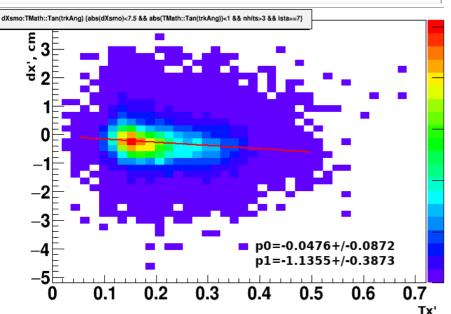


## Previous result, GEM-CSC tracking



## Residuals without field, X and X',

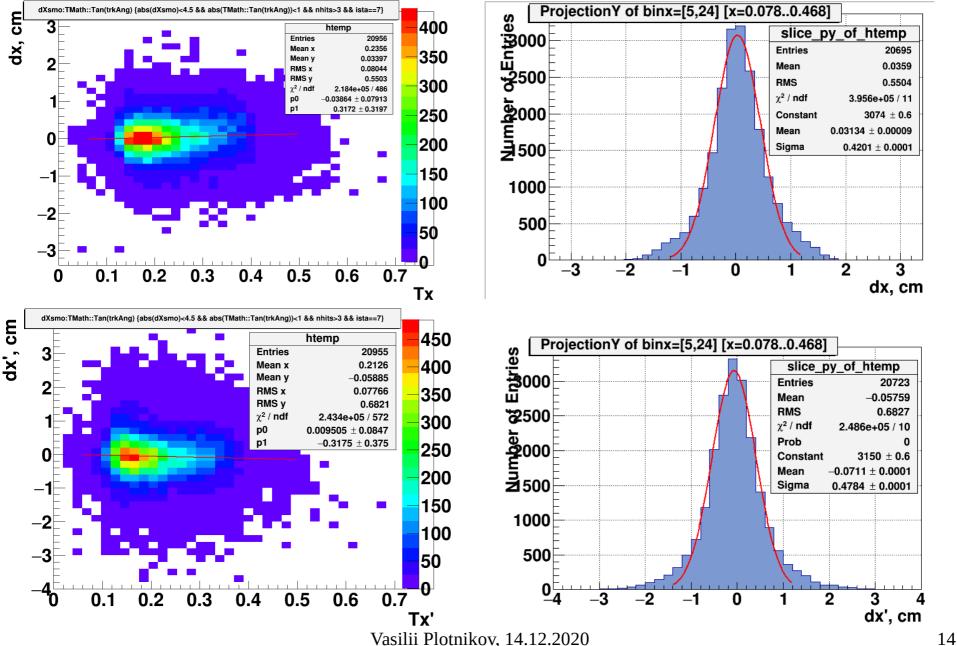




Z<sub>best</sub>+1.5 cm

- Residuals for Z, shifted by 1.5 cm relative to the "optimal" Z
- Negative slope is visible for X and X '
- The slopes are different and correspond to the difference in position along Z ∆Z≈6.5 mm

## Вм@№ Residuals without field, X и X', Z<sub>best</sub>



## ВМ@№ Residuals without field, X и X', Z<sub>best</sub>

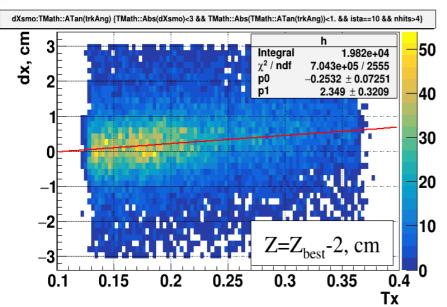
- Residuals were calculated by discarding the CSC hit and extrapolating the track from GEM
- Sigma of residuals about 4 mm
- Zef planes X and X 'are separated by several millimeters in different directions relative to Zcsc (X' is closer to the target in Z)
- Zcsc, implemented in reconstruction, in the middle between X and X '

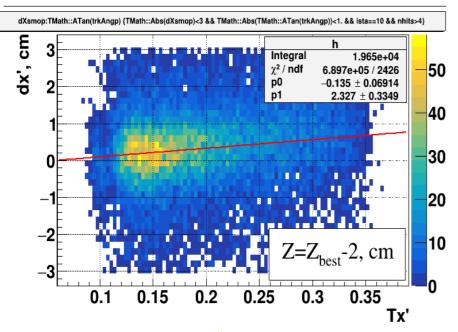


# Si-GEM-CSC extended tracking



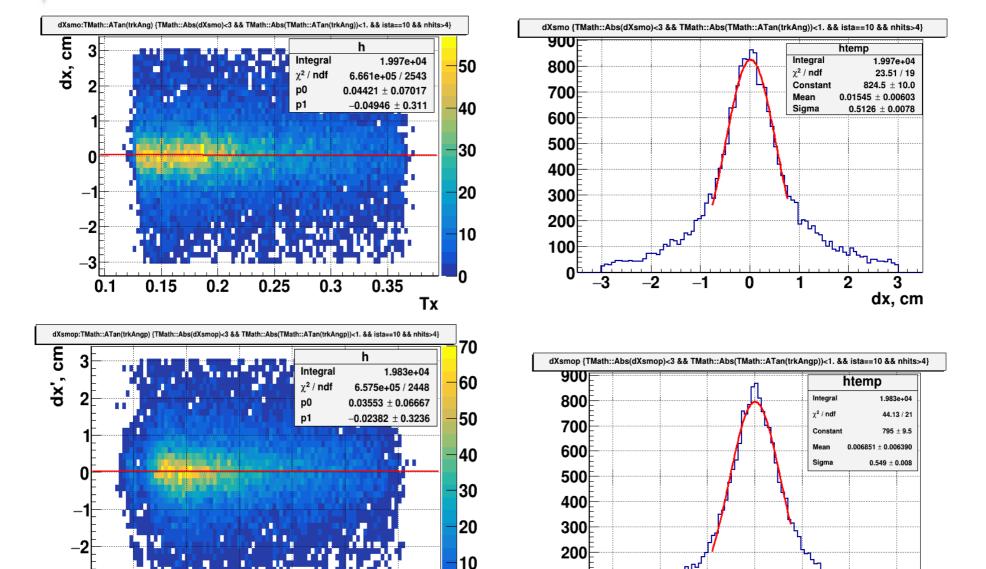
## Residuals w/o field, X and X',





- Z<sub>best</sub>-2 cm
  - Residuals for Z, shifted by 2 cm relative to the "optimal" Z
- Positive slope is visible for X and X '
- The slopes are close to each other

## Residuals w/o field, X and X', Z<sub>best</sub>



0.2

0.15

0.25

0.3

0.35

Tx'

100

dx', cm

## ВМ@№ Residuals without field, X и X', Z<sub>best</sub>

 To get new aligned CSC position following shifts are implemented:

$$-Z_{new} = Z_{old} - 1.01$$
, cm

$$-X_{new} = X_{old} - 0.213$$
, cm

$$- Y_{new} = Y_{old} + 0.085$$
, cm

- Sigma of residuals about 5.3 mm (about 1 mm more than before)
- The slopes for the X and X' planes are close to each other
- The difference in slopes corresponds to a displacement along Z about 200 μm

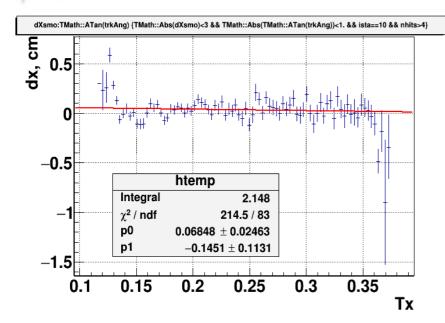


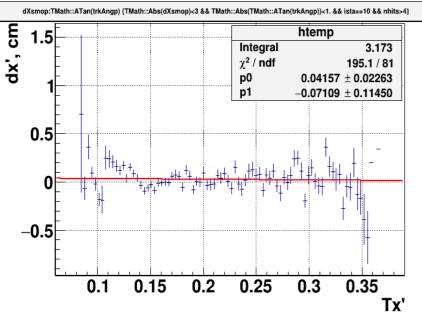
## Displacement of X and X' planes

- X and X' plane displacement issue not reproduced
- The possible reasons are following:
  - New tracking
  - More accurate track selection (≥2 Si hits, ≥3 GEM hits)
  - Smaller binning
  - Using the same X^X' angle in ResidOk as in the reconstruction (influence  $<100 \mu m$ )

#### BM@N

## Residuals w/o field, X and X', Z<sub>best</sub>





- Residuals vs tangent in XZ plane with "prof" option
- Errors are the errors of the mean
- The discrepancy with the alignment results using the "colz" option is about 1 mm