



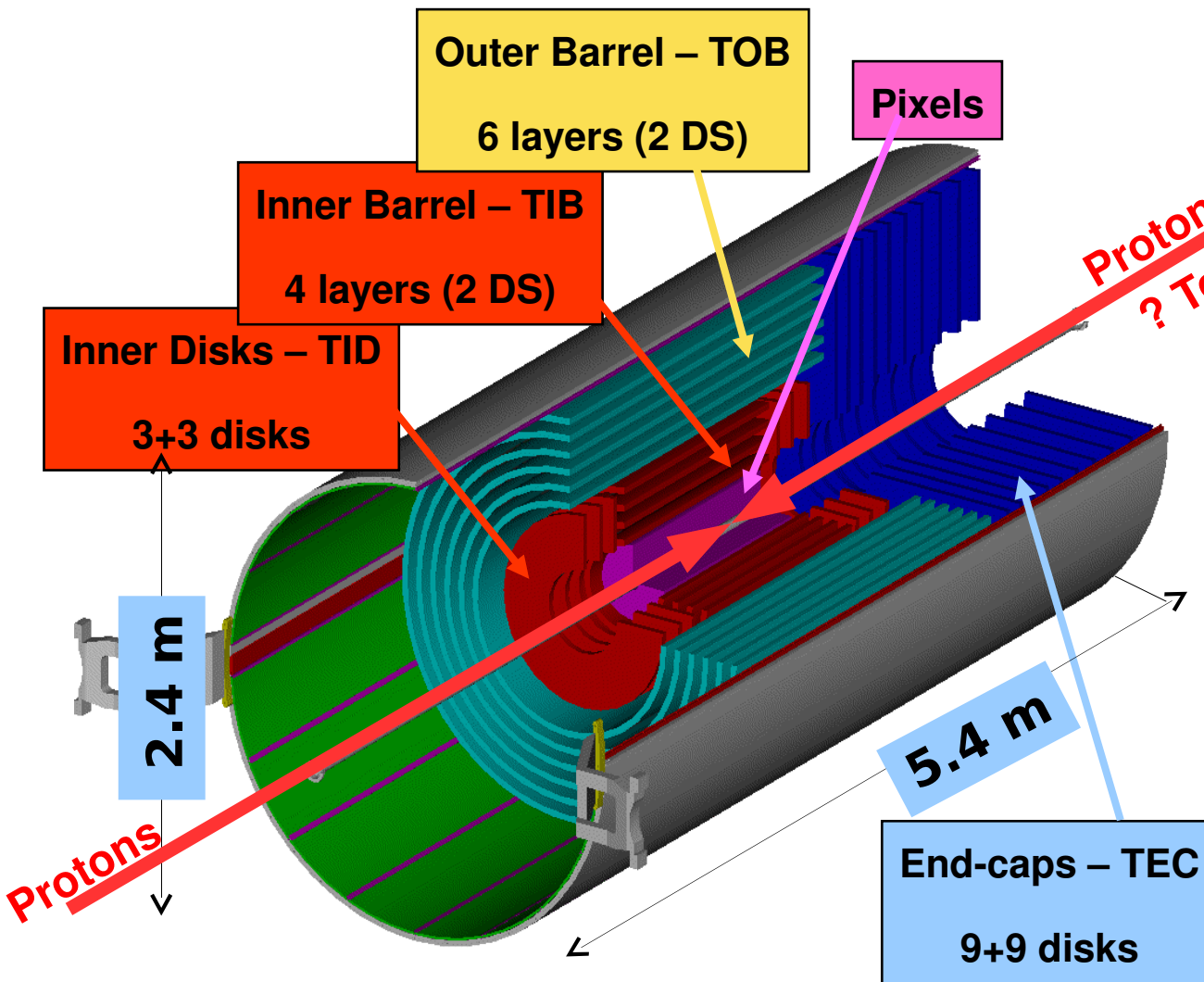
Alignment Position Errors Status

M. Musich

CMS Torino Group / Tracker Alignment Group

– Torino Group Internal meeting –

The CMS Silicon Tracker



Tracker Layout

- Volume 24 m³ / covered area 200 m²
- Running temperature: -10° C
- **STRIP:**
 - **15148 modules** (pitch 80 – 205 μm)
 - single point resolution of 20 – 60 μm
 - 2D measurements from DS modules, mounted back to back (tilt 100mrad)
- **PIXEL:**
 - **1440 modules** (pitch 100(r) x150(z) μm²)
 - resolutions: 9 (r) 20 (z) μm

Why Alignment?

- The CMS tracker is built in order to optimize the particle momenta resolution.
- It depends on two factors:

C_1 depends on the geometry of the detector

$$\frac{\delta p}{p} = C_1 p \oplus C_2$$

C_2 depends on multiple coulomb scattering (MCS)

$$C_1 = \frac{\sigma_{pos}}{\sqrt{N} \cdot B \cdot L^2}$$

B = magnetic field intensity

$\sim 10 \mu\text{m (Si)}$

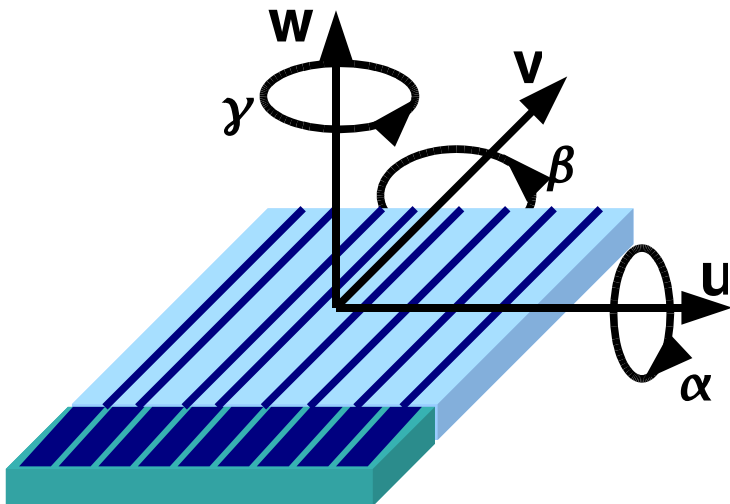
N = number of track hits

L = track length

σ_{pos} = resolution on measured point

$$\sigma_{pos} = \sqrt{\sigma_{intr}^2 + \sigma_{sist}^2}$$

MISALIGNMENT



- The challenge is to determine at **$O(10\mu\text{m})$** corrections for the **6 d.o.f** (3 rotations + 3 translations) of each of the $> 19\text{k}$ modules in CMS Silicon Tracker!

$19\text{k modules} \times 6 \text{ n.d.of.} \approx 100\text{k unknowns!}$

Alignment formalism

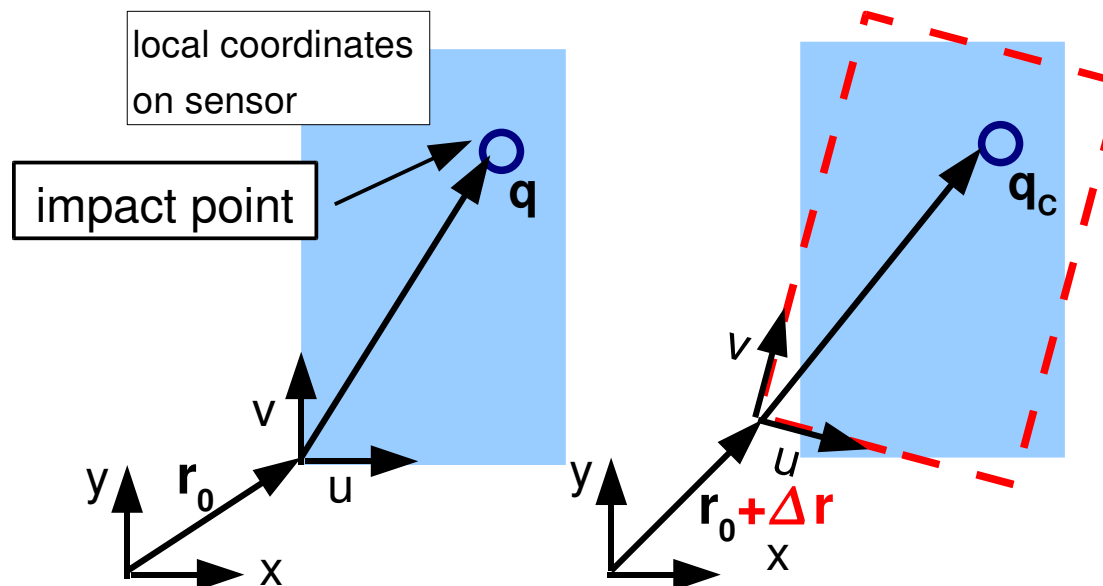
- In the CMS Tracker alignment formalism the hit position in local coordinates of the module is $\mathbf{q} = (\mathbf{u}, \mathbf{v}, \mathbf{w})$ and $\mathbf{r} = (\mathbf{x}, \mathbf{y}, \mathbf{z})$ w.r.t the global reference frame of CMS.
- The two sets of coordinates are related via a roto-translation:

$$\begin{cases} \mathbf{r} = (x, y, z) \Rightarrow \text{global coordinates} \\ \mathbf{q} = (u, v, w) \Rightarrow \text{local coordinates} \end{cases} \quad \mathbf{r} = \mathbf{R}^T \mathbf{q} + \mathbf{r}_0$$

- The alignment procedure determines corrections to the original transformation via an additional rototranslation:

$$\mathbf{r} = \mathbf{R}^T \Delta \mathbf{R} (\mathbf{q} + \Delta \mathbf{q}) + \mathbf{r}_0$$

- The alignment parameters are $\Delta \mathbf{q} = (\Delta \mathbf{u}, \Delta \mathbf{v}, \Delta \mathbf{w})$ which parametrize translations, while the angles α, β and γ appearing in $\Delta \mathbf{R}$ parametrize the rotation



Final goal of alignment:

- Determine for each of the $O(20k)$ detunits the 6 parameters $(\Delta \mathbf{u}, \Delta \mathbf{v}, \Delta \mathbf{w}, \alpha, \beta, \gamma)$ 3 translations and 3 rotations w.r.t the nominal geometry
- Determine for each of the modules the statistical error associated to the aligned position (**APE**)

Track Based Alignment

- Several methods are deployed (optical survey/LAS/track based alignment) ultimate precision $O(10 \mu\text{m})$ reached via track based alignment
- Definition of track χ^2 :

$$\chi^2 = \sum_{i=1}^{n_{\text{hits}}} r_i^T(p, q) V_k^{-1} r(p, q)$$

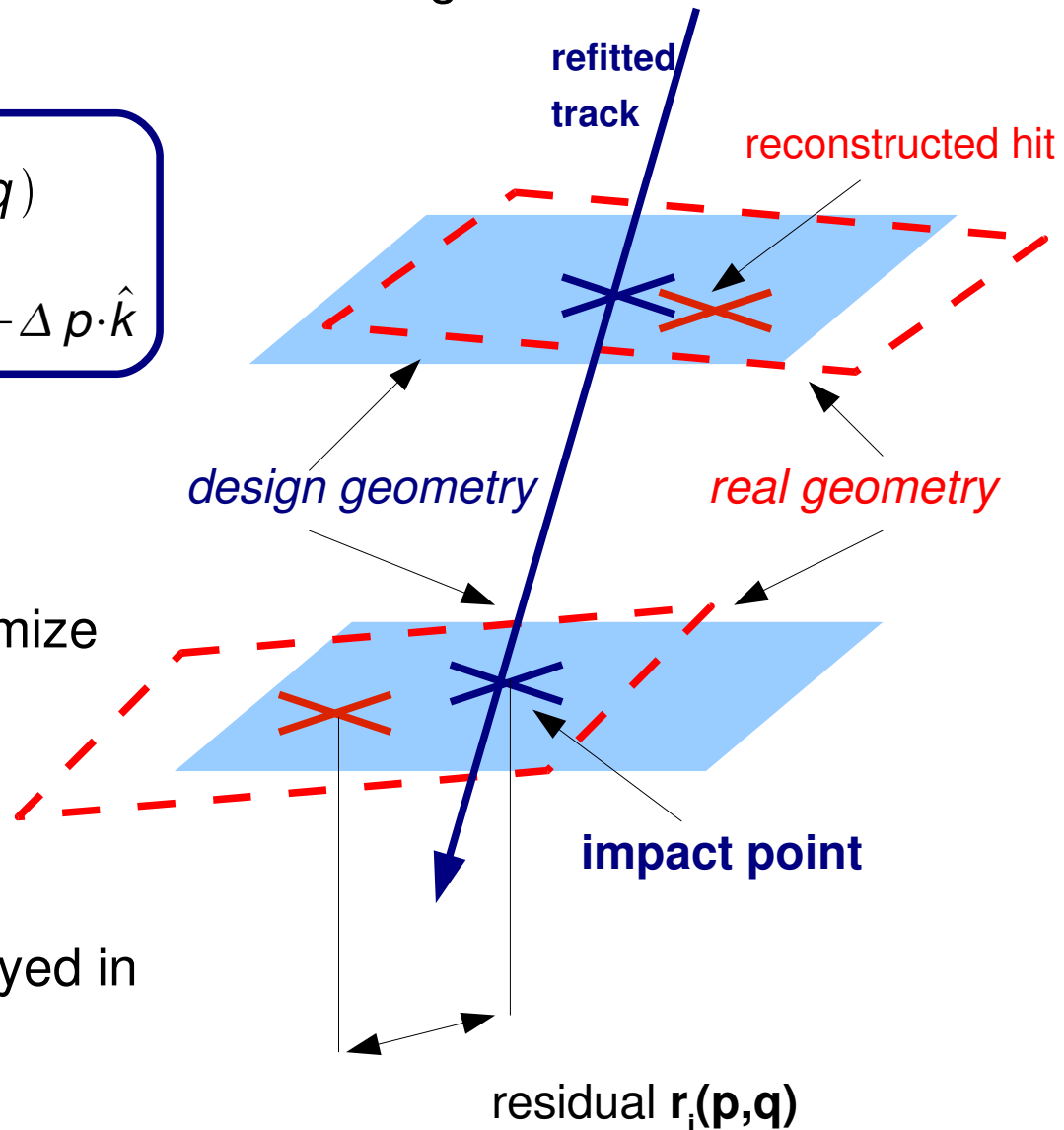
$$r_i(p, q) = u^{\text{hit}} - u^{\text{fit}}(p, q) = u^{\text{hit}} - \Delta p \cdot \hat{k}$$

V = covariance matrix

p = **alignment parameters**

q = track parameters

- Alignment algorithms attempts to minimize this χ^2 function and therefore track residuals
- A complex system of equations to be solved ($O(100\text{k unknowns})$)
- Fast and robust algorithms are deployed in CMS framework



Alignment Position Errors

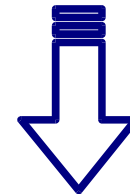
- The alignment position error (APE) **characterizes the measurement uncertainty** of each detector due to misalignment effects.
- The APE is combined with the spacial (intrinsic) resolution of the device giving the total error of hit positioning on the silicon modules:

$$\sigma_{TOT}^{HIT} = \sigma_{intr}^{HIT} \oplus \mathbf{APE}(DET)$$

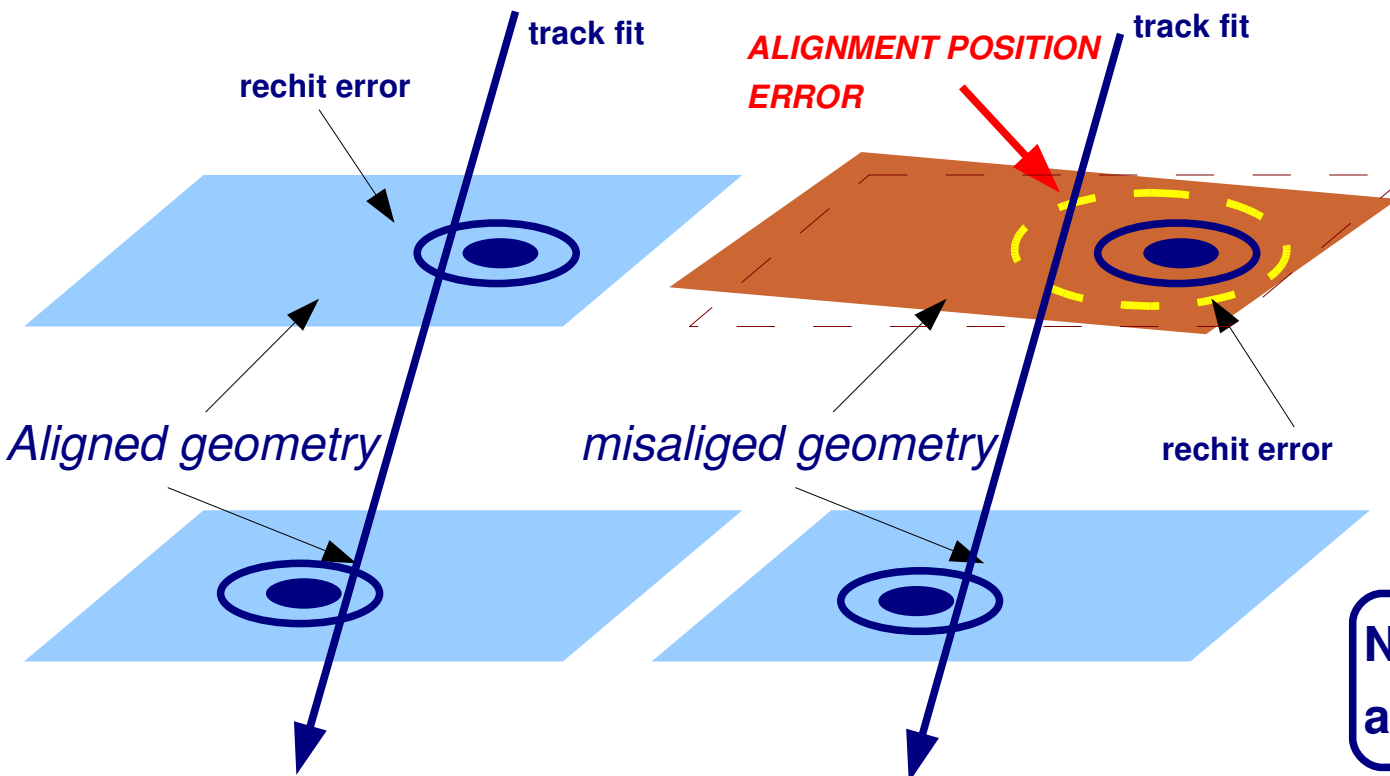
- The APE affects the search window of pattern recognition in track finding

APE have direct impact on:

- **performance / efficiency** of track reconstruction
- **track quality (χ^2)**
- **fake rate**
- **momentum resolution**

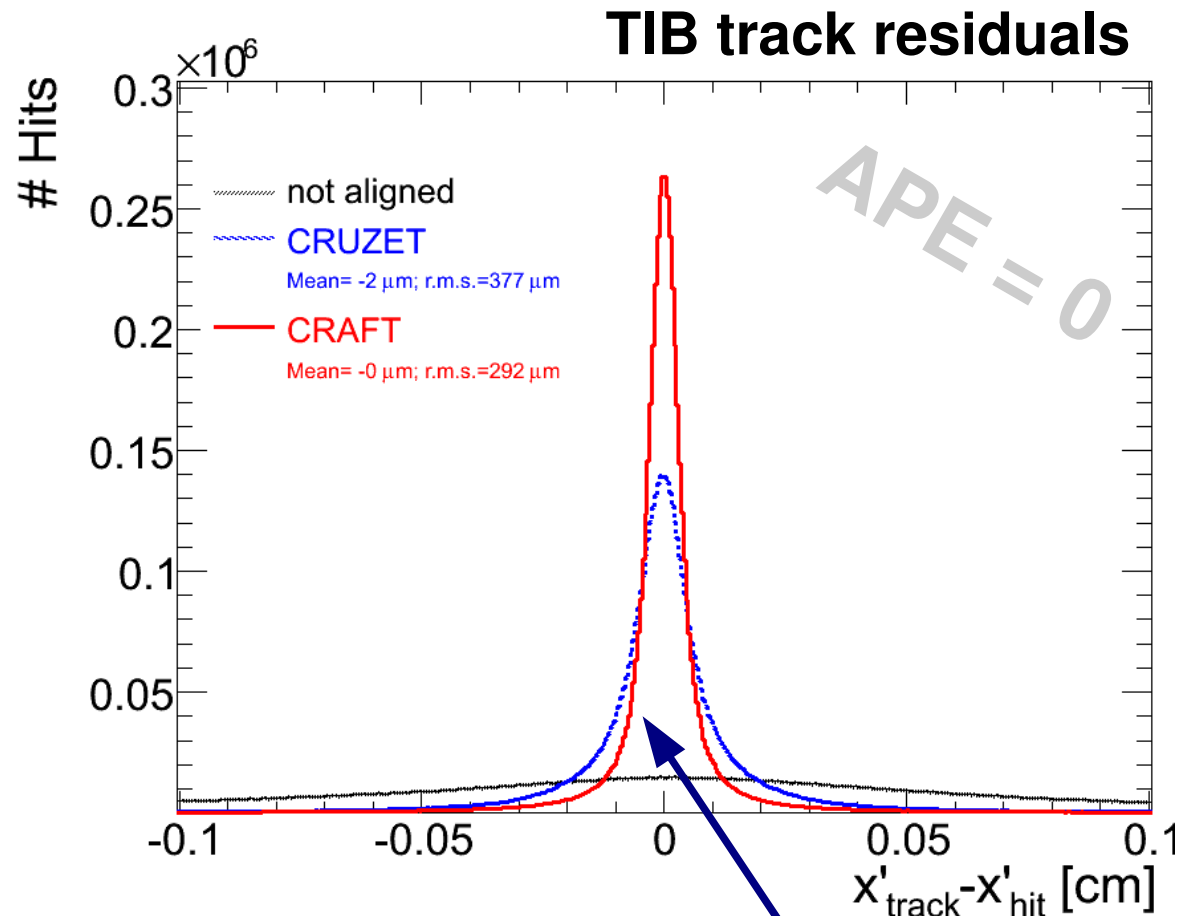


Need good estimation of APE according to alignment status



Track residuals

- To check alignment quality and determine remaining misalignment look to track residuals at Subdet level and layer level.



- Several effects folded in the residuals distributions:

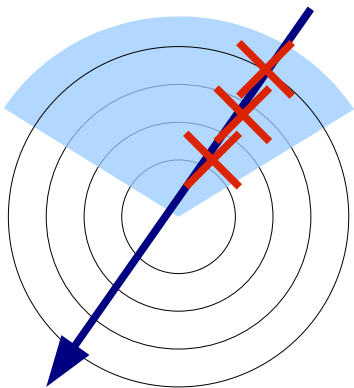
- **hit resolution:**
 - cluster width
 - strip pitch
- **tracking extrapolation**
- **multiple scattering** in silicon:

$$\delta x \simeq l \cdot \delta \theta = l \cdot \frac{1}{p} \sqrt{\frac{t}{X_0}}$$

- **alignment precision**

$$RMS(\Delta X) = \sigma_{\text{hit}} \oplus \sigma_{\text{track}} \oplus \delta X_{MS} \oplus \sigma_{\text{misalign}}$$

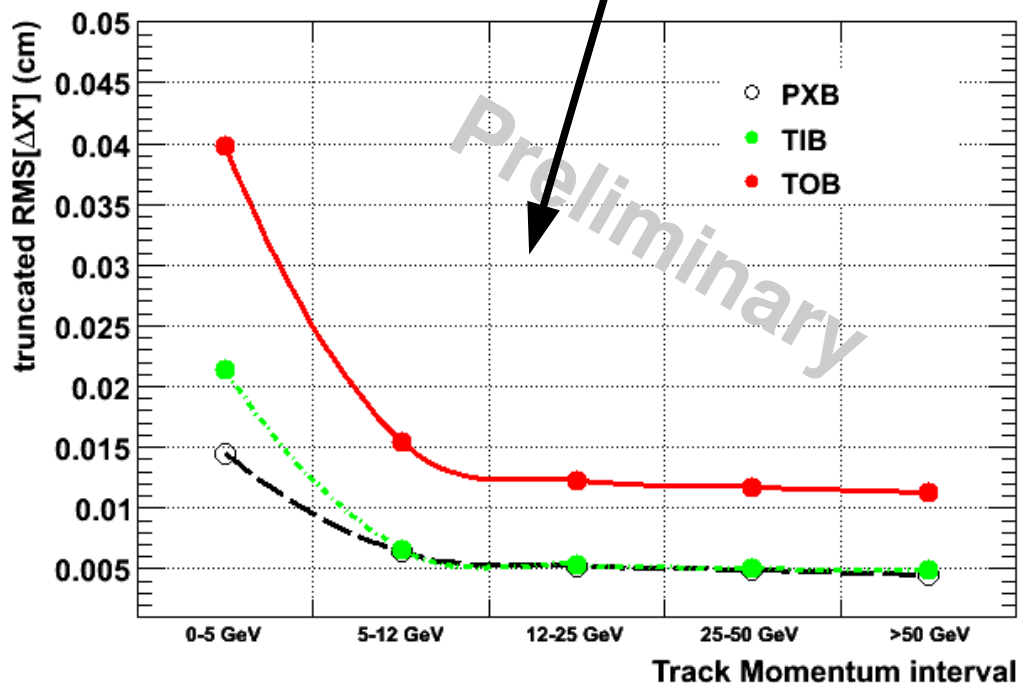
Trends of Residuals



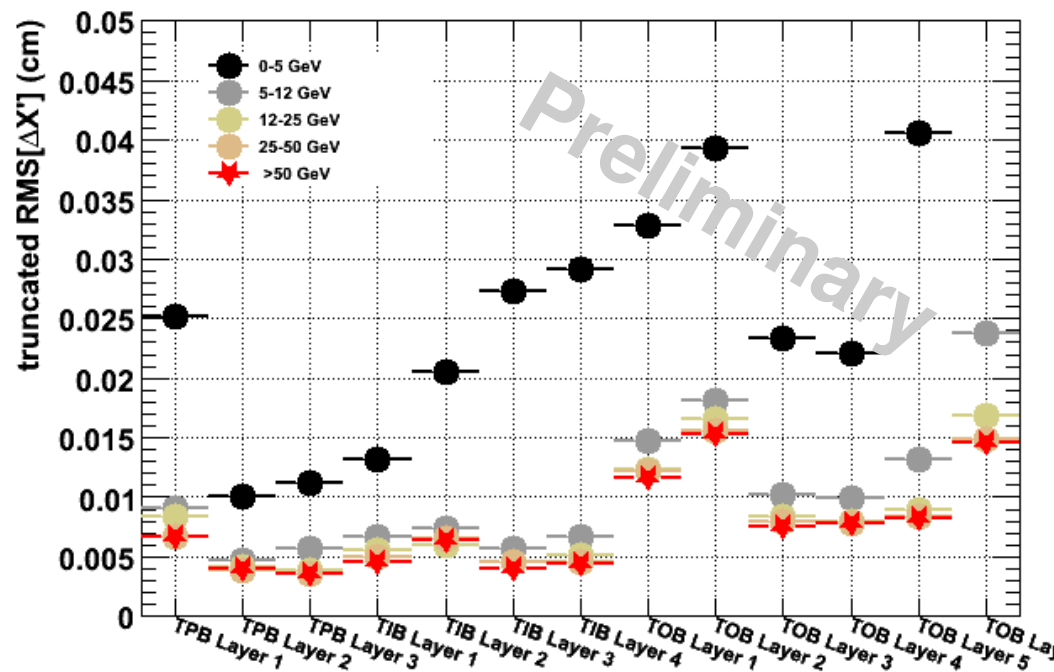
- In order to have a sound **estimate of remaining misalignment** take a well aligned region (upper quarter of Tracker) select tracks hit pattern to satisfy test-beam like geometry and plot residuals as a function of track momenta

Residuals in the different subdets **saturate** at some threshold value ($p > 20 \text{ GeV}$), for which the MCS starts to be dominated by the strip (pixel) pitch and misalignment effects

Subdets Residuals vs momentum



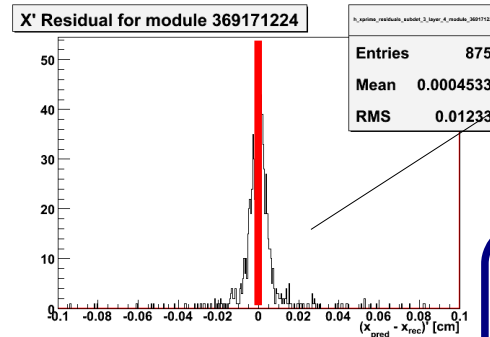
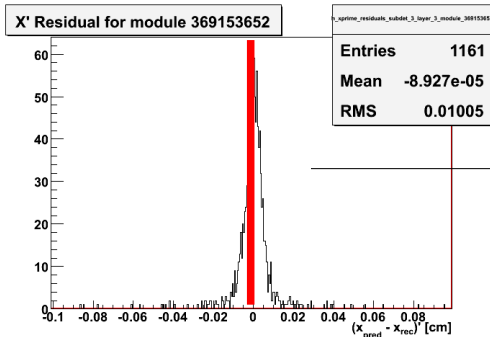
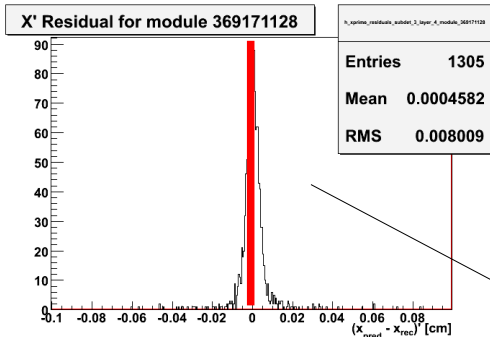
Residuals Barrel Layers



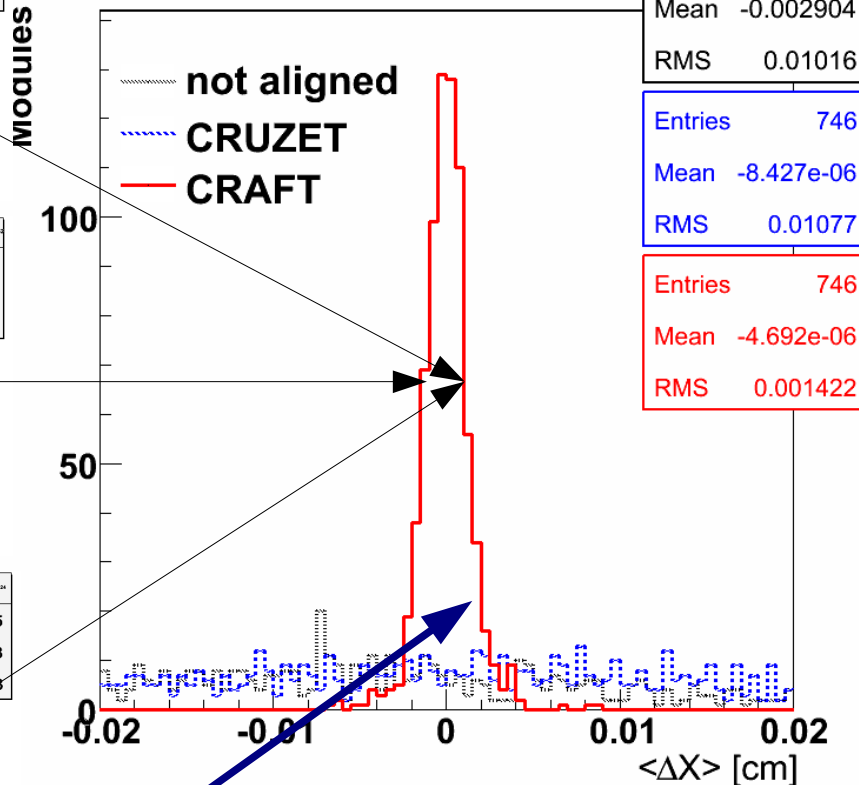
Distribution of Median of Residuals (DMR)

- To check residual misalignment:

- DMR** (distribution of median of residuals) is a better way to disentangle alignment effects



MR of TPB modules (x_{local} coord)



It has been demonstrated using misaligned MC simulation that width of the distribution of median of residual is the best estimator of the input misalignment

for each module take the residual. **If entries > 30 hits** take median and fill the DMR

multiple scattering averages out when considering DMR.

Able to spot uncoherent misalignment of modules respect the others. NOT displacements that leave track χ^2 invariant (weak modes)

•The **RMS of DMR** is taken as width of the remaining statistical misalignment after the alignment procedure

Motivation for module dependent APE

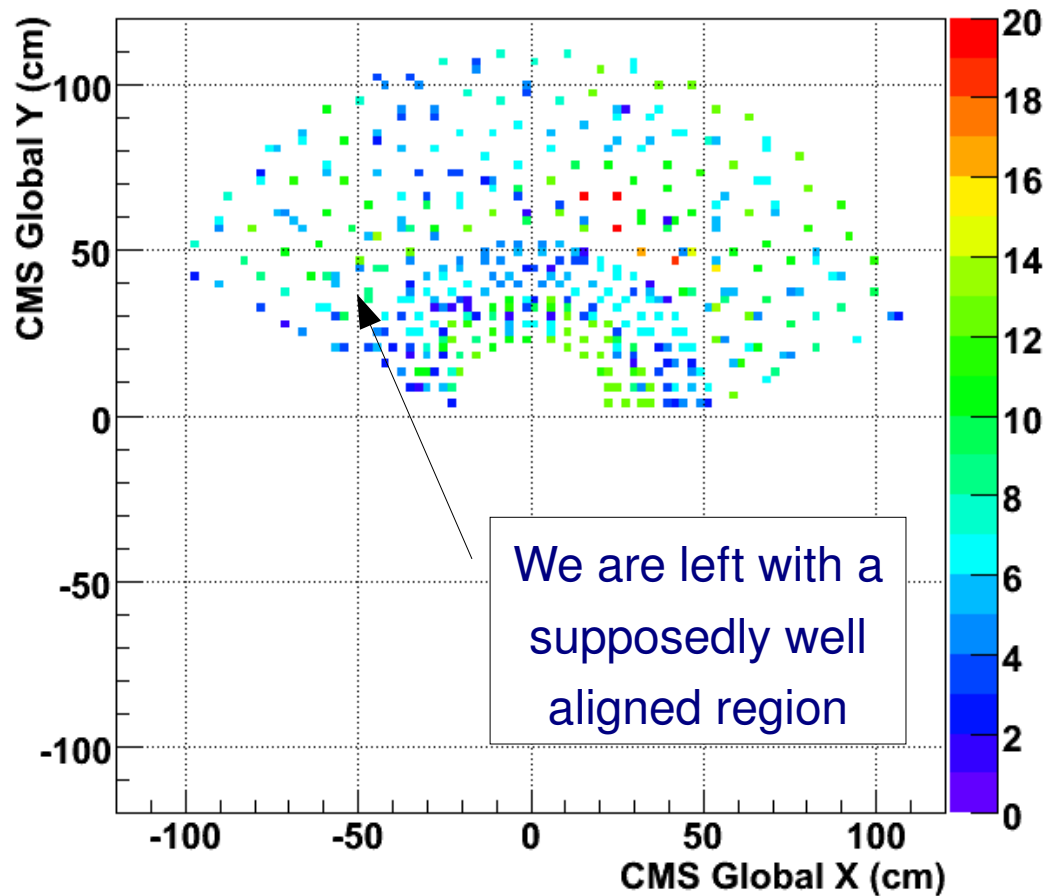
- Old APEs were **much larger** than latest (shown at CRAFT Torino Workshop)
RMS of Distribution of Median of Residuals (= DMR)
- need to define a new set of APEs which reflects better the current status of Tracker alignment
- They need to be module-dependent since there are regions aligned better than others.
- **New code for writing APE object starting from local module dependent input values** (G. Flucke + I. Reid)
- Every study in the following has been performed using the ***CRAFT first reprocessing datasample***, and using the ***CRAFT – signoff alignment object*** (Tracker_Geometry_v3_offline)
- It is the first attempt to determine module level APE for CRAFT alignment

Subdet	RMS OF DMR		
	APE (μm)	Mean (μm)	Median (μm)
TPB	200	41	14
TPE	1000	90	37
TIB	100	18	10
TID	300	46	23
TOB	100	21	9
TEC	300	49	28

Strategy

- Tuning of remaining misalignment (Tracker_Geometry_v3_offline as reference for DATA)
 - selecting tracks / hits where MS and extrapolation are small (**p > 20GeV**)

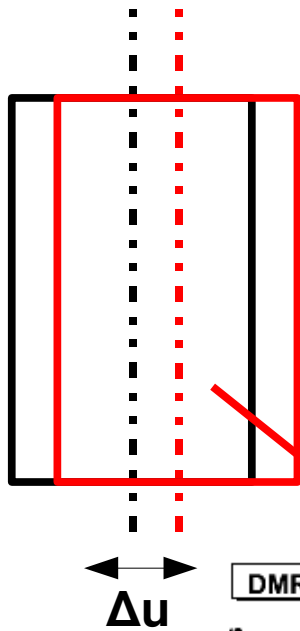
Hit Map XY



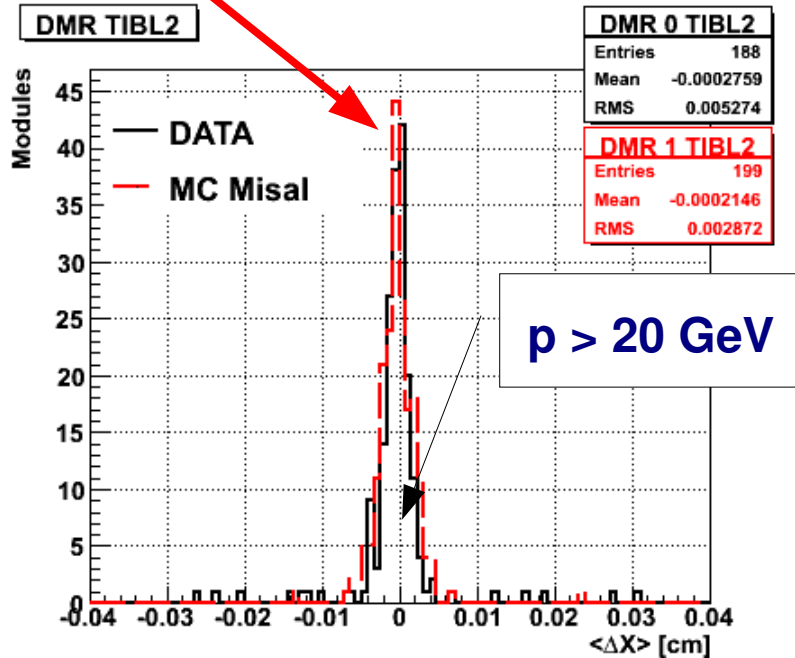
- Track/Hits quality cuts applied
 - **Standard Validation cuts**
 - $N_{\text{hits}} > 10$
 - $N_{\text{hits } -2D} > 2$
 - $S/N_{\text{cluster}} > 18$
 - **Fiducial (pixel-like) volume cuts**
 - $(x_{\text{DCA}}^2 + y_{\text{DCA}}^2)^{1/2} < 11 \text{ cm}$
 - $|z_{\text{DCA}}| < 60 \text{ cm}$
 - **Hit pattern selection**
 - 14 split hits (10 SS + 4 DS)
 - Test-Beam like topology:
 - TOB L6
 - TOB L5
 - ...

Tuning of $\Delta u, (\Delta v), \Delta \gamma$

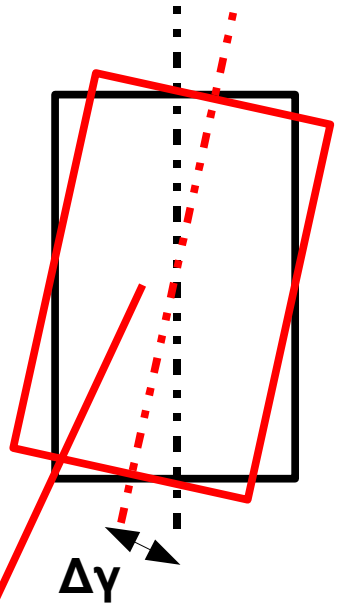
- Look at DMRs and residuals in Barrel Layers and compare Craft data with cosmic MC @ 3.8 T



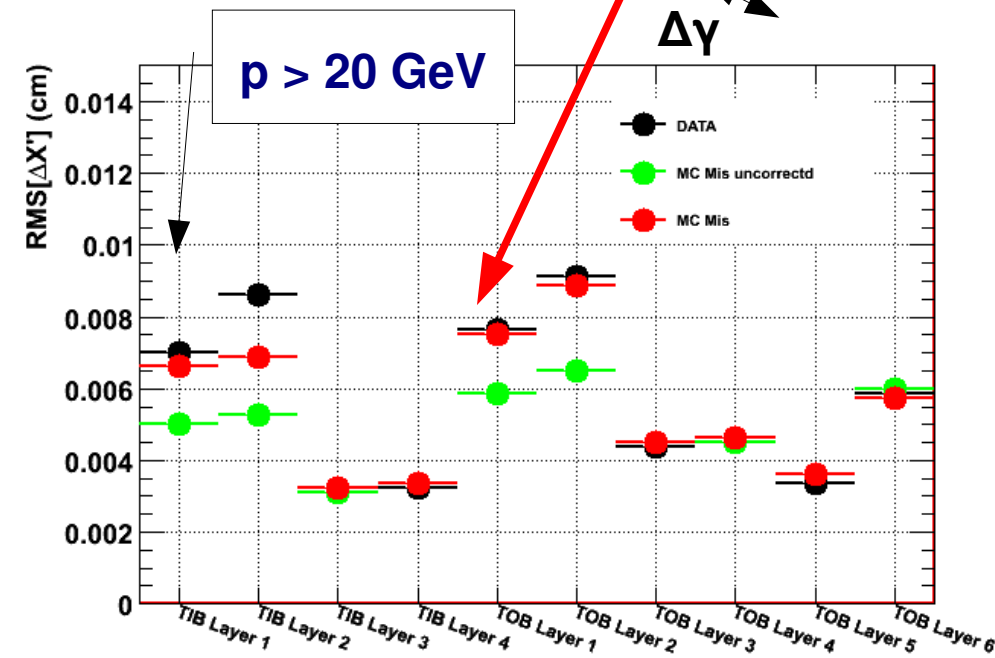
- Δu (Δv) affecting the DMR
- so tune layer by layer Δu comparing **misaligned MC** and **data**



- $\Delta \gamma$ not affecting DMRs but spread in the residuals
- so tune **MC** in order to reproduce the trend of Barrel layer residuals of **data**



Residuals Barrel Layers

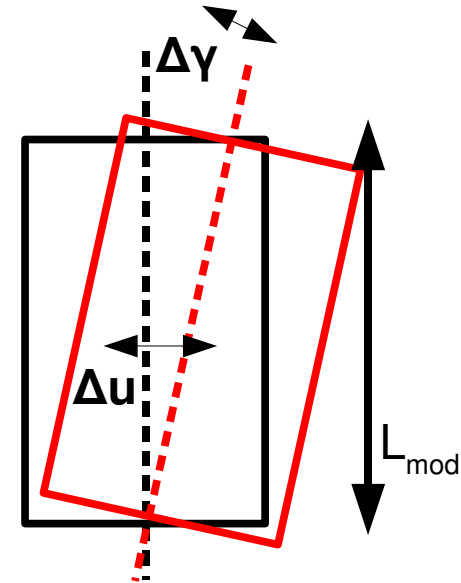


Estimation of new APE

- In **TIB/TOB**

- Misalignment parameters Δu , (Δv for DS), $\Delta \gamma$ obtained as described before are used to define a NEW layer dependent APE (APE_{NEW}) in the local x coordinate

$$APE_{NEW} = \sqrt{\sigma_{uu}} = \underbrace{\Delta u}_{\substack{u \text{ correction} \\ \text{from MC tuning} \\ \text{of DMR}}} \oplus \underbrace{\frac{L_{mod}}{4}}_{\substack{\text{average} \\ \text{lever arm}}} \underbrace{\Delta \gamma}_{\substack{\gamma \text{ from} \\ \text{MC tuning} \\ \text{of residuals}} \oplus \underbrace{(C \delta v)}_{\substack{\text{ad hoc correction} \\ \text{for DS}}}$$



- In **TPB/TPE/TID/TEC** (Endcap and Pixels)

- since a detailed analysis of layer dependent matching with misaligned MC was not performed → Take the **DMR**

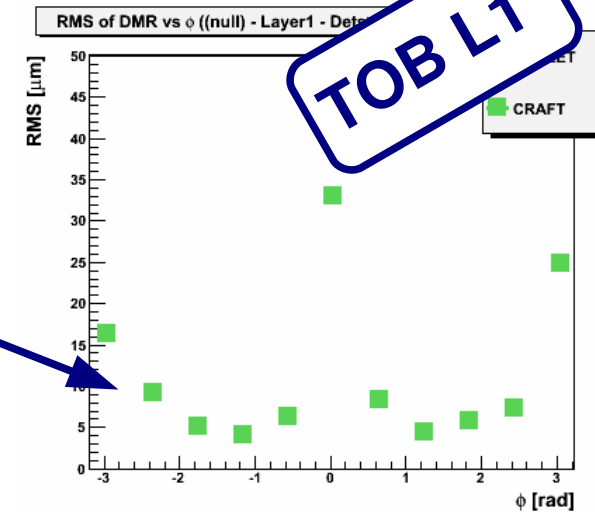
$$APE_{NEW} = \sqrt{\sigma_{uu}} = \text{Median}(\text{Residual}_{x'})$$

Subdet	Median (μm)
TPB	14
TPE	37
TID	23
TEC	28

Scaling Law

- We know that the quality of Alignment is ϕ -dependent, so introduce a scaling law, which increases the APE in modules having fewer hits in the alignment procedure:

Structure in DMR(ϕ) clearly visible



- so said N , the number of hits/module

$$\left\{ \begin{array}{l} \langle |residual_x| \rangle > 3 APE_{old} \\ N < N_{min} \\ N > N_{max} \end{array} \right. \quad APE = \langle |residual_x| \rangle$$

$$N < N_{min}$$

$$N > N_{max}$$

$$APE = APE_{old}$$

$$APE = k APE_{new}$$

$$N_{min} < N < N_{max}$$

$$APE = k APE_{new} \cdot \sqrt{\left(\frac{N_{max}}{N} \right)}$$

Subdet	Old APE (μm)
TPB	200
TPE	1000
TIB	100
TID	300
TOB	100
TEC	300

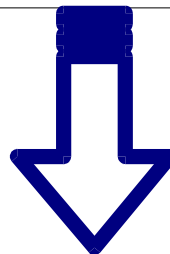
- k , N_{MAX} , N_{MIN} parameters to be tuned!
- This procedure should avoid introducing errors too small to bad aligned modules (which have very large median of residuals / too few hits)

Current status

I. Reid +
G. Flucke

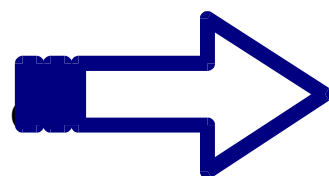
- Using the numbers as shown in the previous slides we define the following parameters:

	K^*APE0 (μm)	Nmax	Nmin
TPB	19	400	25
TIB L1/L2	20/16	4000	100
TIB L3/L4	19	4000	100
TOB L1/L2	38/23	8000	200
TOB L3/L4	16	8000	200
TOB L5/L6	15	8000	200
TPE	55	100	25
TID	35	1500	500
TEC	31	1600	30



to rescale

- Local coordinate input given to generate module dependent APE



- First module dependent APE object successfully produced.
- set $\sigma_{uu} = \sigma_{vv} = \sigma_{ww}$
- “spherical” local APE → “spherical” global APE

$$V_{uvw} = \begin{pmatrix} \sigma_{uu} & 0 & 0 \\ 0 & \sigma_{vv} & 0 \\ 0 & 0 & \sigma_{ww} \end{pmatrix} = \begin{pmatrix} \sigma_0 & 0 & 0 \\ 0 & \sigma_0 & 0 \\ 0 & 0 & \sigma_0 \end{pmatrix}$$

369120493	0.00475	0.00475	0.00475
369120494	0.00628	0.00628	0.00628
369120501	0.00418	0.00418	0.00418
369120502	0.00723	0.00723	0.00723

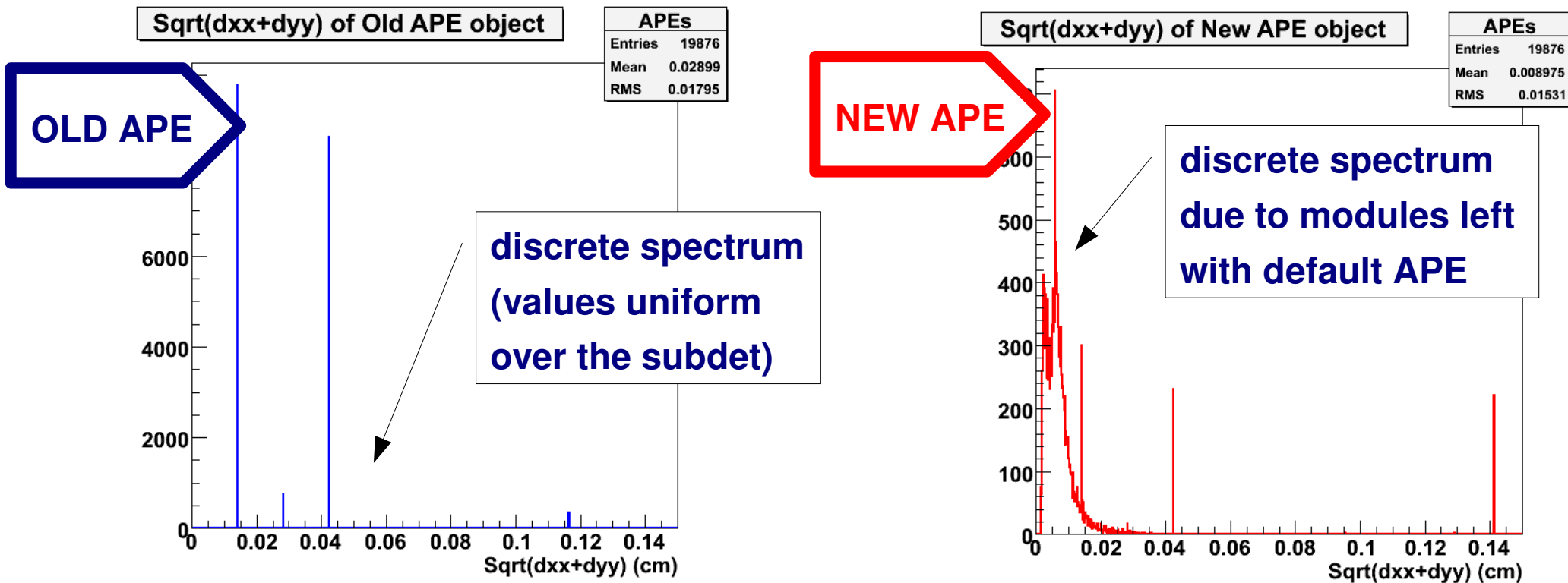
moduleId	σ_{uu}	σ_{vv}	σ_{ww}
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Error “spectrum”

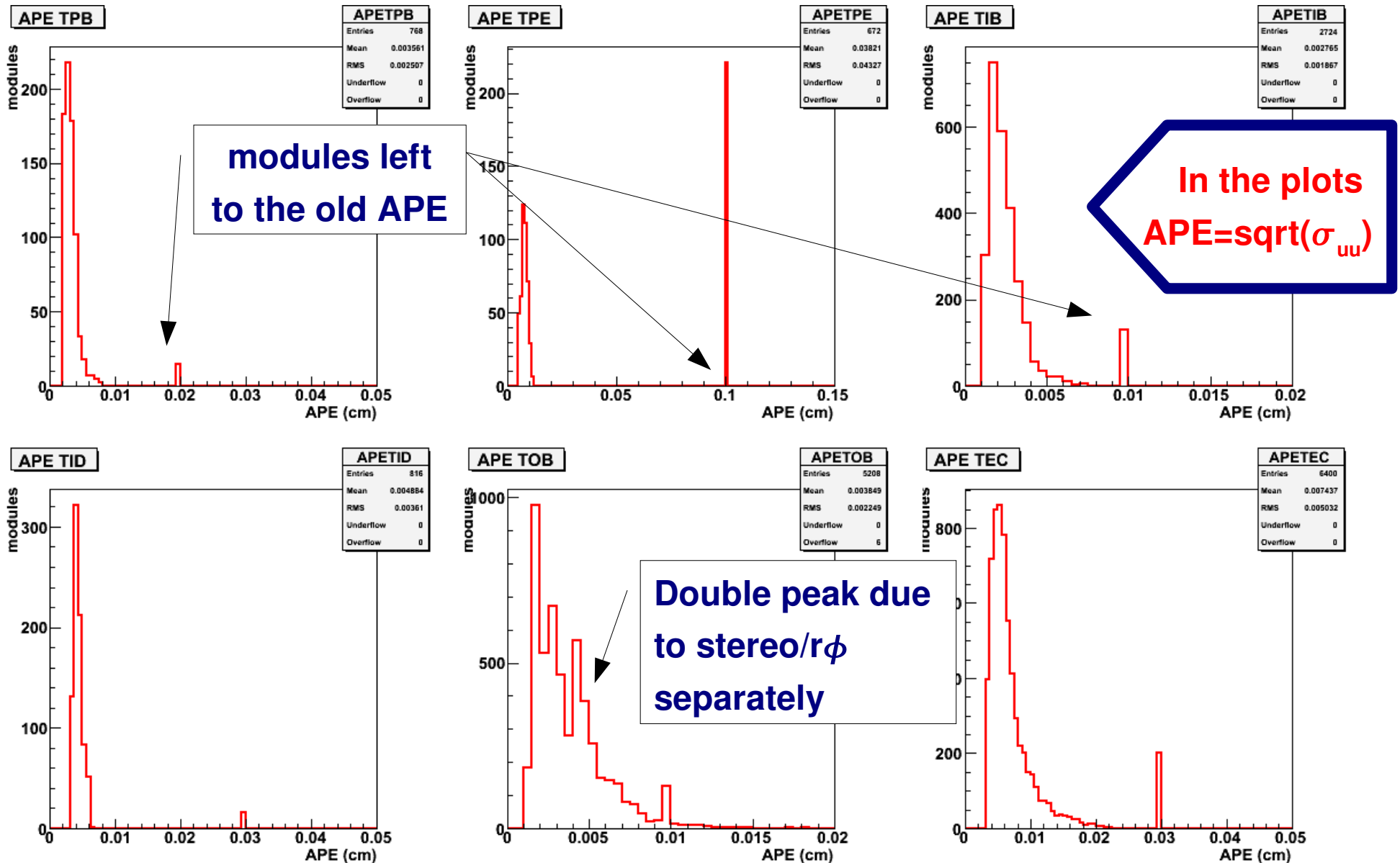
- Define the error in the rp plane as the squared sum of the global X and Y errors

$$error = \sqrt{(\sigma_{xx} + \sigma_{yy})} = \sqrt{(dxx + dyy)}$$

- Plot it for “default” APE (TkGeomErr_Offline_v3) and new **module-dependent APE**;

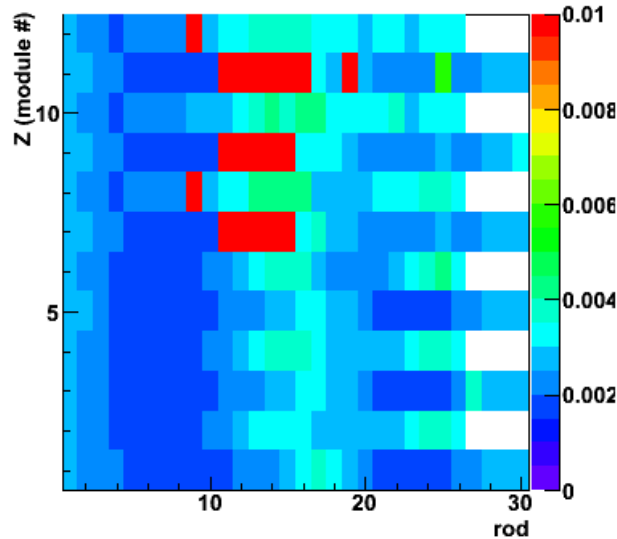


Error "spectra" for Subdets

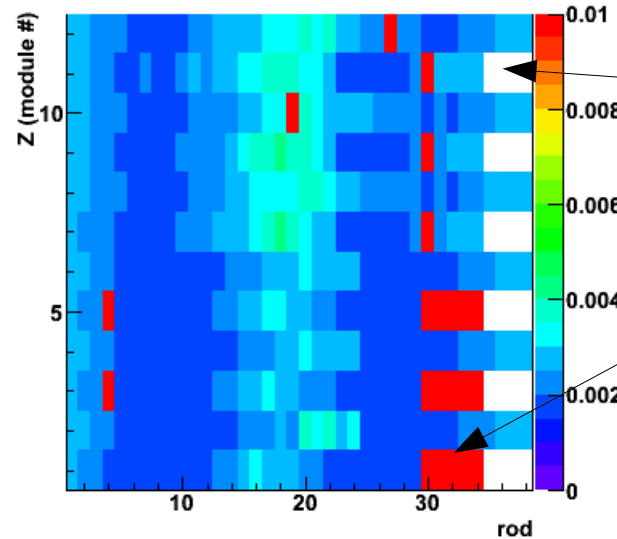


2D map of APE - TIB

APE TIB L1



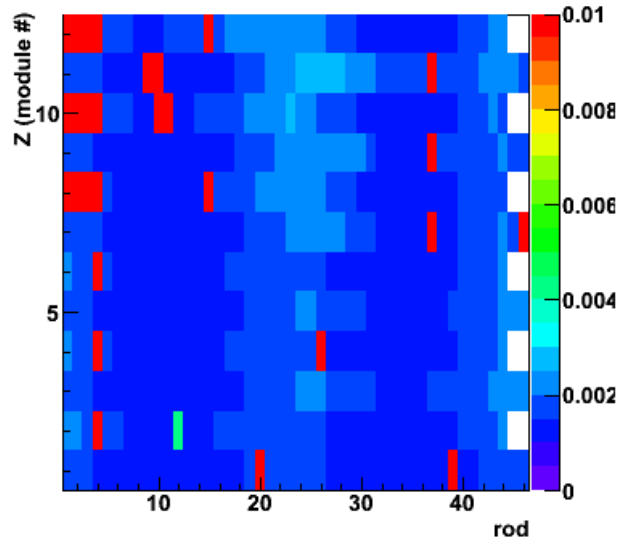
APE TIB L2



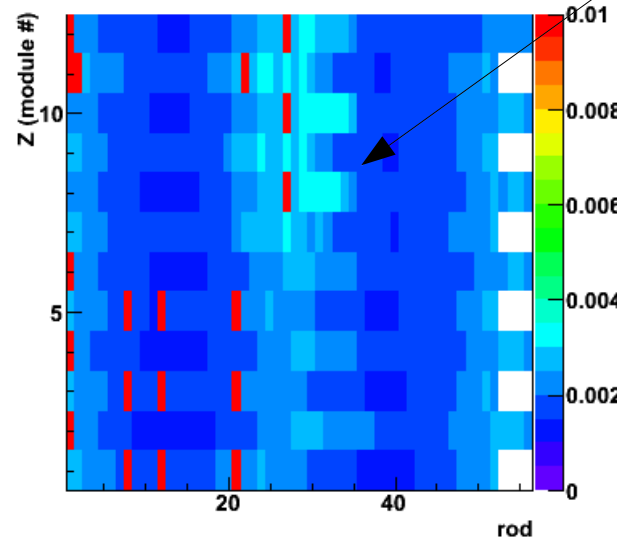
white spots are due to binning issues (internal/external strings)

red spots are modules left with default APE

APE TIB L3



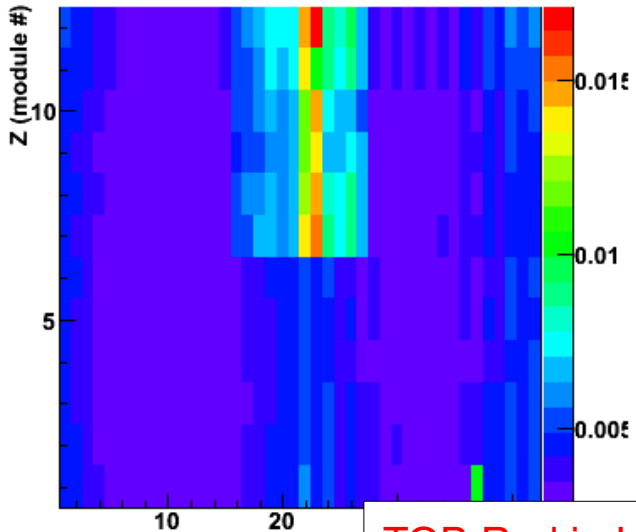
APE TIB L4



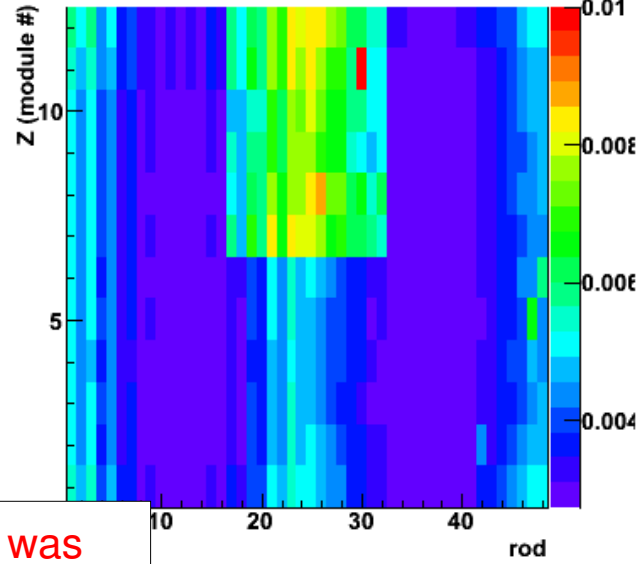
values in-between are due to the modulation as a function on the number of entries (structure Top-Bottom visible)

2D Map of APE - TOB

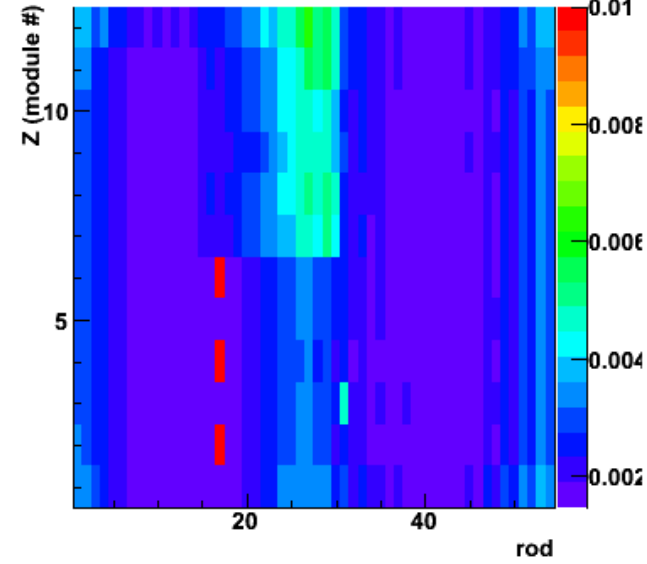
APE TOB L1



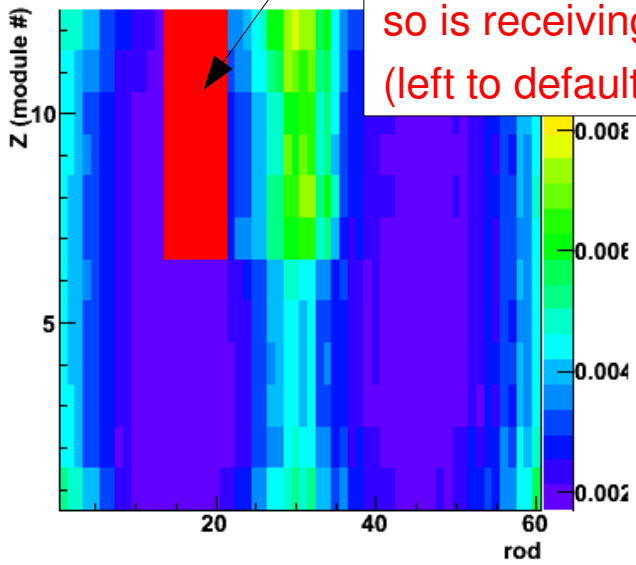
APE TOB L2



APE TOB L3

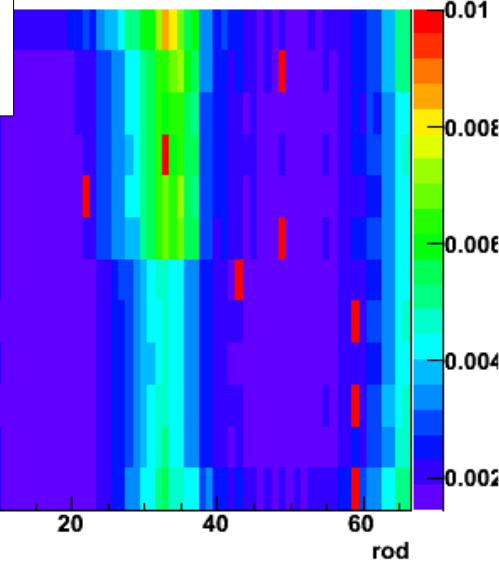


APE TOB L4

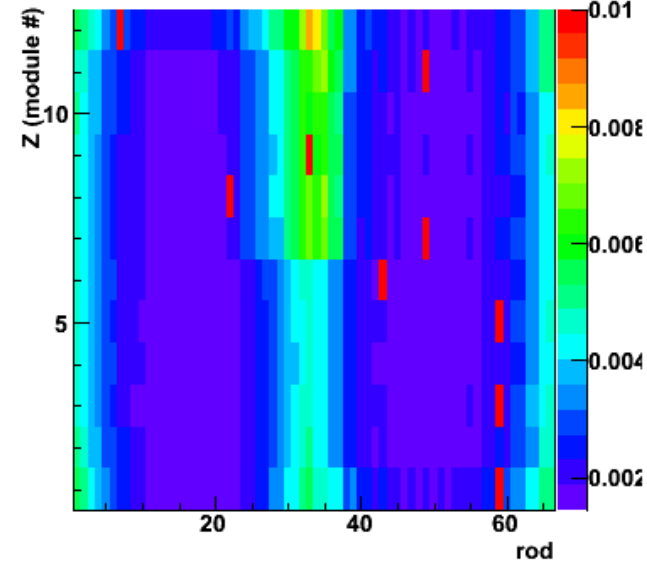


TOB Rod in L4 was out of the DAQ and so is receiving no hits (left to default APE)

APE TOB L4



APE TOB L5

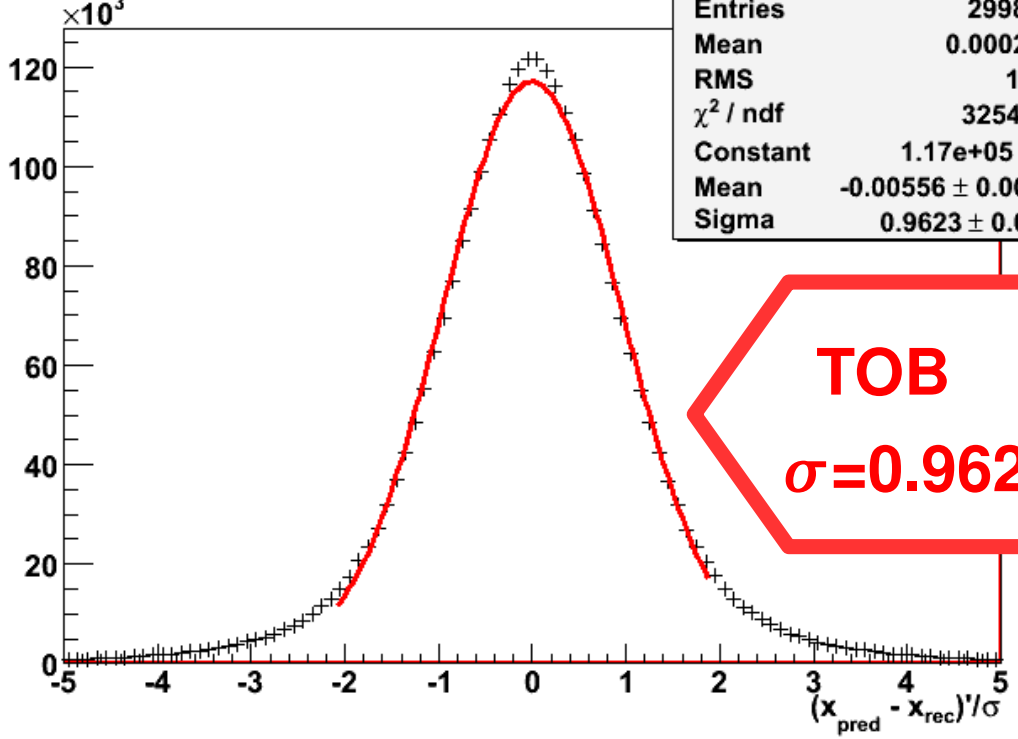


Validation

J. Hauk

Residual for TOBBarrel 3 in Strip

h_NormXprime_TOBBarrel_3	
Entries	2998853
Mean	0.0002552
RMS	1.184
χ^2 / ndf	3254 / 37
Constant	1.17e+05 ± 94
Mean	-0.00556 ± 0.00065
Sigma	0.9623 ± 0.0006



First rough validation, using normalized track residuals:

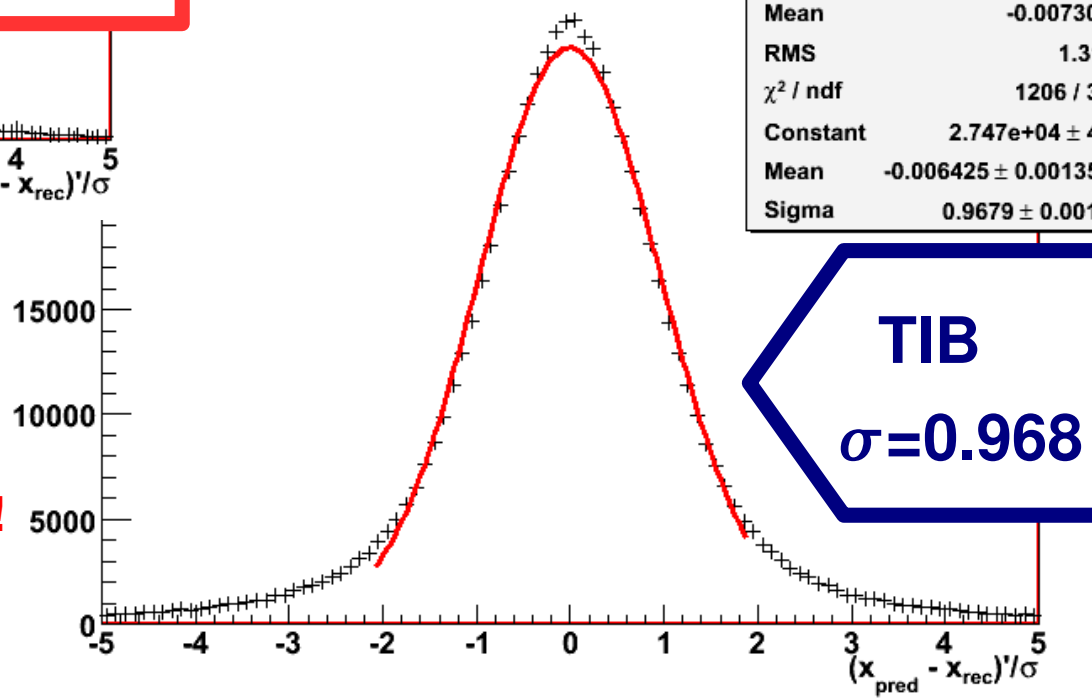
$$r_i = \frac{u_i^{hit} - u_i^{fit}}{\sigma_i}$$

$$\sigma_i = \sigma_i(APE, hit)$$

If the errors were correctly estimated the RMS should be 1

TIBBarrel 0 in Strip

h_NormXprime_TIBBarrel_0	
Entries	745699
Mean	-0.007308
RMS	1.311
χ^2 / ndf	1206 / 37
Constant	2.747e+04 ± 46
Mean	-0.006425 ± 0.001359
Sigma	0.9679 ± 0.0014



- Take the width of a gaussian fit (~1 in the subdets) and use it to adjust calibration
- **It does not take into account tails yet!**

Cosmic Track Splitting Validation

- Take a tracker track:
 - split it along its **PCA** (Point of Closest Approach)
 - refit separately the two hits collections coming from the the two cosmic halves
 - compare the track parameters of the the two legs updated at the PCA:

$$X = (d_{xy}, d_z, p_T, \theta_{tk}, \phi_{tk})$$

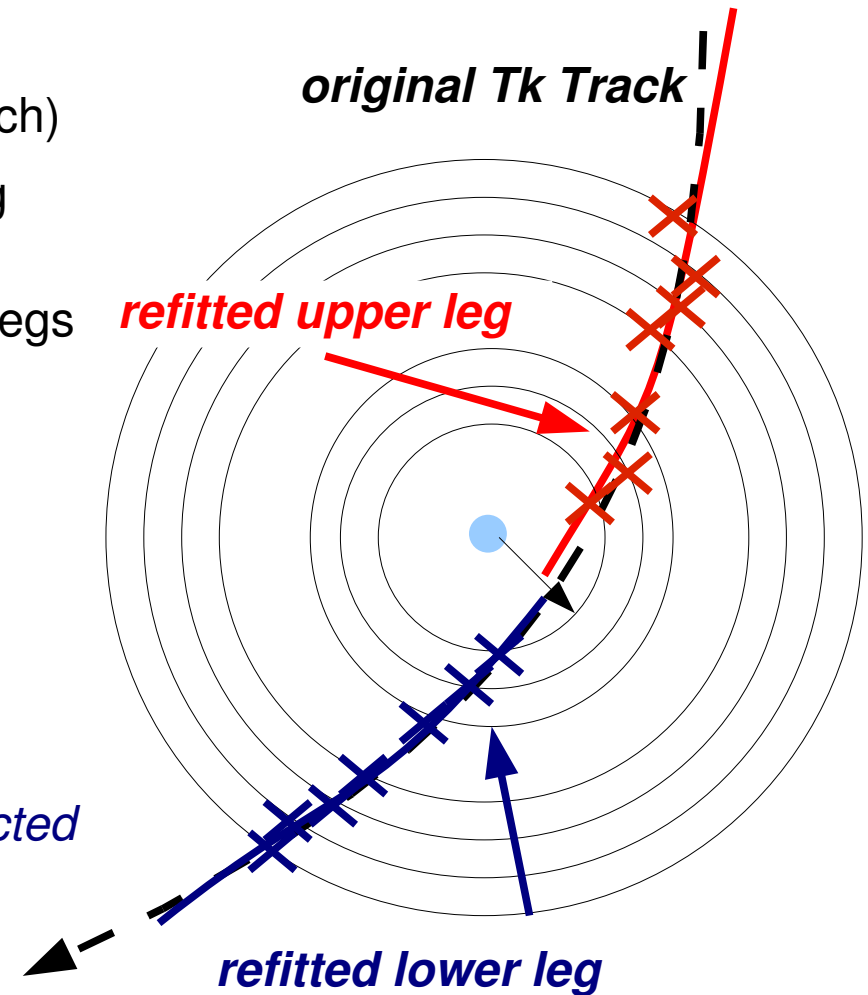
- define residuals r_x as the difference of the parameters from above and below

$$r_x = \Delta_x = X(PCA)_{TOP} - X(PCA)_{BOT}$$

- if alignment is good the two parameter sets should coincide and *small residuals are expected*
- Correct estimation of errors is reflected in the normalized residuals or pulls

$$\frac{r}{\sigma_r} = \frac{\Delta X}{\sigma_{\Delta X}} = \frac{X_{top} - X_{bot}}{\sqrt{\sigma_{X_{top}}^2 + \sigma_{X_{bot}}^2}}$$

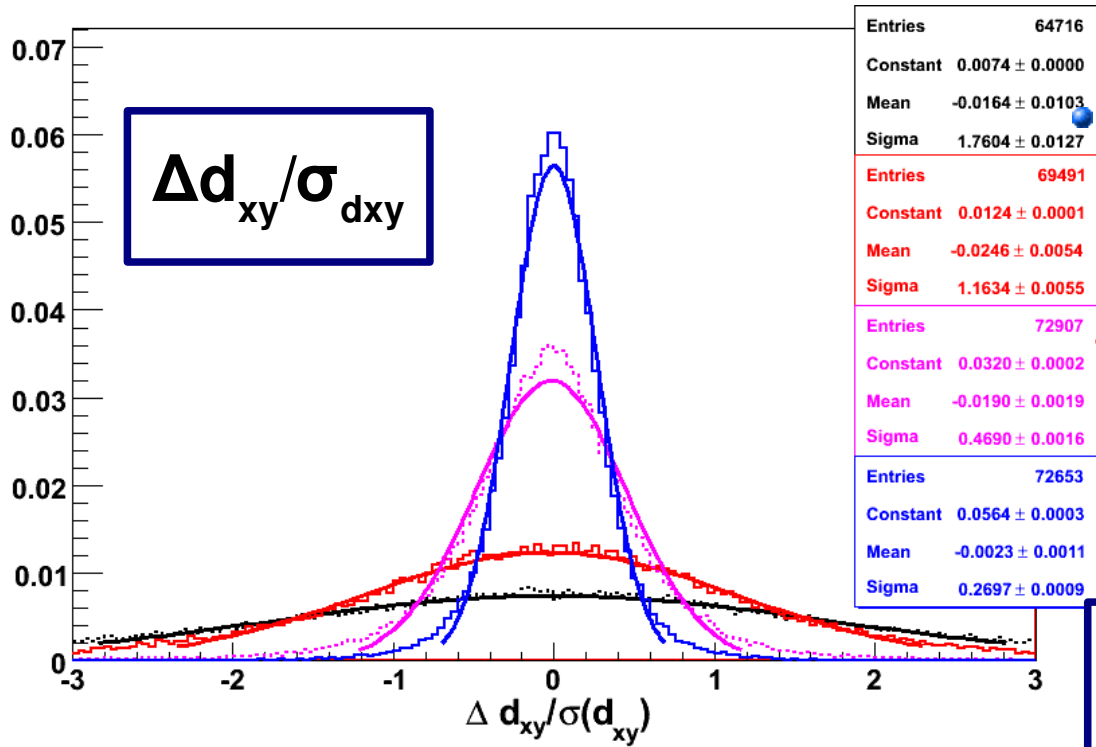
RMS of normalized residuals should be 1



Cosmic Track Splitting Validation*

N. Tran

Pairs of Split Tracks



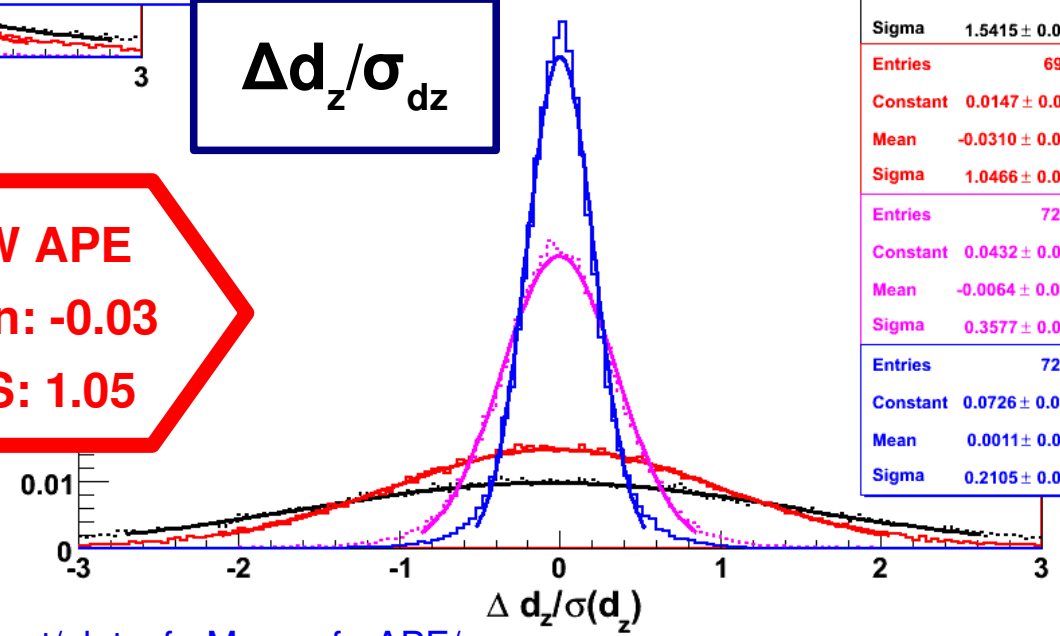
Pull of impact parameters d_{xy} and d_z

NEW APE
mean: -0.02
RMS: 1.16

$\Delta d_z / \sigma_{d_z}$

NEW APE
mean: -0.03
RMS: 1.05

Entries	64716
Constant	0.0098 ± 0.0001
Mean	-0.0556 ± 0.0080
Sigma	1.5415 ± 0.0089
Entries	69491
Constant	0.0147 ± 0.0001
Mean	-0.0310 ± 0.0047
Sigma	1.0466 ± 0.0047
Entries	72907
Constant	0.0432 ± 0.0002
Mean	-0.0064 ± 0.0014
Sigma	0.3577 ± 0.0013
Entries	72653
Constant	0.0726 ± 0.0004
Mean	0.0011 ± 0.0008
Sigma	0.2105 ± 0.0008

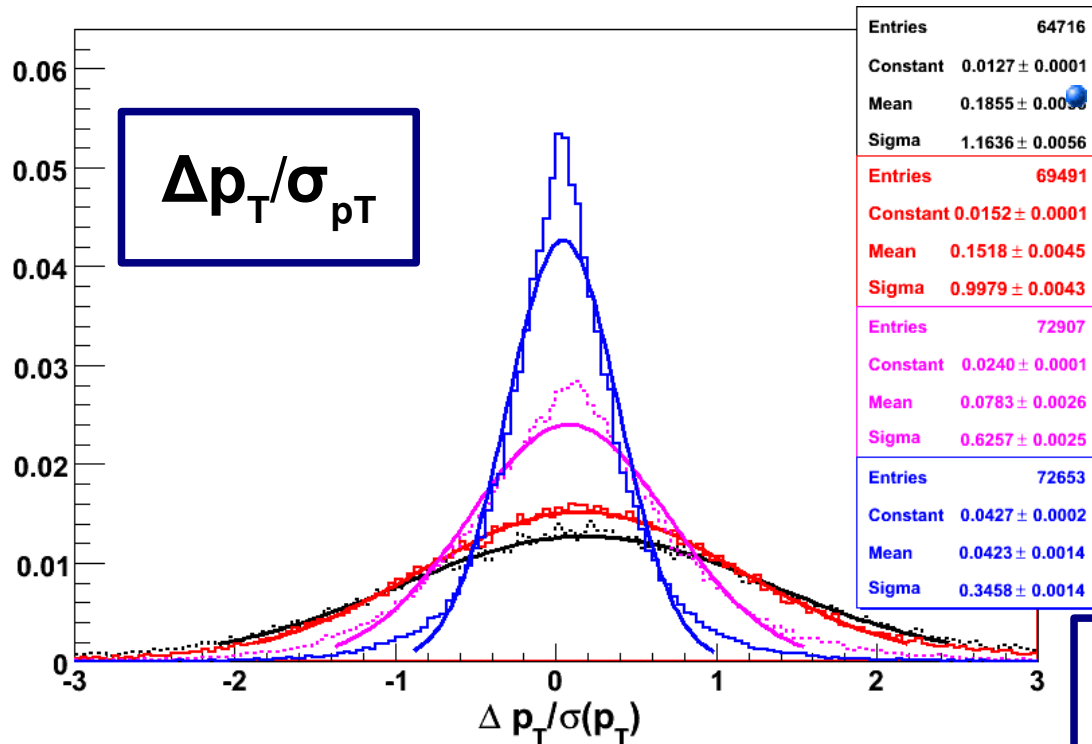


- Four APE objects considered:
- CRAFT 0 APE
- CRAFT New APE
- CRAFT Default APE
- CRAFT Inflated APE (default * 100)

*see: http://www.pha.jhu.edu/~ntran/cms/splitTracks/alignment/plots_forMarco_forAPE/

Normalized Residuals (p_T / κ)

Pairs of Split Tracks

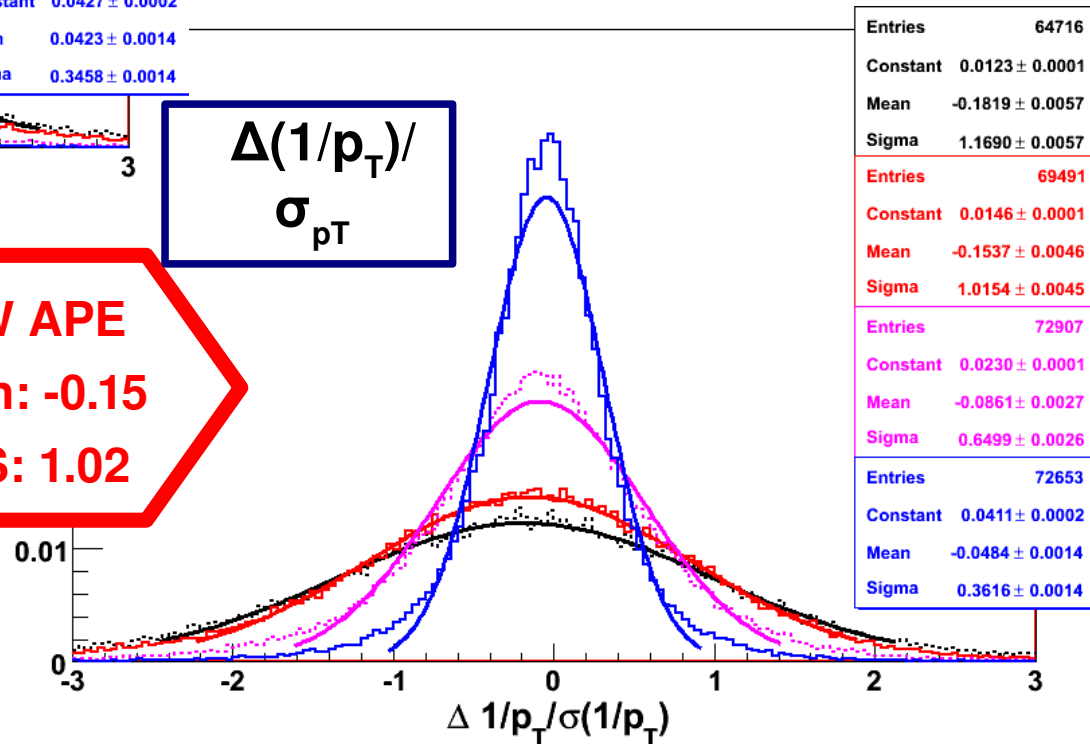


Pull for momentum/curvature $p_T / 1/p_T$

NEW APE
mean: 0.15
RMS: 0.99

$\Delta(1/p_T)/\sigma_{pT}$

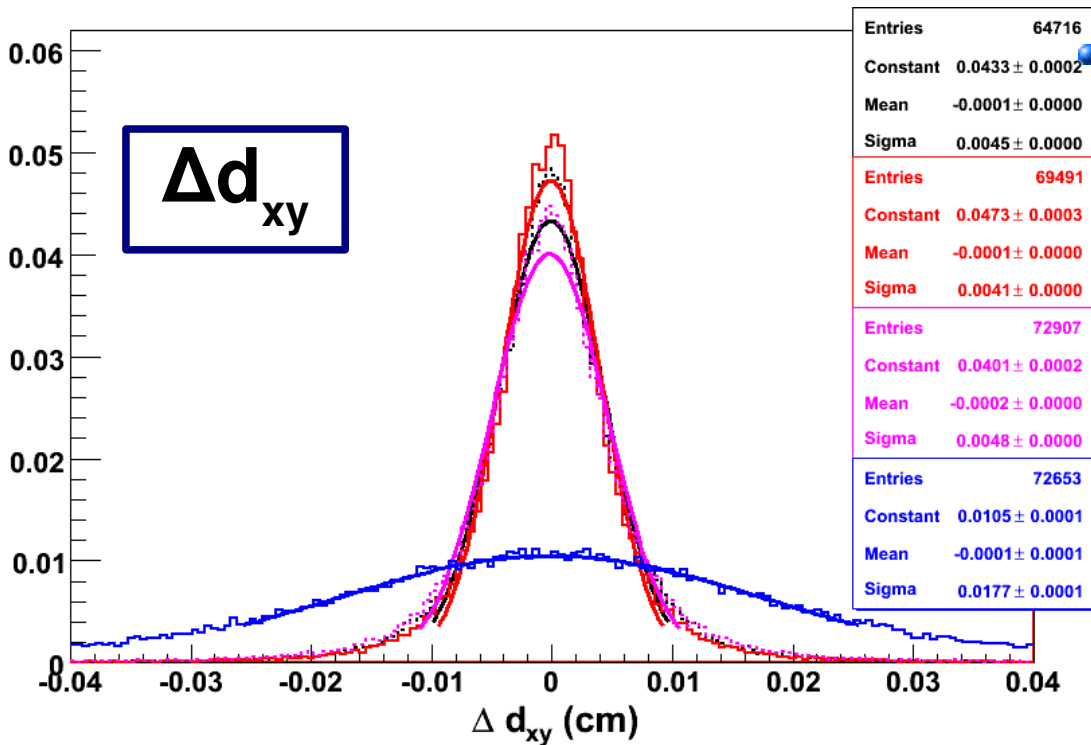
NEW APE
mean: -0.15
RMS: 1.02



• Pulls in general show a slight underestimation of the errors

Absolute Residuals

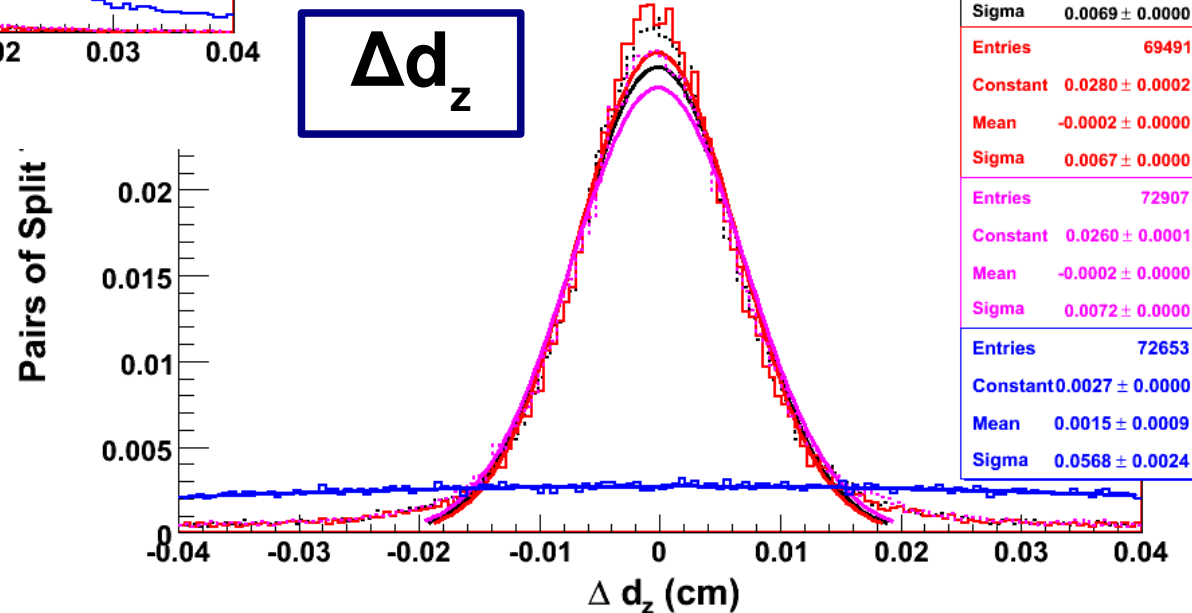
Pairs of Split Tracks



Four APE objects considered:

- CRAFT 0 APE
- CRAFT New APE
- CRAFT Default APE
- CRAFT Inflated APE

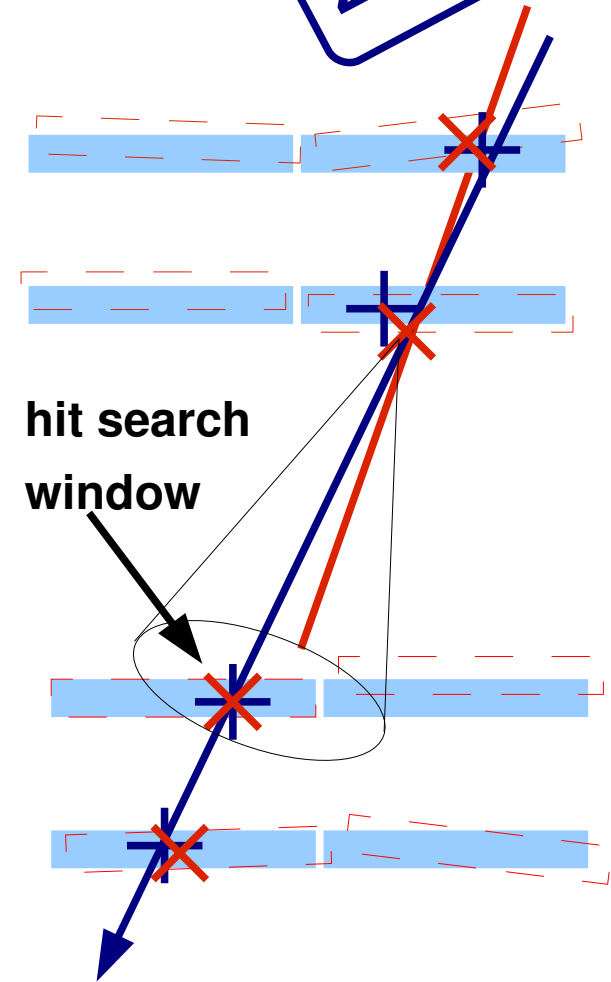
- Absolute residuals show:
 - little dependence on APEs
 - the **new APE** object has the best performance



APE in tracking efficiency

Z. Guo

- APE have a **direct impact on tracking efficiency** since:
 - the search window of hits in pattern recognition is tuned on APE (hit is taken if it does not deteriorate the track χ^2 more than some value)
 - track extrapolation is sensible to APE \Rightarrow in the refit procedure hits are "weighted" with the APE
- APE-related efficiency is a responsibility of Tracker Alignment Group
- Idea: Re-reco ~ 3k tracks from CRAFT**
 - Number of tracks with at least a TXX (TIB/TEC/...) hit



Within the **same tracking algo**, very little differences are observed among the different APE objects

CTF	PXB	PXE	TIB	TID	TOB	TEC
Zero	22	15	466	256	1456	724
New	22	18	464	256	1450	720
Default	24	19	474	261	1453	736

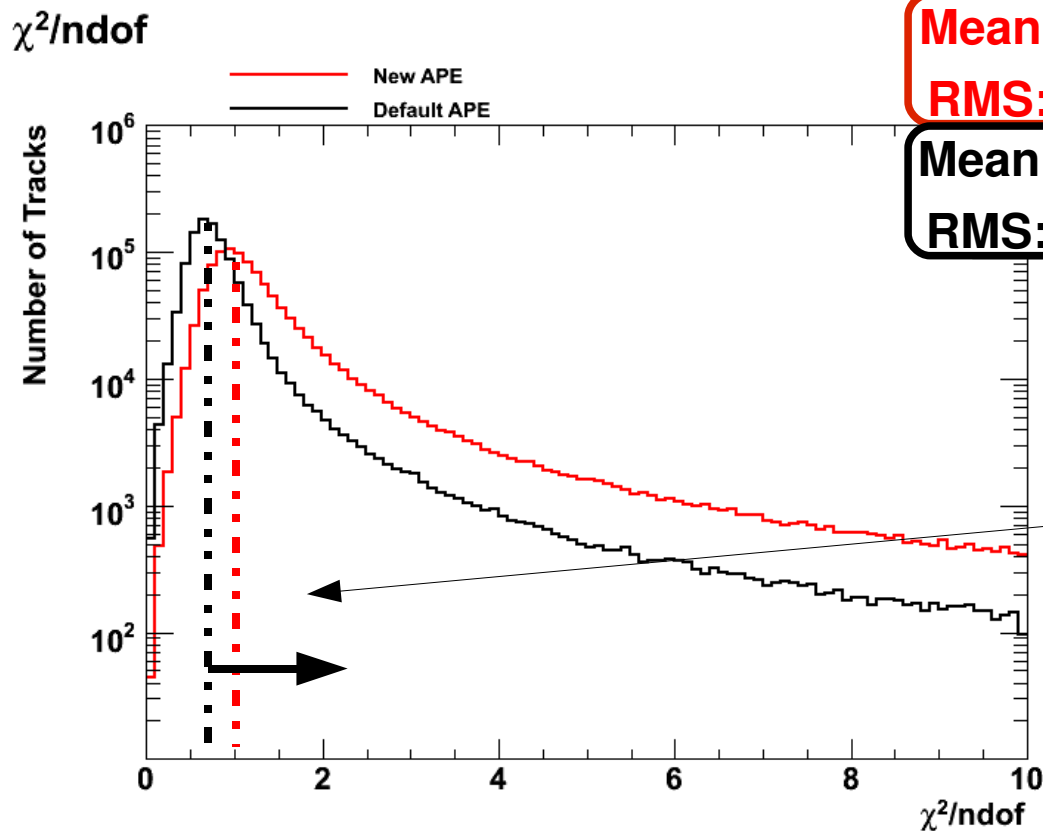
Cosmic TF	PXB	PXE	TIB	TID	TOB	TEC
Zero	25	20	469	262	1502	1070
New	24	19	471	262	1514	1079
Default	25	23	482	264	1536	1100

Track χ^2 (Default Vs New APE)

- Definition of track χ^2 :

$$\chi^2 = \sum_i^{N_{hits}} \frac{r_i^2(p, q)}{\sigma_i^2} = \sum_i^{N_{hits}} \frac{(u^{hit}(p, q) - u^{fit}(p, q))^2}{\sigma_i^2}$$

$$\sigma_i = \sigma_{i, track}(\mathbf{APE}) \oplus \sigma_{i, hit} \oplus \sigma_{APE}$$



Mean: 1.57

RMS: 1.35

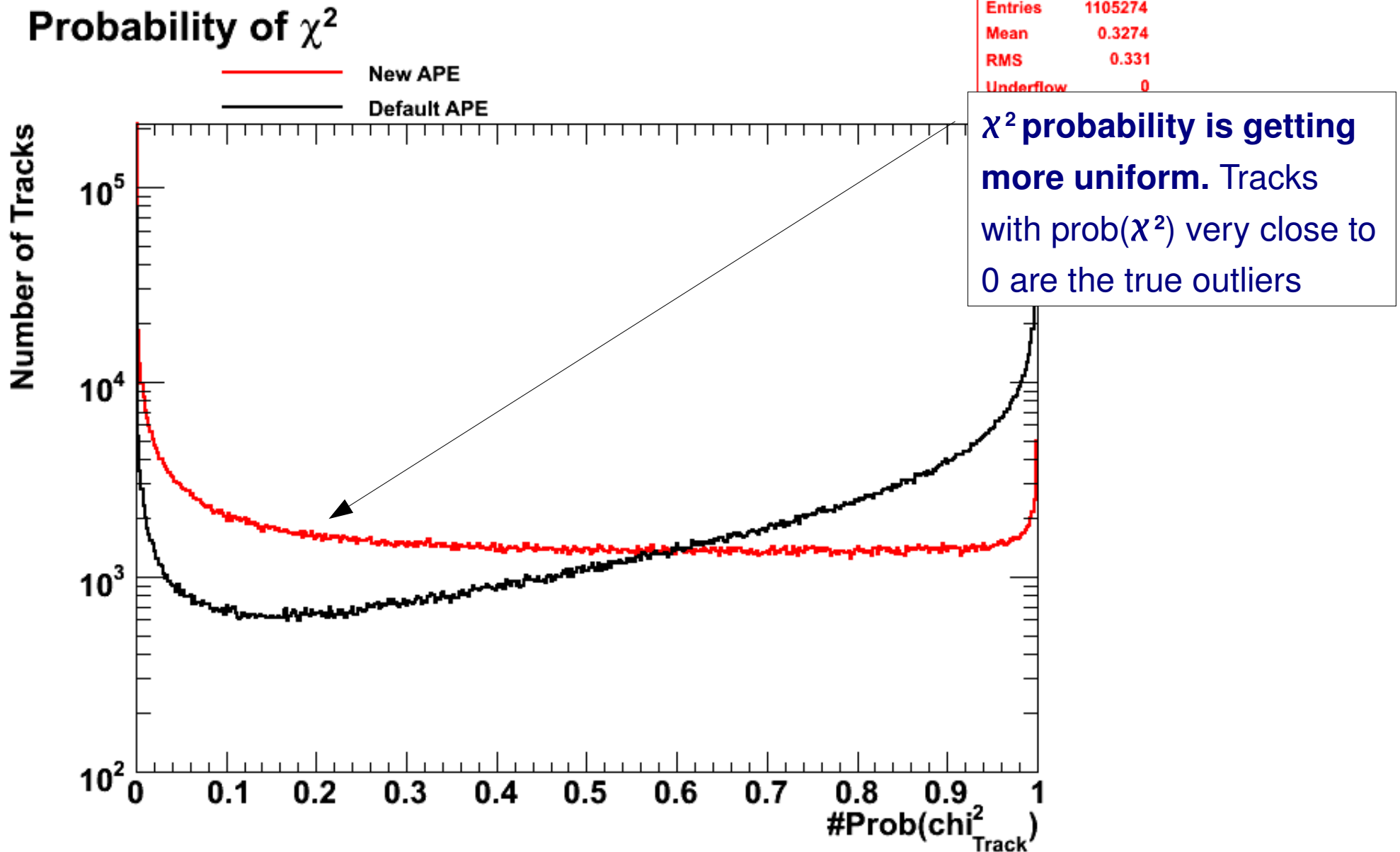
Mean: 0.94

RMS: 0.87

- The track χ^2 depends strongly on the **Alignment Position Error**
- Idea: refit tracks with new and old APE and check that the χ^2 shifts and indeed peaks at 1.

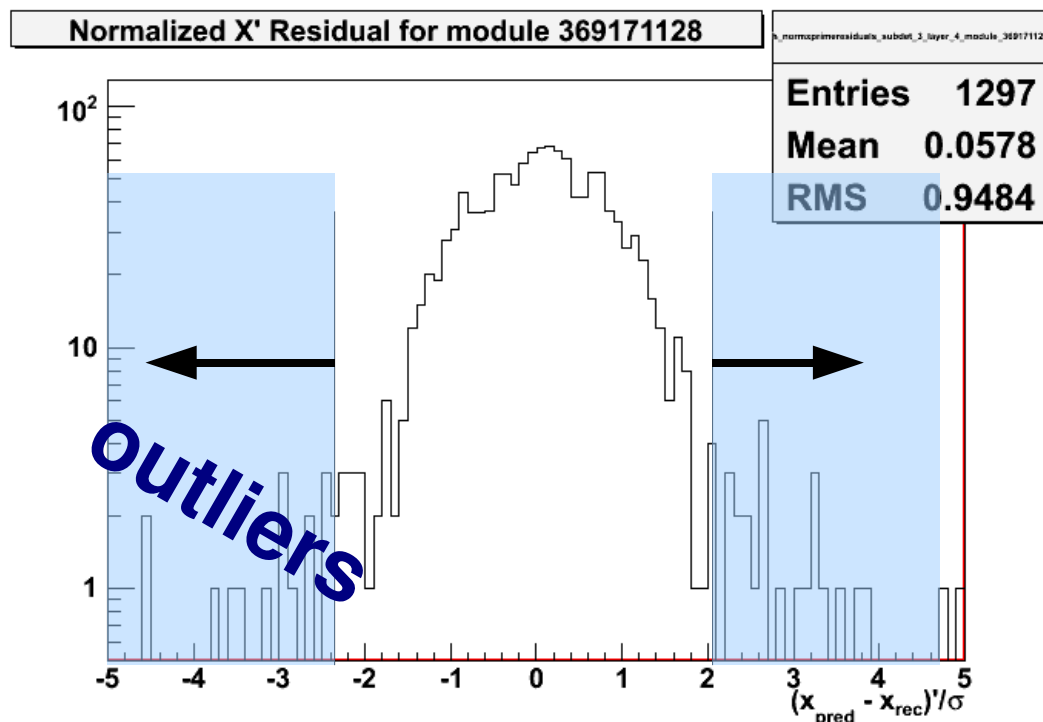
χ^2 peak shifting to 1. Mean values is still to high due to the heavy tail. More sensible to fit the distribution and extract the curve parameters?

Probability of χ^2



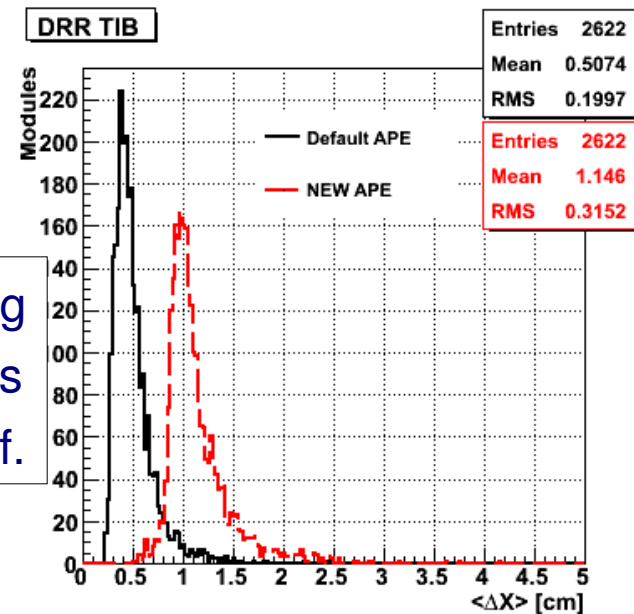
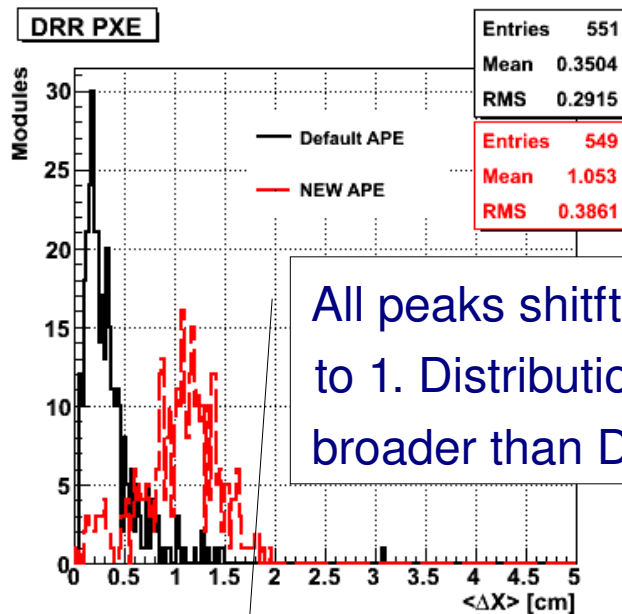
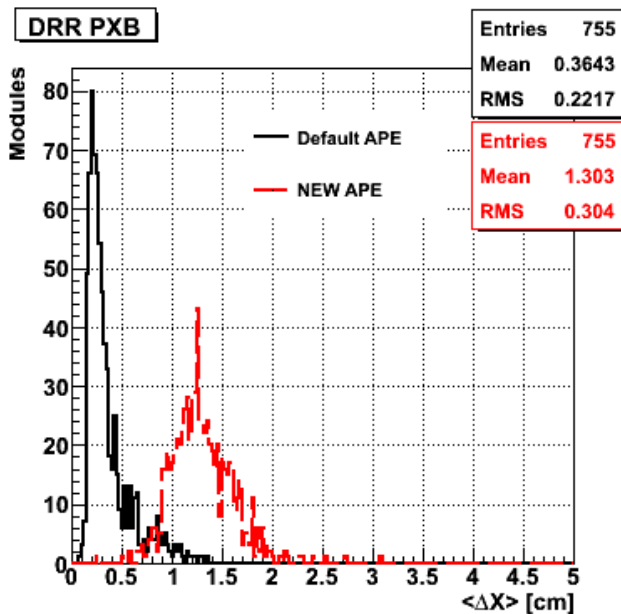
Further Validation of APE object

- Perform Standard Validation using **Tracker_Geometry_v3_offline** on **~ 1.5 M Tracks** (half of CRAFT Datasample)
- Extract at **module level** the width of the distribution containing 95.44% (i.e. $\pm 2\sigma$ if dealing with perfect gaussians) of the **normalized residuals**

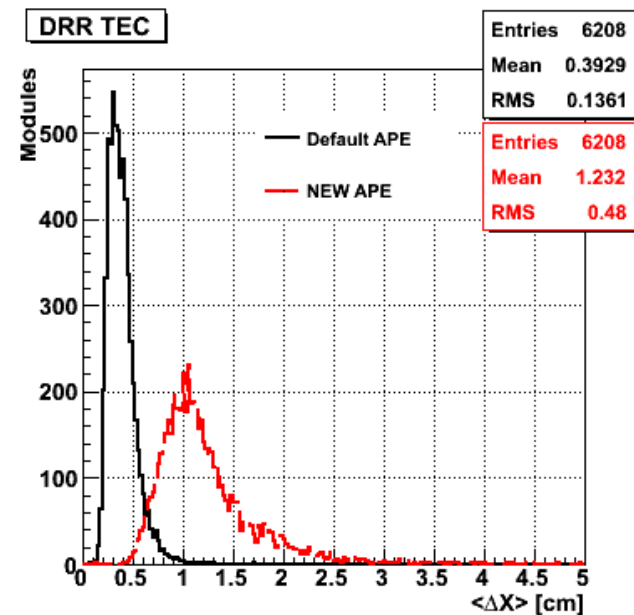
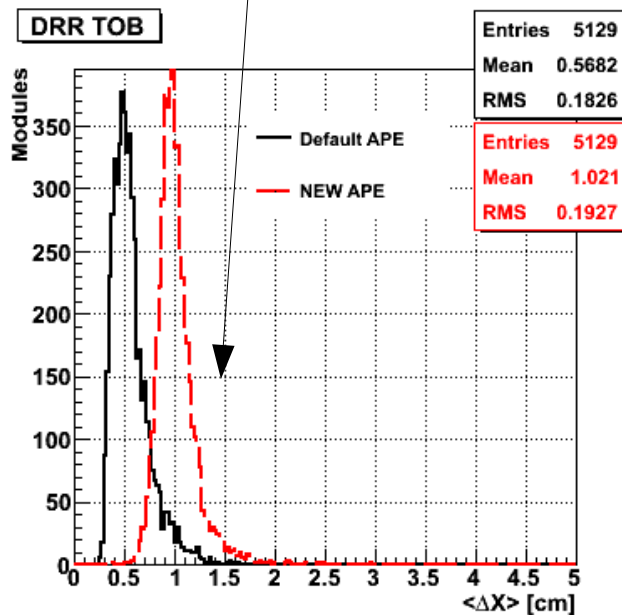
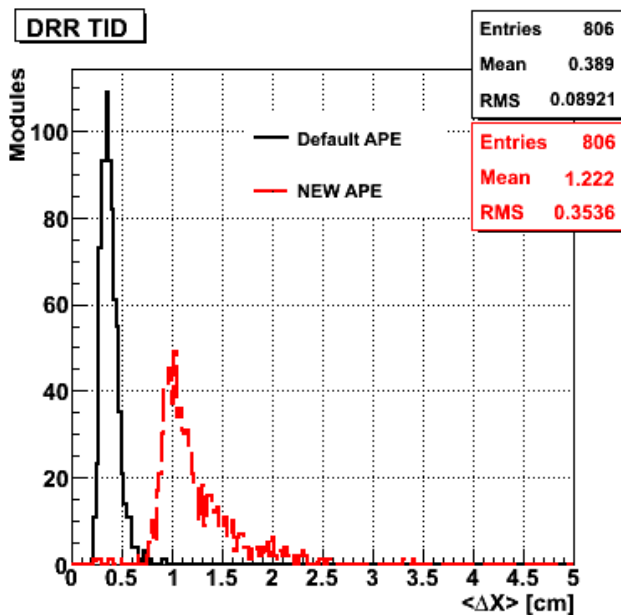


- Look at 1D distribution of Truncated RMS of normalized residuals at subdet and Layer level for Strip Barrel (Ideal world \Rightarrow peak to 1, as narrow as possible)
- Look at the TH2 distribution of Truncated RMS at Layer level for **TPB/TIB/TOB** for each module (check for inhomogeneities)

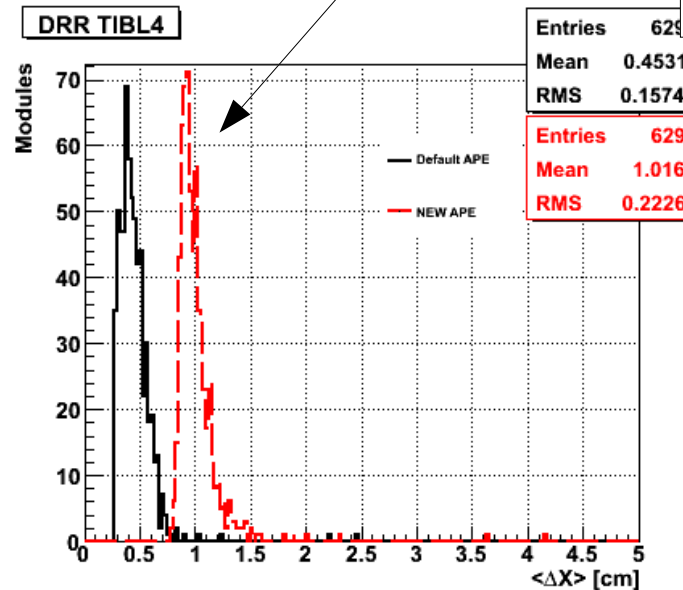
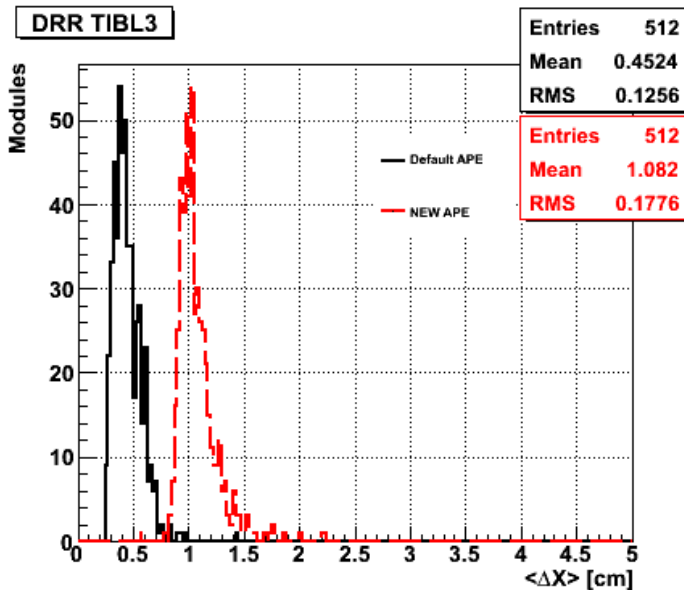
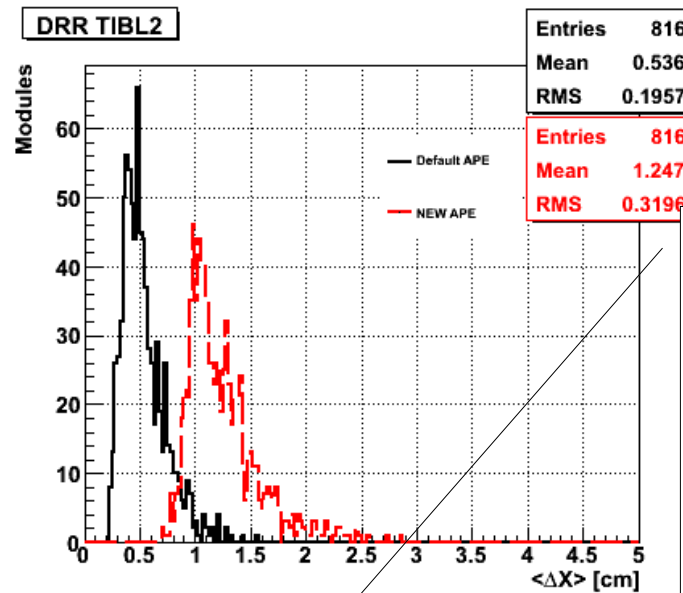
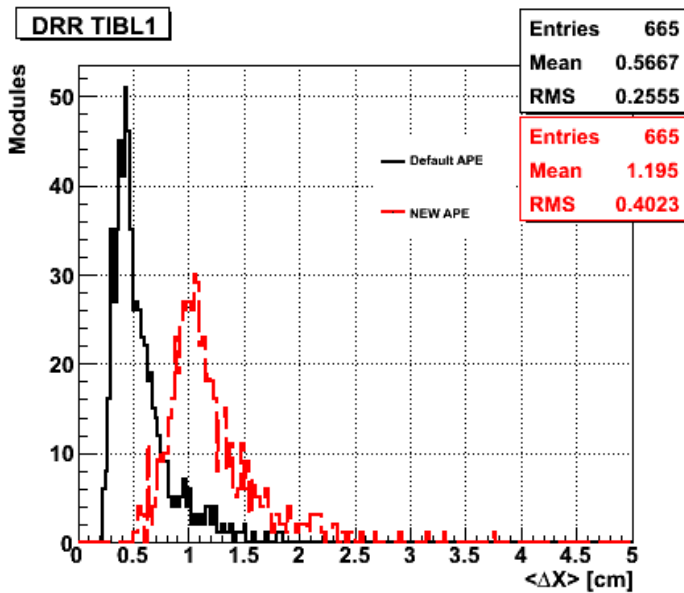
DRR – Subdet level



All peaks shifting to 1. Distributions broader than Def.

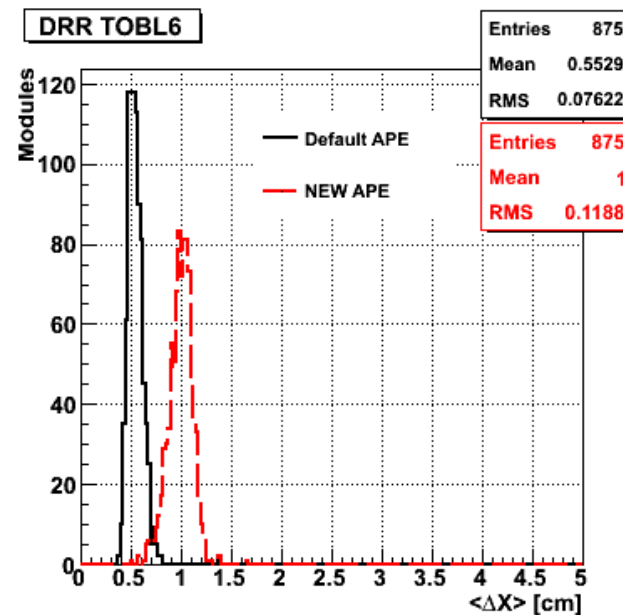
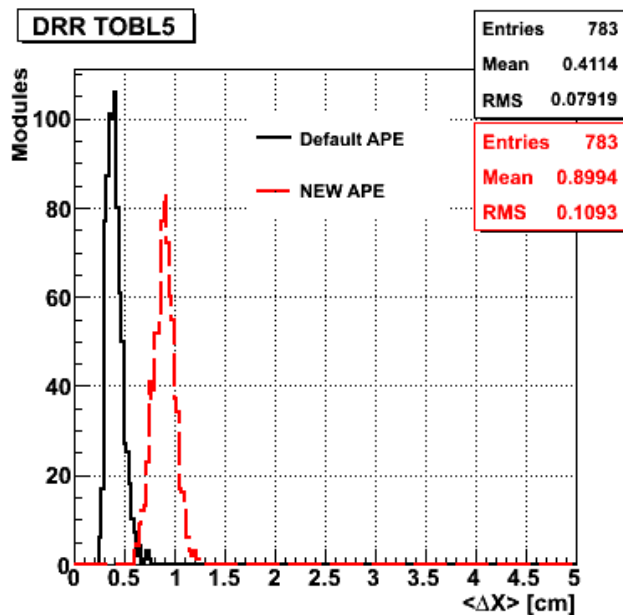
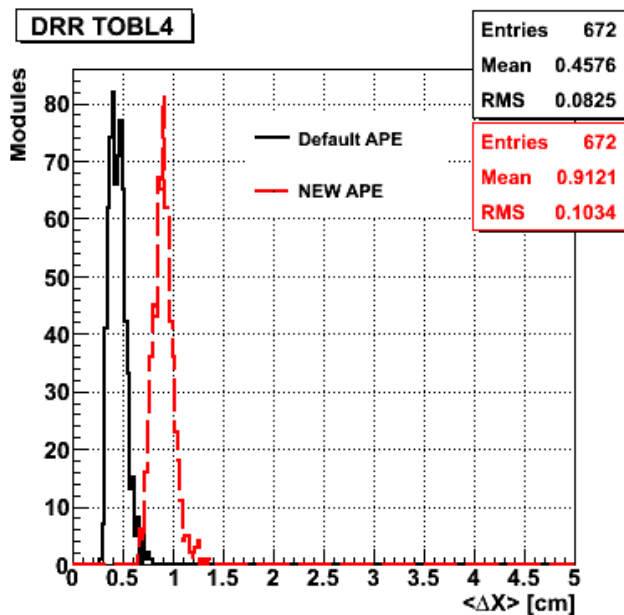
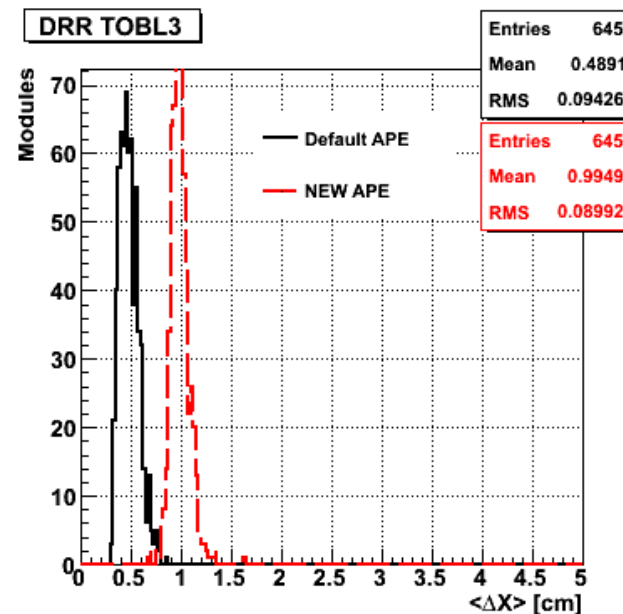
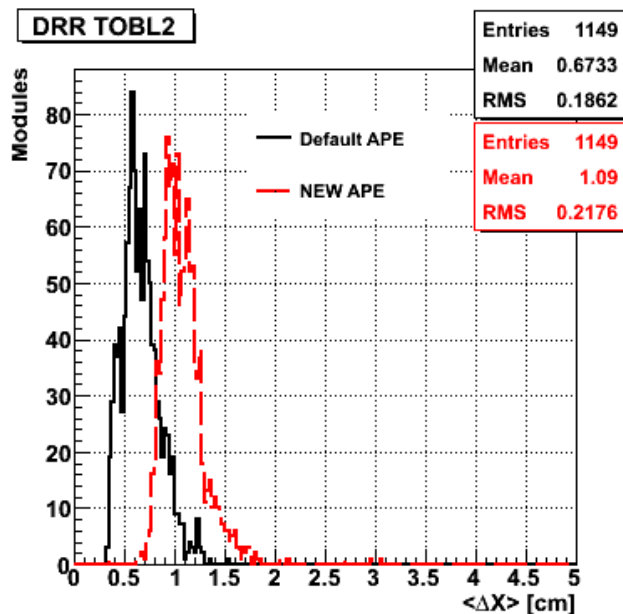
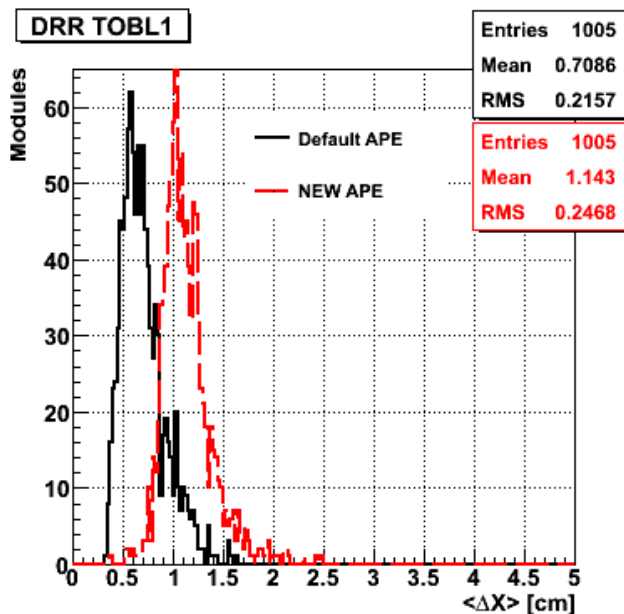


DRR – TIB (Layer Level)



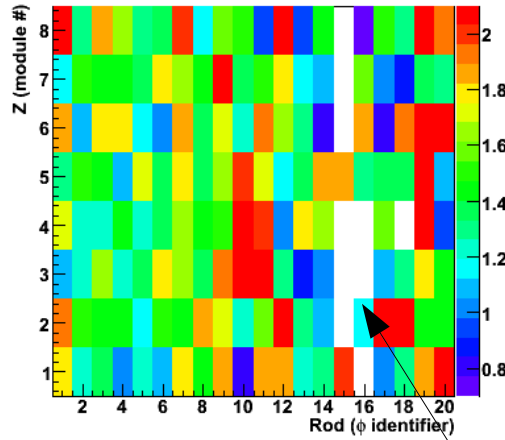
All peaks shifting to 1.
Distributions broader than Default. Distributions look crudely ok for SS Layers (L3/L4) while too broad in DS (L1/L2)

DRR – TOB (Layer Level)

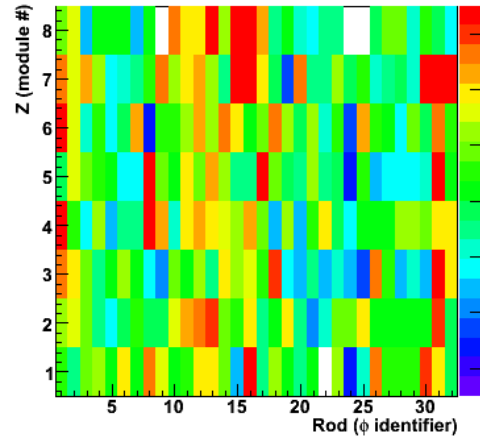


“Thermal Maps” of RMS - PXB

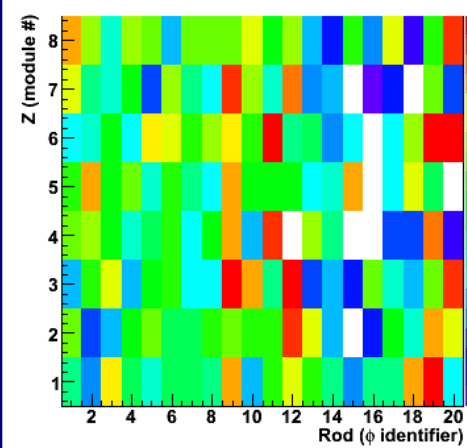
Truncated RMS Normalized Residuals PXB L1



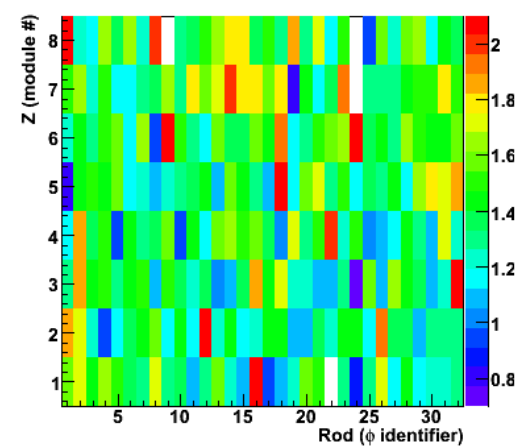
Truncated RMS Normalized Residuals PXB L2



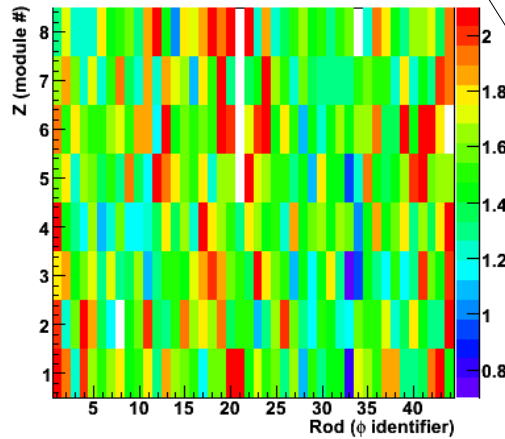
Truncated RMS y Normalized Residuals PXB L1



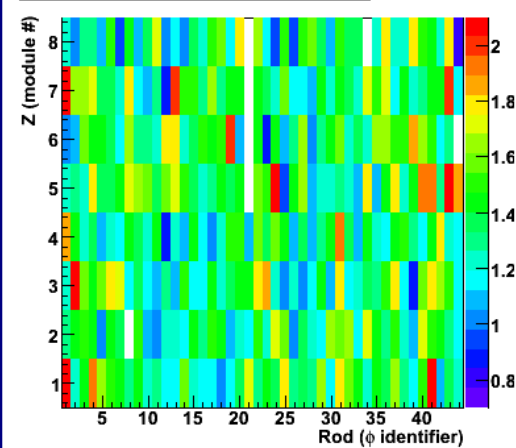
Truncated RMS y Normalized Residuals PXB L2



Truncated RMS Normalized Residuals PXB L3



Truncated RMS y Normalized Residuals PXB L3



X - residuals

Y - residuals

White spots are modules receiving too few hits to extract sensible RMS.

“Thermal Maps” of RMS - TIB

R ϕ

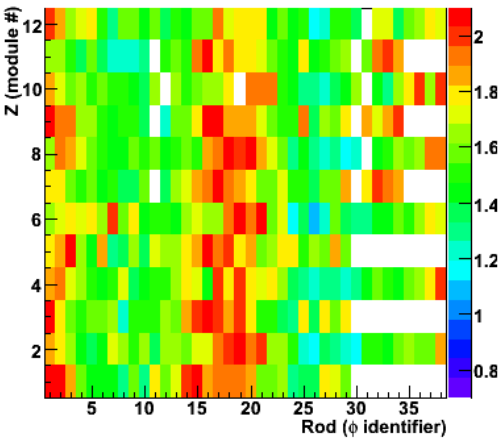
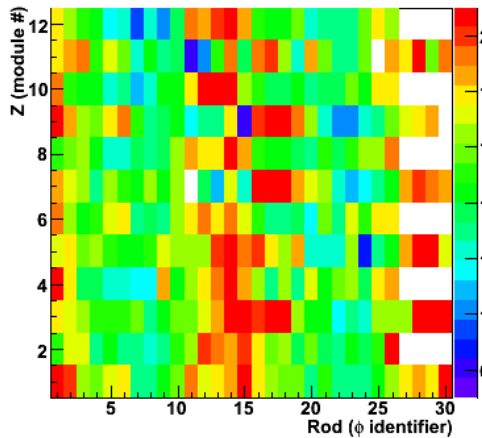
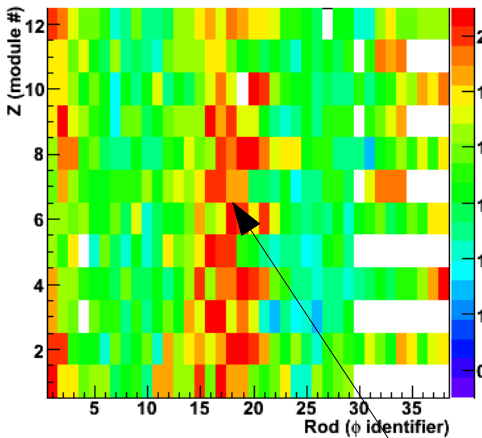
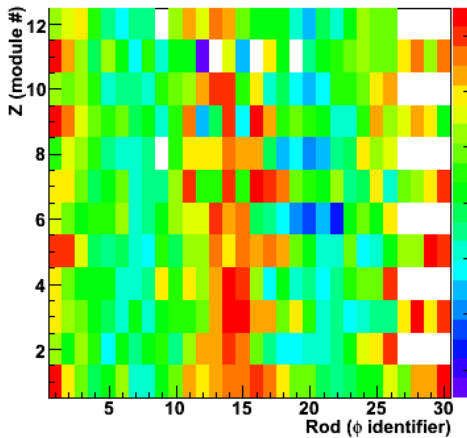
Stereo

Truncated RMS Normalized Residuals TIB L1

Truncated RMS Normalized Residuals TIB L2

Truncated RMS Normalized Residuals TIB L1

Truncated RMS Normalized Residuals TIB L2

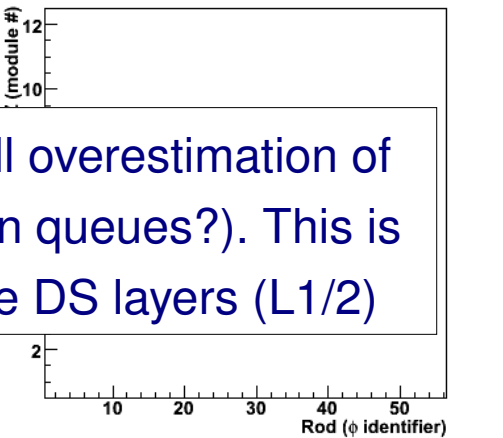
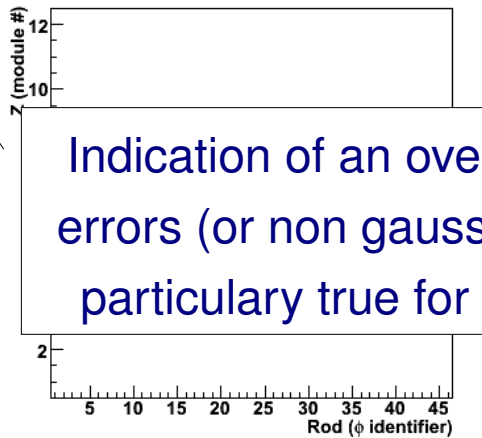
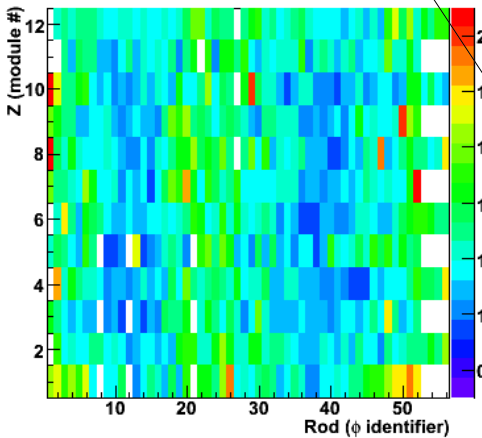
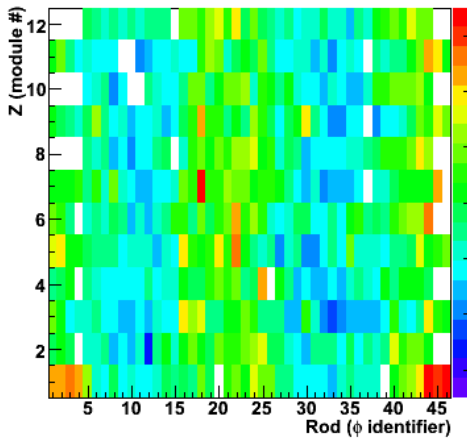


Truncated RMS Normalized Residuals TIB L3

Truncated RMS Normalized Residuals TIB L4

Truncated RMS Normalized Residuals TIB L3

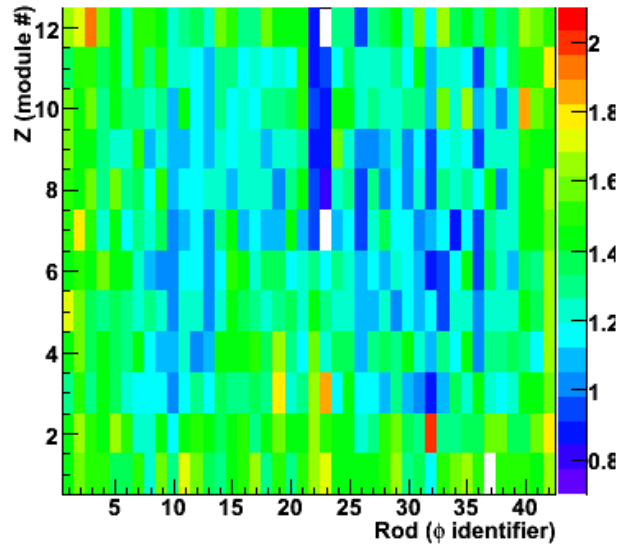
Truncated RMS Normalized Residuals TIB L4



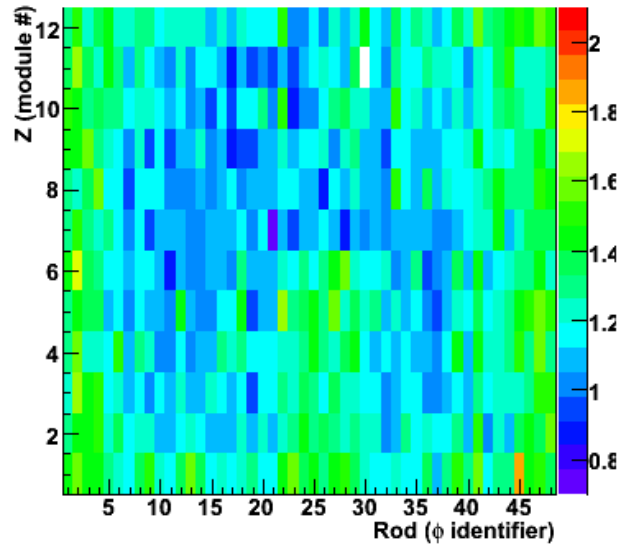
Indication of an overall overestimation of errors (or non gaussian queues?). This is particularly true for the DS layers (L1/2)

“Thermal Maps” of RMS - TOB ($r\phi$)

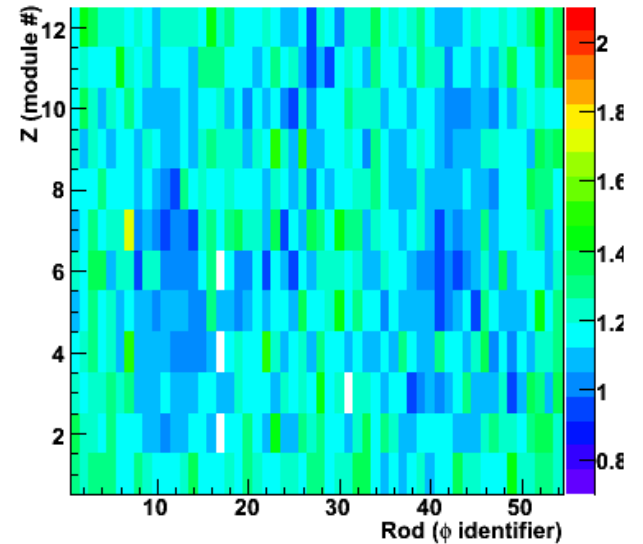
Truncated RMS Normalized Residuals TOB L1



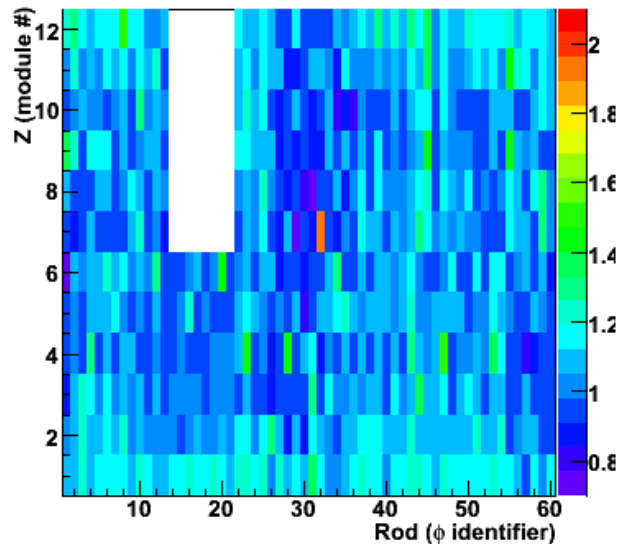
Truncated RMS Normalized Residuals TOB L2



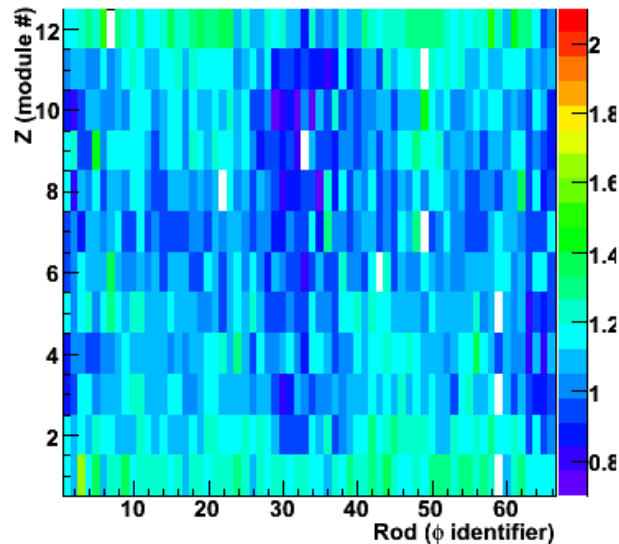
Truncated RMS Normalized Residuals TOB L3



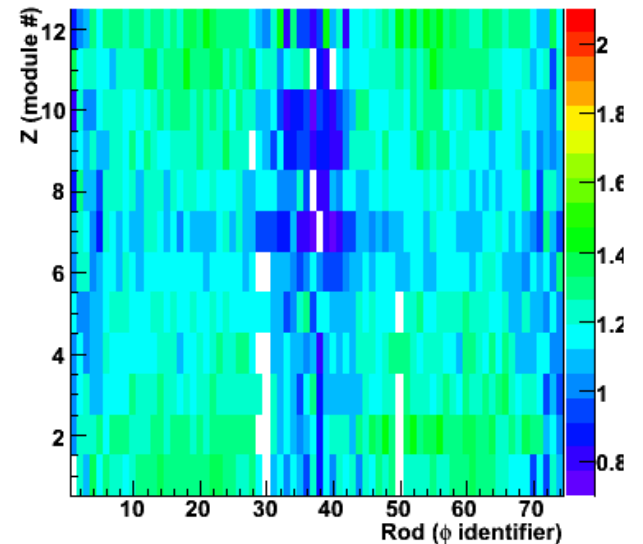
Truncated RMS Normalized Residuals TOB L4



Truncated RMS Normalized Residuals TOB L5

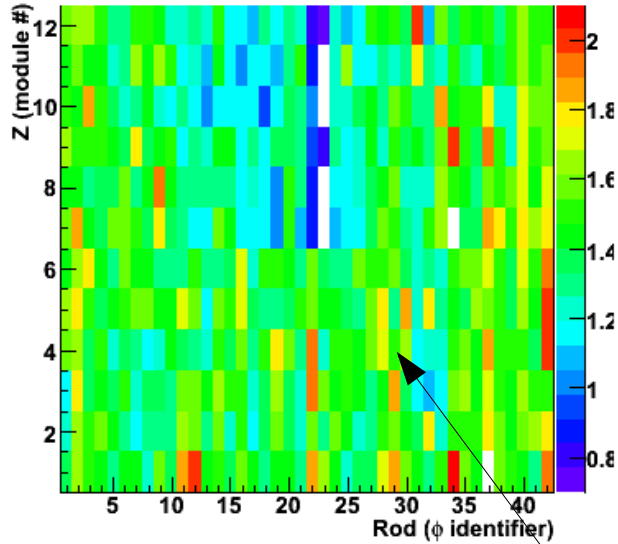


Truncated RMS Normalized Residuals TOB L6

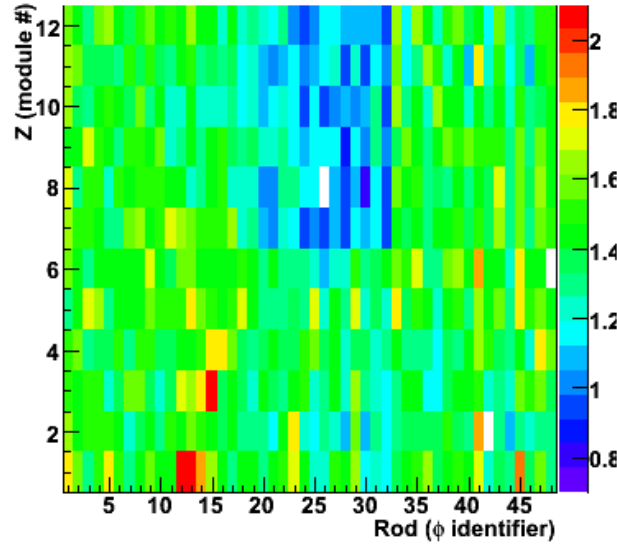


“Thermal Maps” - TOB (stereo)

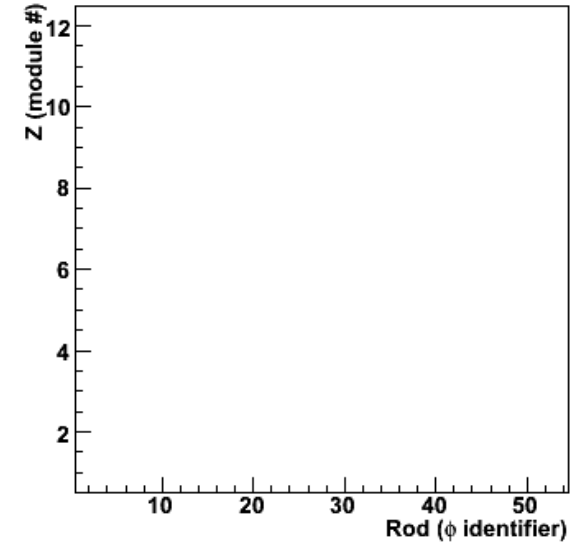
Truncated RMS Normalized Residuals TOB L1



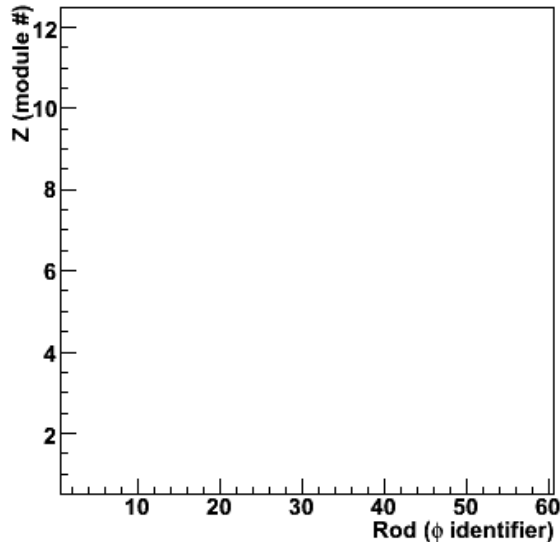
Truncated RMS Normalized Residuals TOB L2



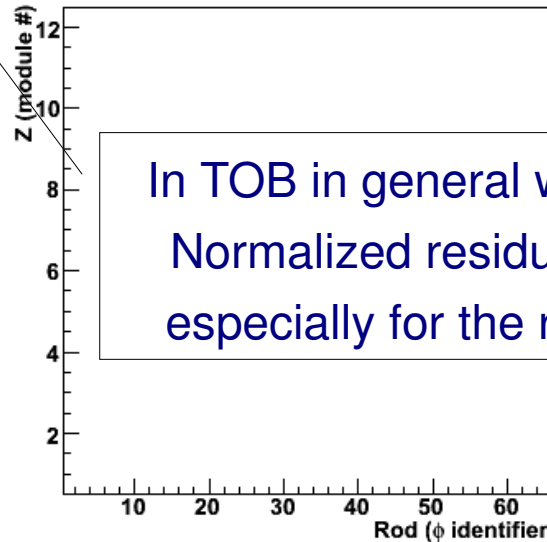
Truncated RMS Normalized Residuals TOB L3



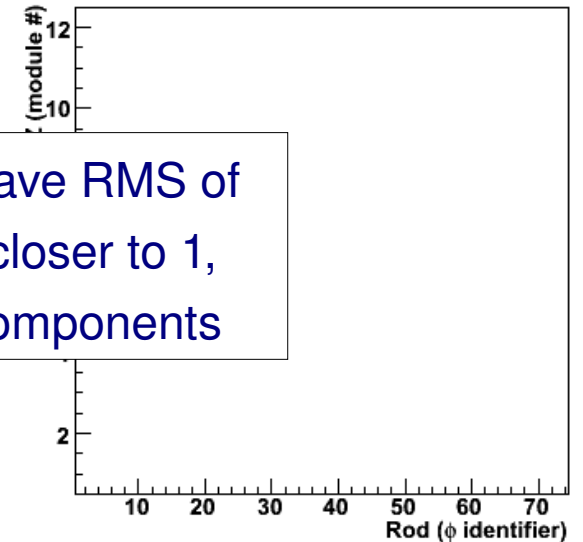
Truncated RMS Normalized Residuals TOB L4



Truncated RMS Normalized Residuals TOB L5



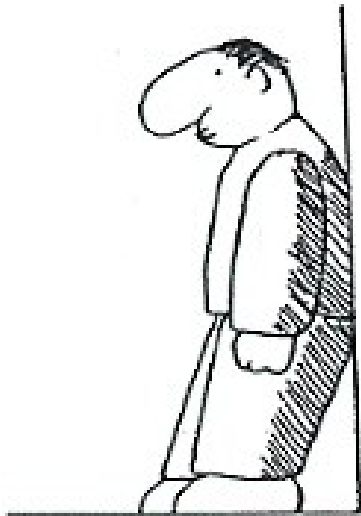
Truncated RMS Normalized Residuals TOB L6



In TOB in general we have RMS of Normalized residuals closer to 1, especially for the $r\phi$ components

Conclusions

- Motivation for module-dependent APE:
 - Old APEs (*TrackerGeometryErr_V3_offline*) were too large wrt to the RMS of DMRs.
 - Alignment is not uniform in the whole Tracker
- A first rough **module dependent APE object has been created** using newly developed code, using as an input “spherical” errors. It was produced mixing several ingredients:
 - MC tuning of remaining misalignment to match DMR and Residuals in a “well aligned” region in TOB/TIB
 - scale law with the number of hits on each DetUnit
- **Validation loop** looking at Normalized Residuals/ Cosmic Track Splitting / Tracking efficiencies completed
 - Newly determined APE entered the CMS Tracker conditions database
 - will eventually go in a new GlobalTag for new CRAFT analyses



Back-up Slides

Tracking Efficiency

CTF	PXB	PXE	TIB	TID	TOB	TEC
Zero	62	18	3435	586	16079	7013
New	66	27	3488	623	16173	7272
Default	68	35	3580	682	16352	7677

Cosmic TF	PXB	PXE	TIB	TID	TOB	TEC
Zero	73	28	3567	650	15470	5784
New	76	31	3616	650	15654	5924
Default	80	38	3662	672	15986	6212

The number of hits associated to tracks re-recoed with new APE is larger than zero APE (= no hit loss)