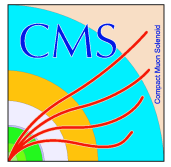


Track-based alignment note and 6-dof procedure

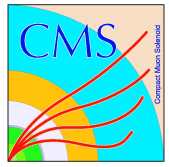
Jim Pivarski

Alexei Safonov

Texas A&M University

14 April, 2009

Track-based alignment news



- 1st draft of comprehensive CMS Note on globalMuon alignment
  - contains method, plotting/validation procedures, but not results
  - method described in paper in sync with latest developments
  - includes CSC Overlaps procedure with complete 2008 results
  - posted on this Indico page (confId=56657)
- Procedure extends CRAFT alignment to 6 d.o.f.
- Status of extended CRAFT alignment:
  - algorithm works, verified with MC
  - optimizing scheme of which parameters to align for which chambers in CRAFT

Outline for this talk

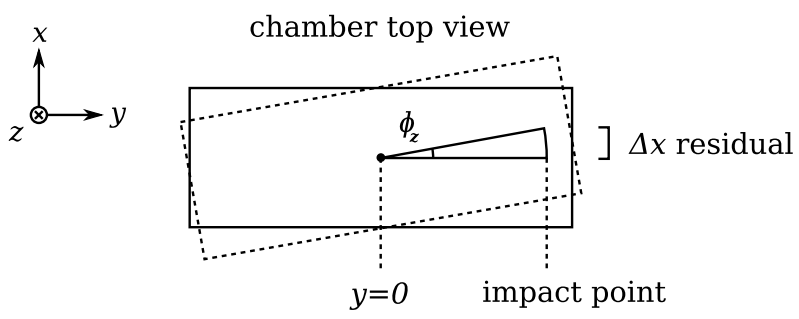
- Highlights from the paper
- Plots of preliminary CRAFT alignment

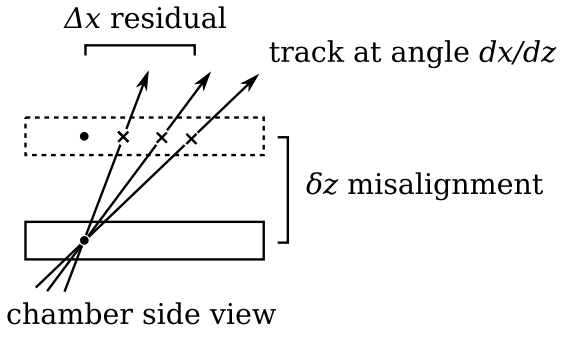
Table of contents

Contents

Alignment procedure in brief

- Fit tracks to tracker, propagate into muon system
- Collect residuals with respect to tracks in two bins: μ^+ and μ^-
- Fit residuals to theoretical curve, accounting for
  - correlations that yield alignments: ϕ_z and local z
  - other significant correlations that may distort the shape





- Average the fit results from the two bins and update geometry
- Iterate if necessary
  - in principle, iteration is not necessary because track-fitting is independent of alignment
  - if imperfectly modeled by fit function, correlations between parameters (especially angles) can be resolved by iteration

Summary of fitting methods

Fits to DT superlayers 1 and 3 super-residuals

fit to Δx residuals	fit to φ_y residuals
δx: peak of the distribution, independent of impact	φ_y peak of the distribution
δz: dependence of the peak on dx/dz track angle	slope vs. dy/dz: control for φ_z
φ_z: dependence of the peak on y impact point	
σ, Γ: width of the distribution	σ, Γ: width of the distribution
slope of Δx vs. φ_y: model scattering	

Fits to DT superlayer 2 super-residuals

fit to Δy residuals	fit to φ_x residuals
δy: peak of the distribution, independent of impact	φ_x peak of the distribution
φ_z: dependence of the peak on x impact point	
σ, Γ: width of the distribution	σ, Γ: width of the distribution
slope of Δy vs. φ_x: model scattering	

Fits to CSC super-residuals

fit to $\Delta r\varphi$ residuals	fit to φ_y residuals
$r\delta\varphi$: peak of the distribution, independent of impact	φ_y peak of the distribution
δz: dependence of the peak on d(rφ)/dz track angle	
φ_z: dependence of the peak on y impact point	
σ, Γ: width of the distribution	σ, Γ: width of the distribution
slope of Δx vs. φ_y: model scattering	

Accessible parameters

DT	δ_x	δ_y	δ_z	φ_x	φ_y	φ_z (two ways)
CSC	δ_x	inaccessible	δ_z	inaccessible	φ_y	φ_z

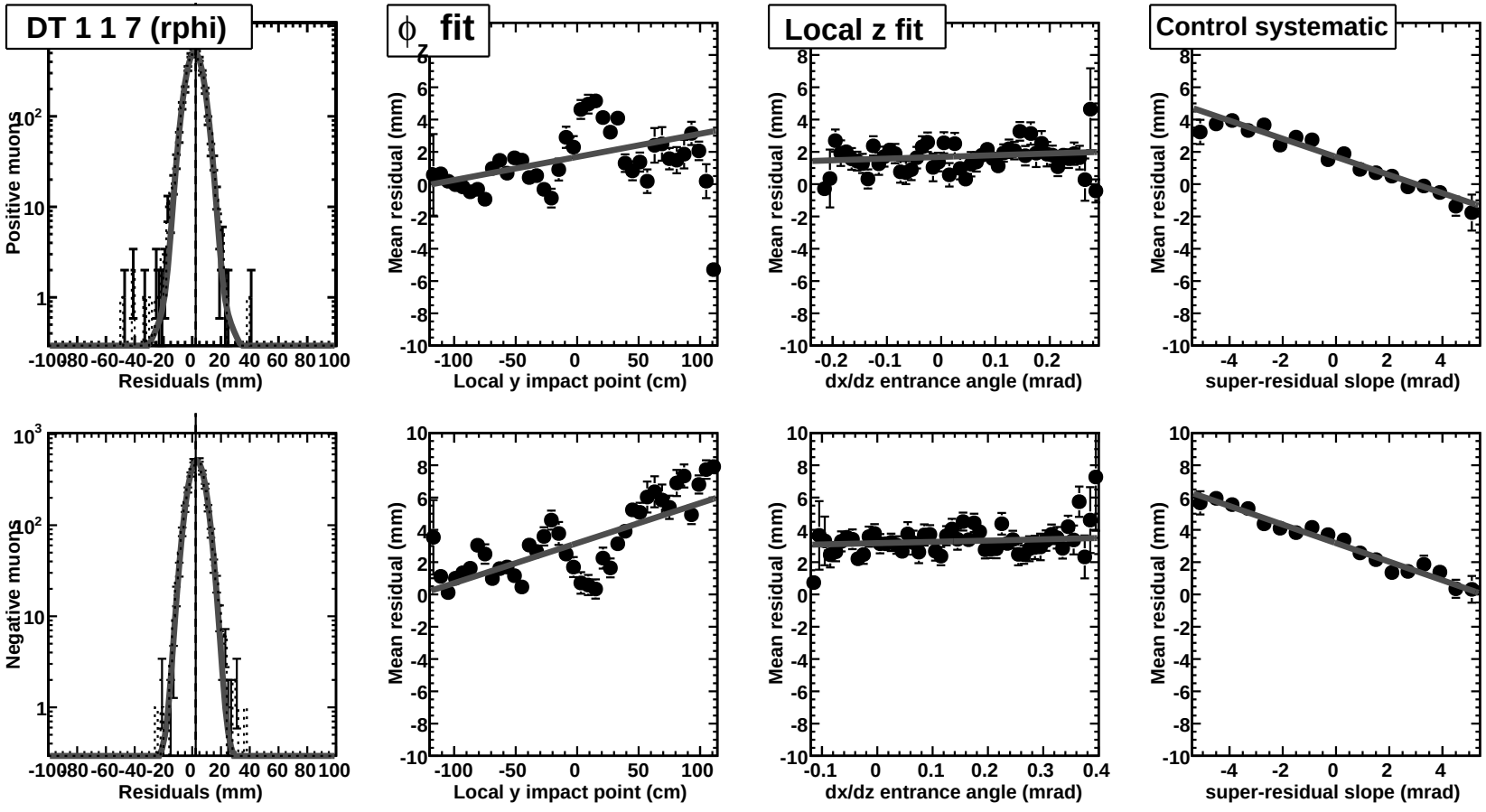
Figure 12: The six independent fits needed to align one DT chamber and one CSC.

Sample fits 1/3 (MC)

Two independent fits: μ^+ in top row, μ^- in bottom row

Lines are crest of peak function in different projections

Vertical line on bell curve is average of μ^+ and μ^-

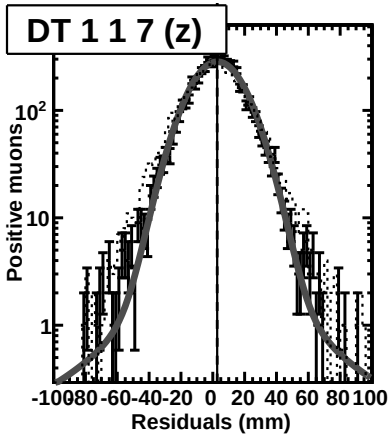


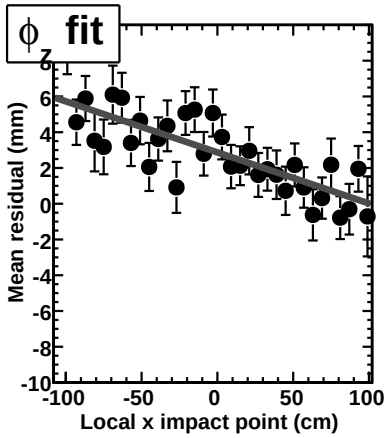
Sample fits 2/3 (MC)

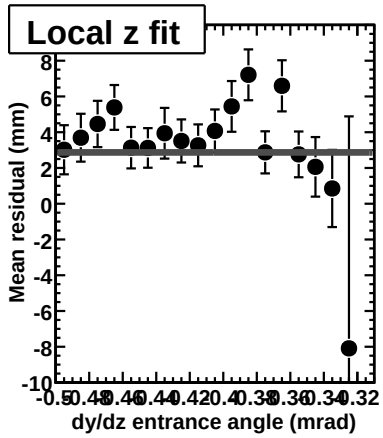
Superlayer 2 fit is independent of superlayer 1&3

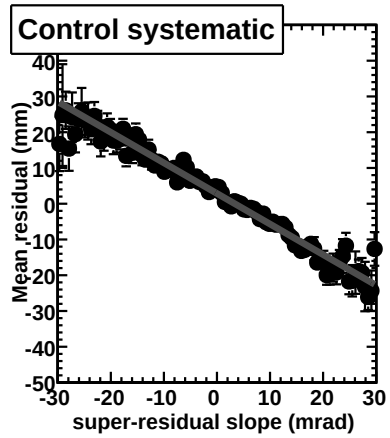
Can cross-check ϕ_z and local z measurements (opposite sign convention)

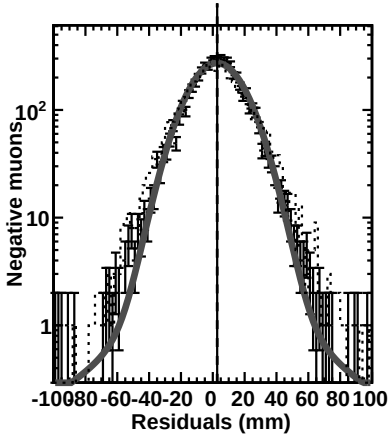
But lower precision (local z is held fixed in this example)

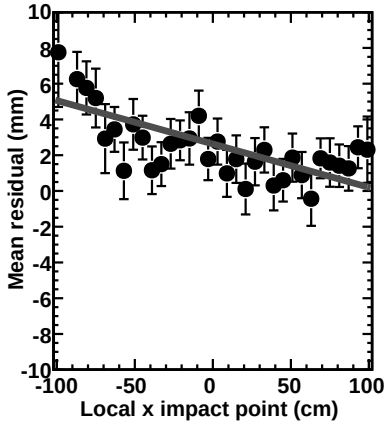


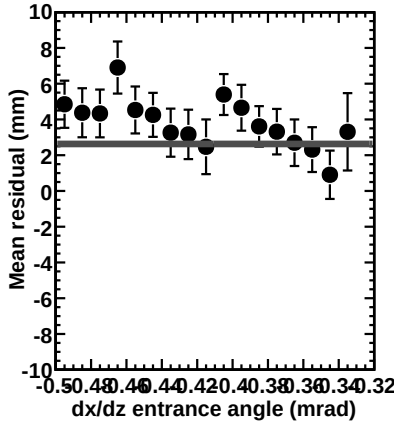


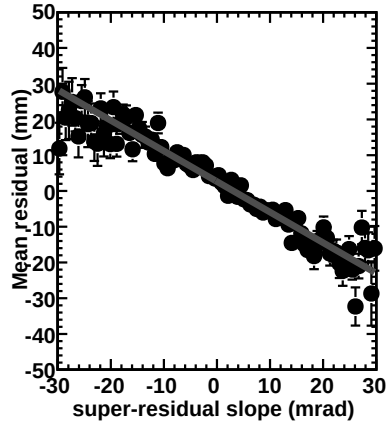




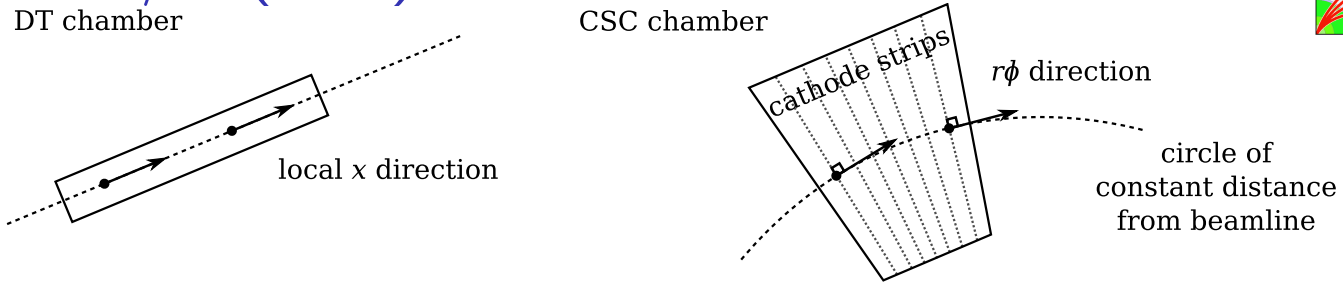




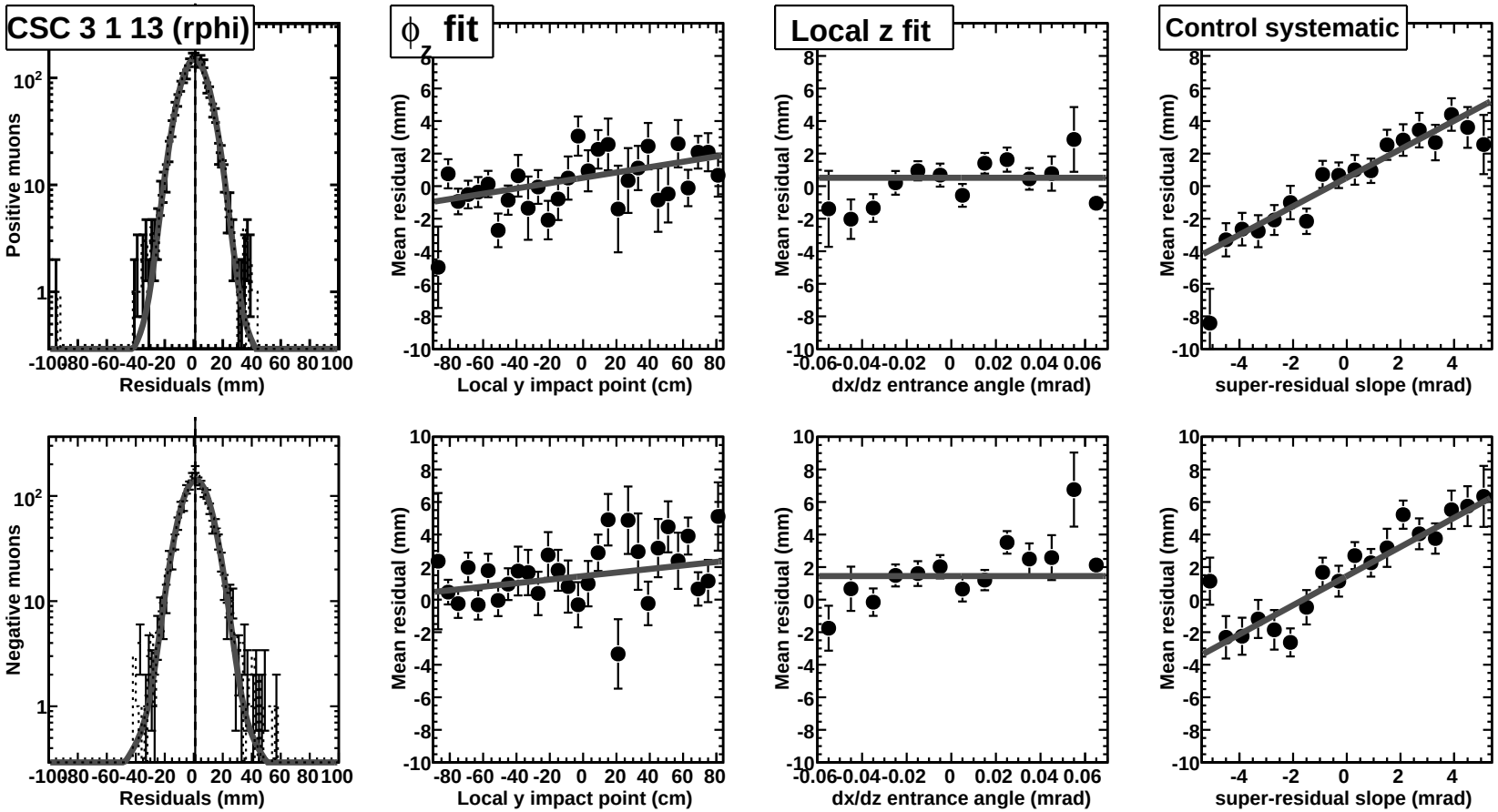




Sample fits 3/3 (MC)



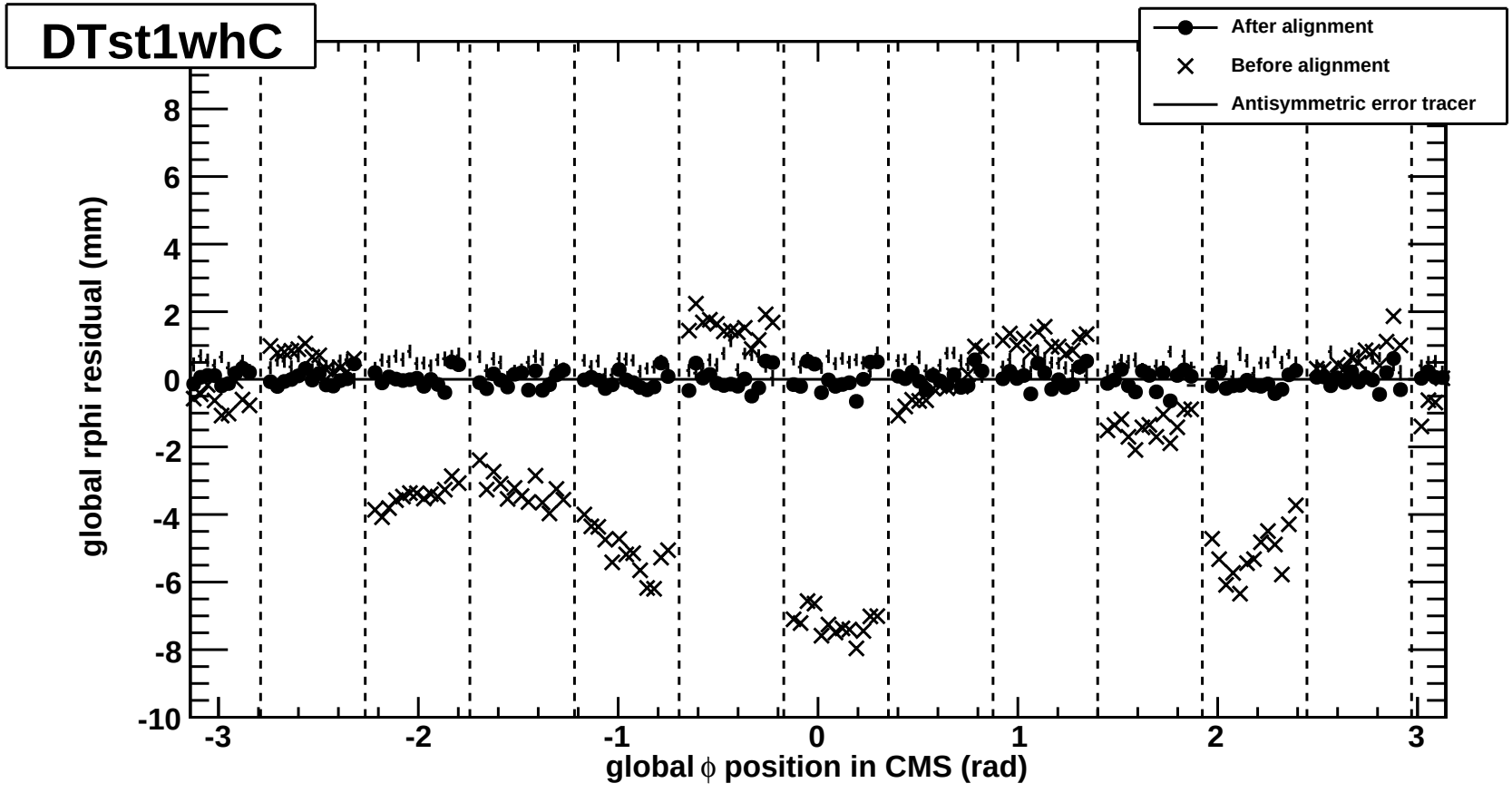
CSCs included in the same way, except that correction is in curvilinear $r\phi$, rather than cartesian local x



New residuals maps 1/3 (MC)

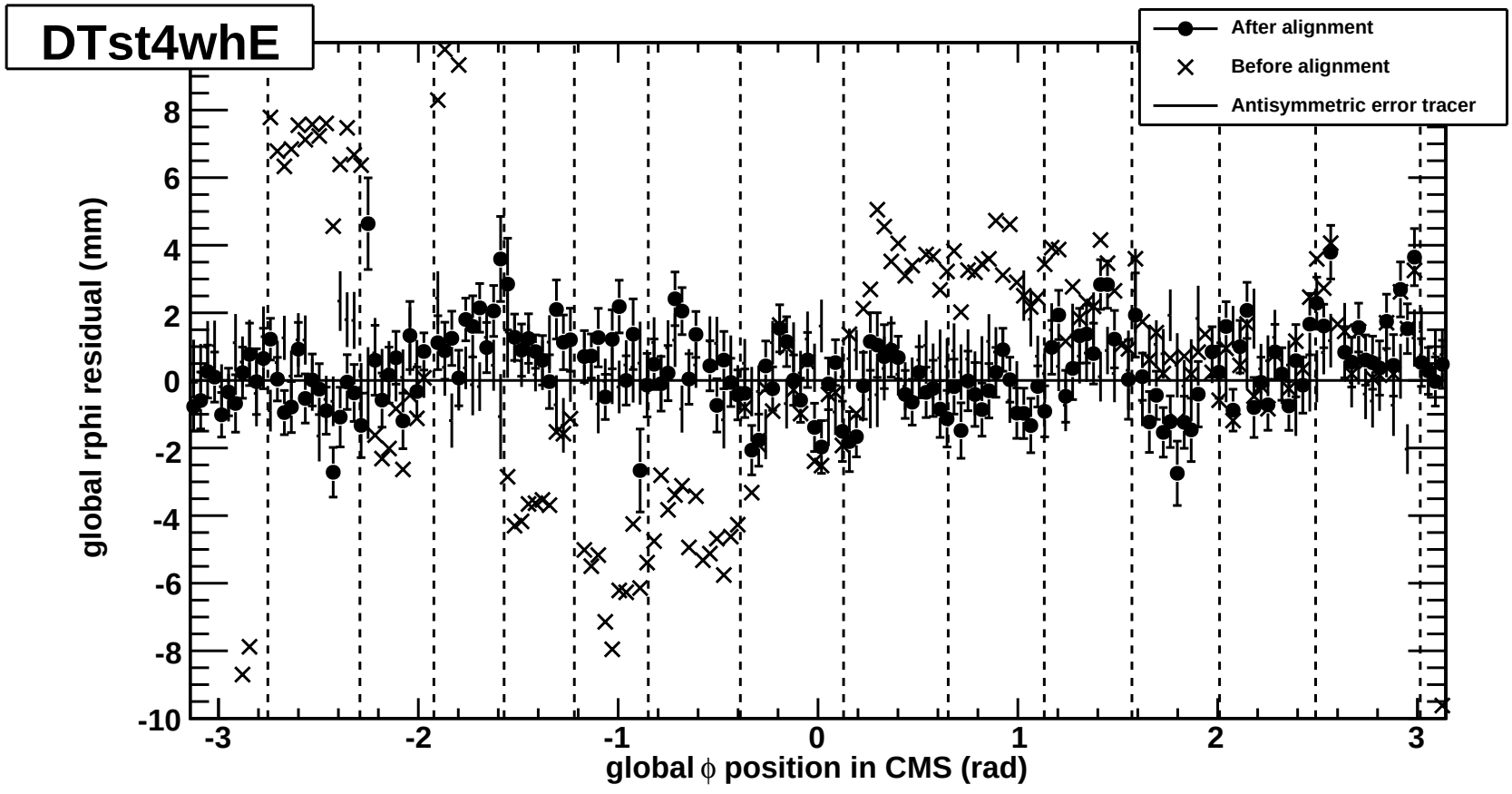
Best DT station (1) and wheel (0) with 50 pb^{-1}

No tracker misalignment included yet



New residuals maps 2/3 (MC)

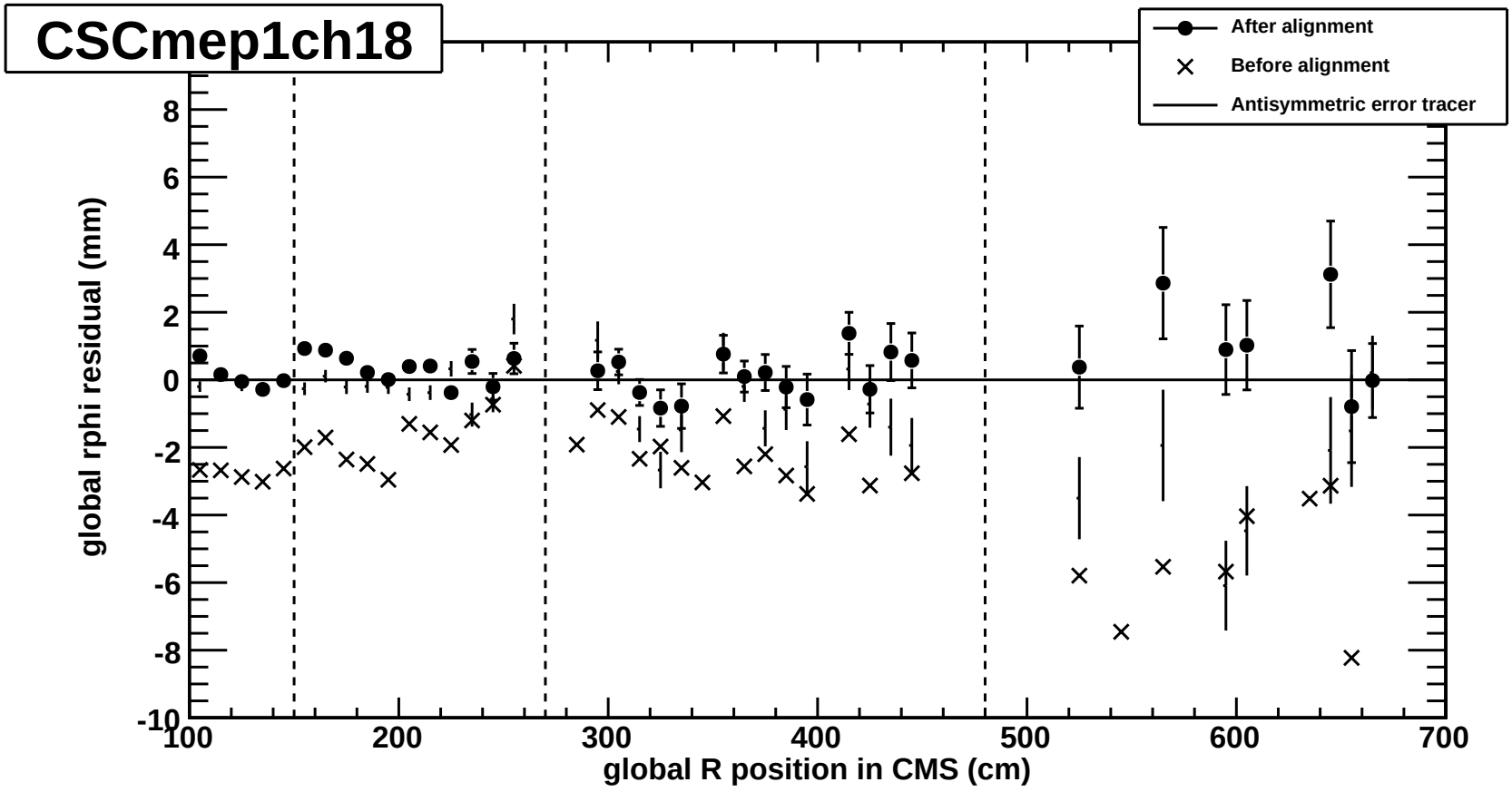
Worst DT station (4) and wheel (± 2), same $\int \mathcal{L}\, dt$



New residuals maps 3/3 (MC)

Jim Pivarski

CSC plots are vs. ϕ and vs. R (ME+1/1a, 1/1b, 1/2, 1/3 below)



Full CSC Overlaps write-up

Method and 2008 results in complete detail (11 pages), polished and final

so the matrix equation is now

$$\begin{pmatrix} \alpha_{12} - \alpha_{51} \\ \alpha_{23} - \alpha_{12} \\ \alpha_{34} - \alpha_{23} \\ \alpha_{45} - \alpha_{34} \\ \alpha_{51} - \alpha_{45} \end{pmatrix} = \left[\begin{pmatrix} 2 & -1 & & & -1 \\ -1 & 2 & -1 & & \\ & -1 & 2 & -1 & \\ & & -1 & 2 & -1 \\ -1 & & & -1 & 2 \end{pmatrix} + \frac{1}{N^2} \begin{pmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 & 1 \end{pmatrix} \right] \begin{pmatrix} A_1 \\ A_2 \\ A_3 \\ A_4 \\ A_5 \end{pmatrix}. \quad (19)$$

It has a unique solution in which the average correction (Eqn 17) minimized to exactly zero. Actually, adding any non-zero constant to every element would yield the same solution as the physically-motivated $\frac{1}{N^2}$.

The circular ring of chambers also provides an internal cross-check: the sum of the means of pairwise residuals must be zero. If not, no combination of alignment corrections can center all of the residuals, because

$$\text{closure} = \sum_{i=1}^{N} \alpha_{i,\,i+1} - (A_i - A_{i+1}) = \sum_{i=1}^{N} \alpha_{i,\,i+1}$$

is independent of $\{A_i\}$. (Note that $\sum_{i=1}^{N} A_{i+1}$ is just a reindexing of $\sum$ arithmetic is understood to be mod N.) With non-zero closure, th uniformly distributes residuals so that they all have non-zero means, chamber disagrees with its neighbor about where the tracks are. Unclos imply

- the average distance of the chambers from the beamline is incor
- the presumed width of the chambers is incorrect.

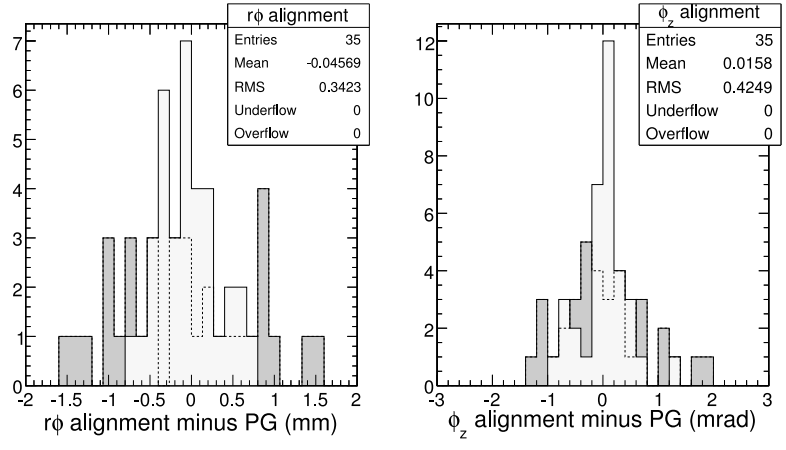
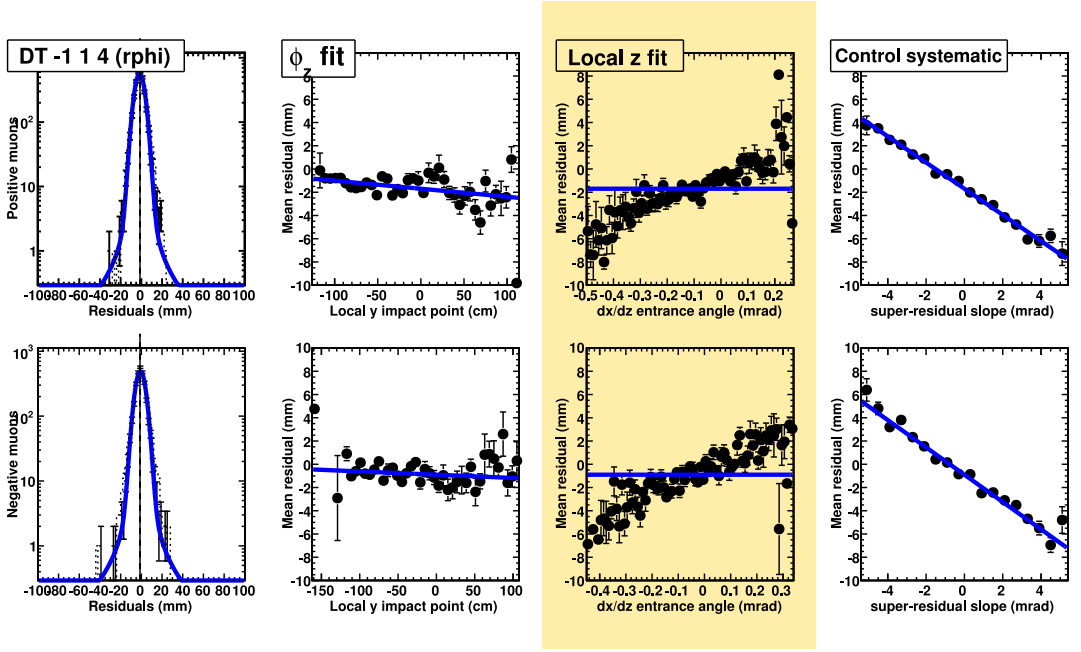
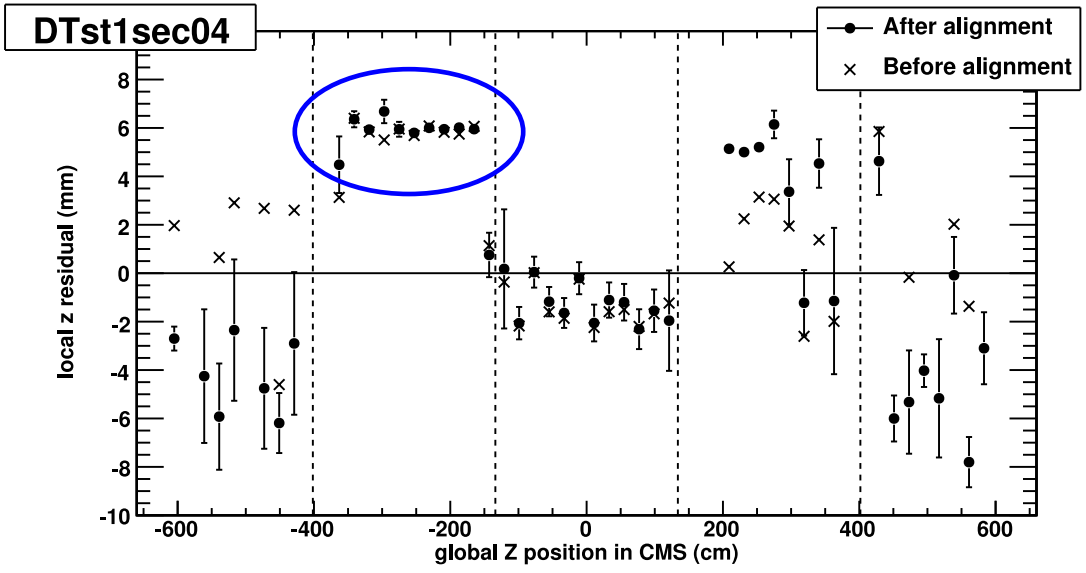


Figure 25: Chamber-by-chamber verification of the beam-halo alignment with photogrammetry. The dark histogram is before alignment; the light histogram and statistics box are after alignment.

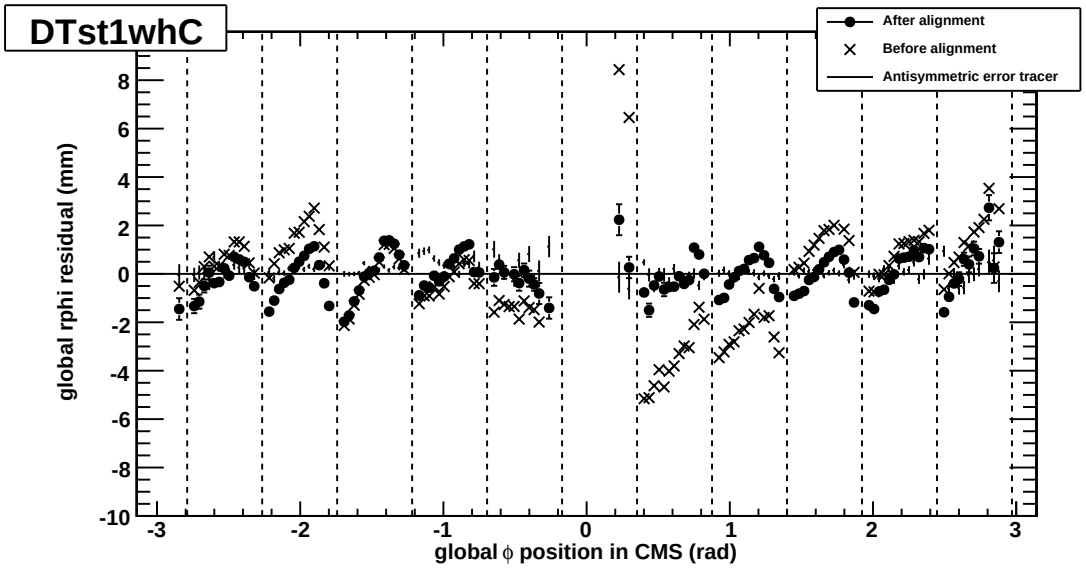
Plots from CRAFT data

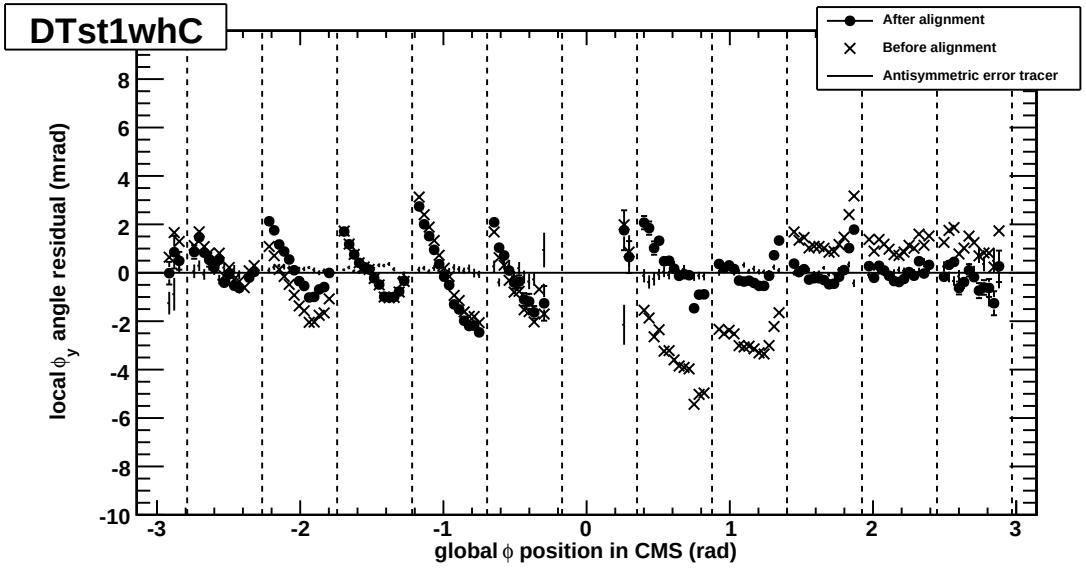




- Observations of radial misalignments in highest-statistics chambers
- Radial corrections restricted to zero in this example
- Statistically significant in some chambers, not in others

Sawtooth still present

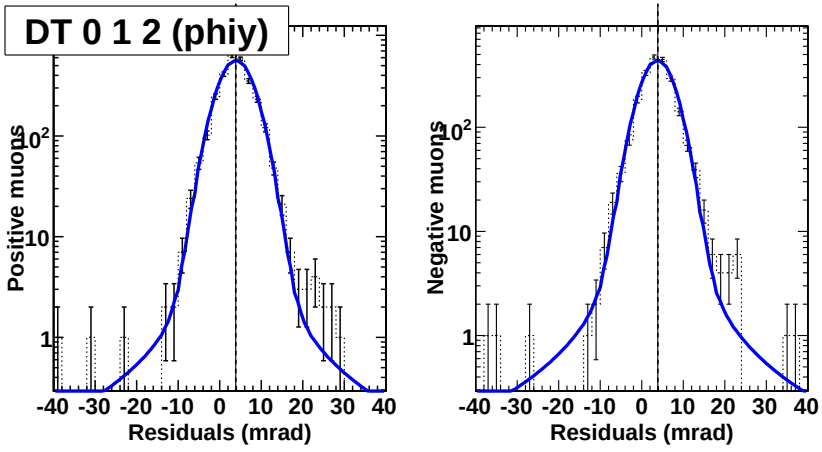




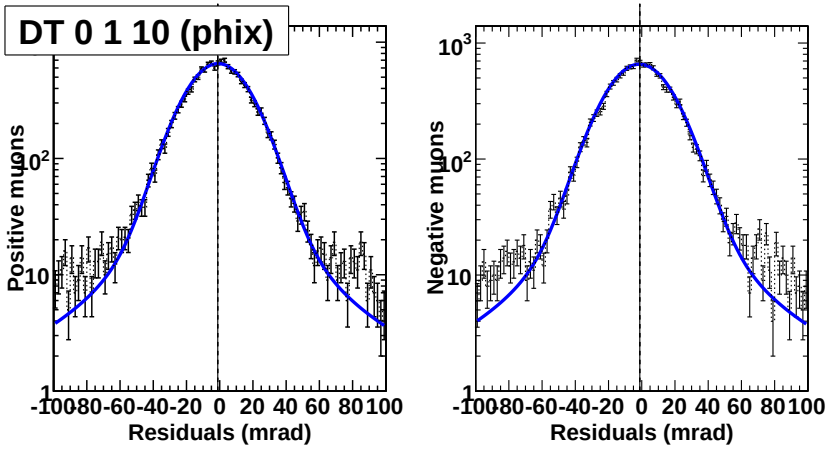
- "Sawtooth" is unexplained $r\phi$ residual vs. ϕ slopes within chambers
- Also present in ϕ_y residuals vs. ϕ (expected from single-chamber studies)
- Full presentation of single-chamber studies in April 2 DT-DPG

Angular alignment corrections

Largest ϕ_y example I could find with high statistics: 3.86 ± 0.06 mrad



Largest ϕ_x example I could find with high statistics: -1.17 ± 0.11 mrad

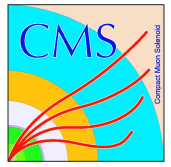


- ϕ_y measured with track-segment angle differences (see note for "super-residuals")
  - some are significant and large: few mrad
- ϕ_x: same technique with superlayer 2
  - generally small and/or low resolution
- Vertical line is again μ^+/μ^- average

What will be for sign-off?

- We'll be signing off the procedure as described in the note
  - already presented in final, digestable form
- Sign-offable *constants* will require some tweaks:
  - need to decide which parameters to align for which chambers
  - how many iterations are sufficient (to work out couplings between parameters)
  - in what order (some parameter dependencies are one-way) for example, CSC Overlaps was optimized by $\phi_y \rightarrow x \rightarrow \phi_z$
- Final constants for tracker-pointing re-processing will need to be generated with new tracker alignment, when it becomes available

Conclusions



- Read the note! What is written is in final or nearly-final form
  - this is the detailed CMS Note that will back up a shorter publication, to be written (by abridgement)
- It includes everything about the CSC Overlaps procedure and results
- We can now align globalMuon-accessible DTs in any of 6 d.o.f. with highly descriptive residuals fits
  - 6 mm radial misalignments observed
  - 4 mrad ϕ_y rotations observed (important for q and p_T)
  - most ϕ_x are small or consistent with zero
- Basic procedure established; working on details of iteration strategy
- Documentation is kept in sync with results