Proposed Constants for Muon Alignment

Jim Pivarski

Alexei Safonov

Texas A&M University

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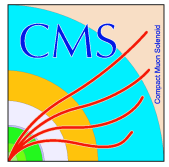
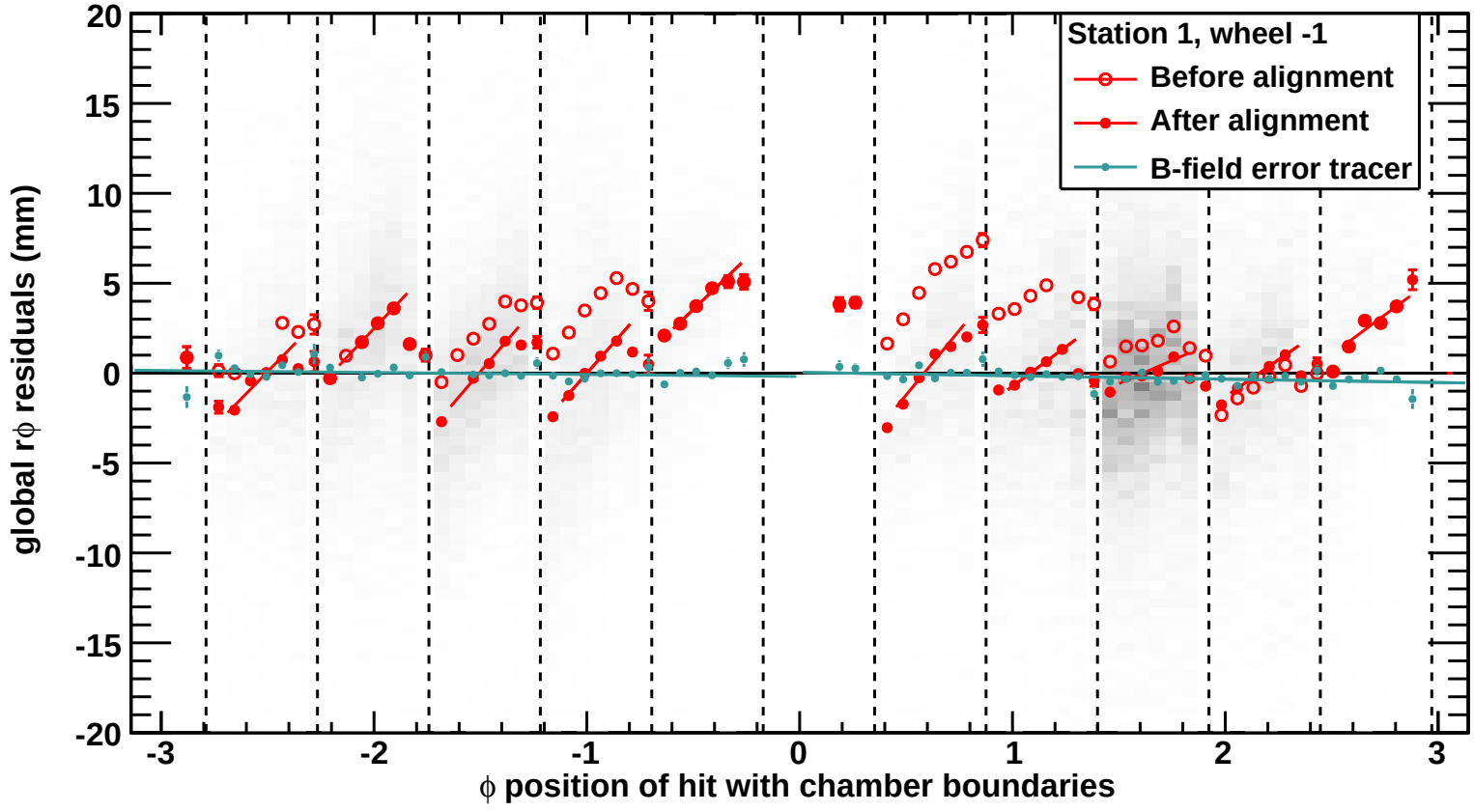
Recommended constants



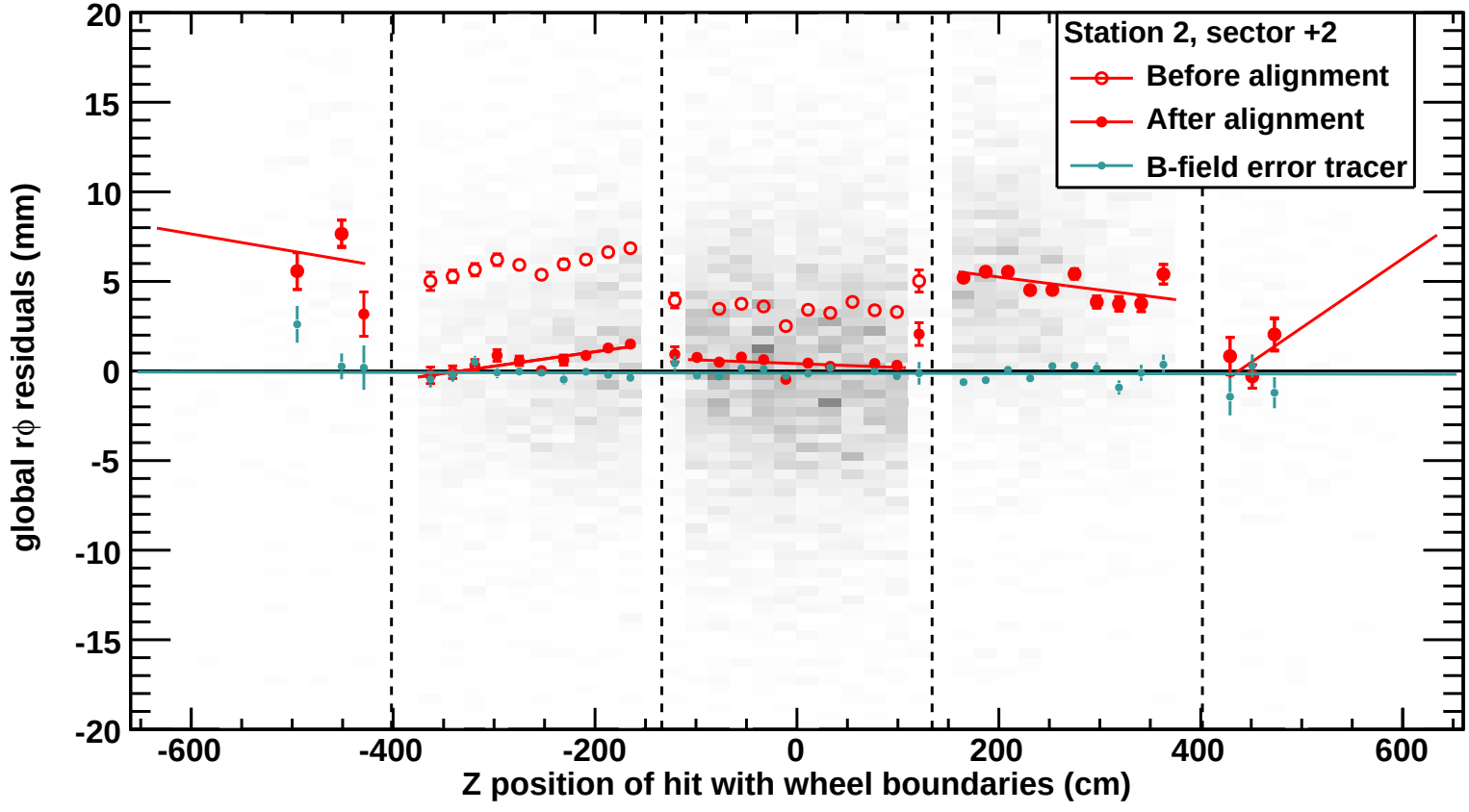
- Minor modification of the CRAFT_ALL_V4 (first re-processing): correct the $r\phi$ positions of the highest-statistics chambers
  - pattern of residuals versus ϕ, z indicates a chamber-by-chamber phenomenon
  - alignment study used tracks from the TIB and TOB only (most trusted)
  - rigorous fitting procedure insensitive to $\vec{B}$-field errors and variation of track distribution across chamber surface
  - passes a track-based validation with unbiased residuals (following slides)
  - tested by Javier (this is the .db on CASTOR)

Example residuals plot



- Alignment moved center of chambers to zero in $r\phi$ (note: center of *chambers*, not center of mass of track distribution)
- "Sawtooth mountain" shape is still there, because we didn't do anything to correct for it

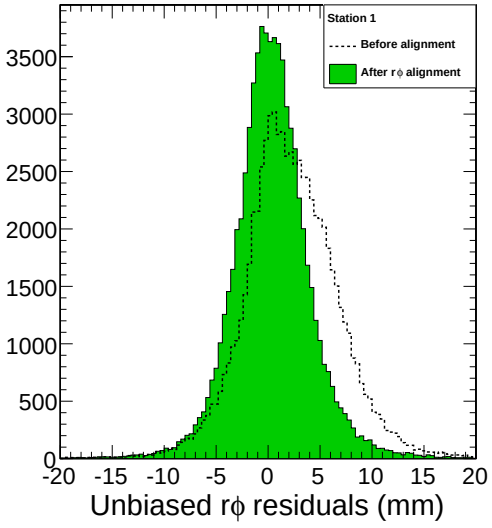
Other projection



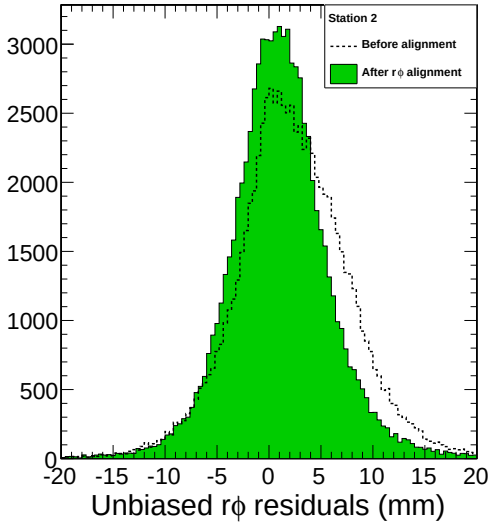
- Makes sense in the vs. z projection as well
- Not all chambers were aligned, only the ones with at least 800 well-distributed tracks (overly conservative?)

Residuals summary

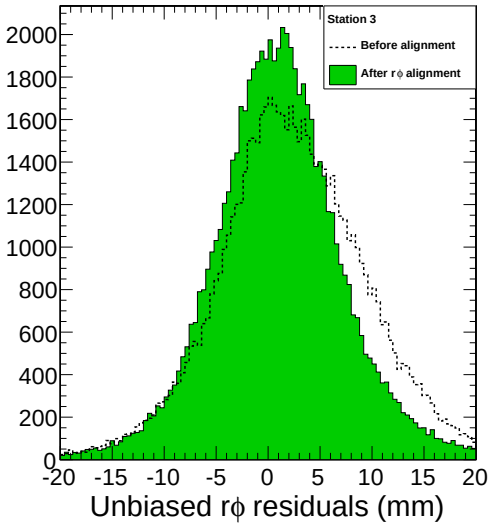
Station 1



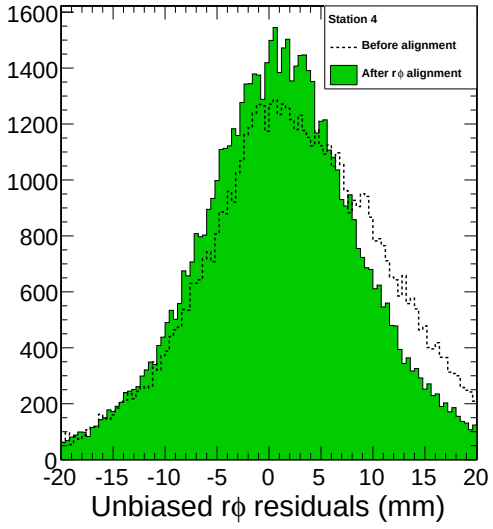
Station 2



Station 3



Station 4



- Not everyone can look at all the hundreds of plots
- Summarize with raw residuals distributions
- Not a very sensitive measure because chamber corrections are smaller than intrinsic width

Other evident effects

- This was a local x alignment only; there is no barrier to aligning x, y, and ϕ_z (the three most important parameters)
  - I have such an alignment partially validated, but not in time for this meeting (and way too late for Javier)
- Very important: the "sawtooth mountain" structure is due to a non-alignment effect. The only misalignments that can cause it are
  - radial, or local z: causes a linear slope in local x residuals vs. local x and local y residuals vs. local y
    - both cannot be accomodated with a local z correction (I tried it)
  - a ϕ_y misalignment of 70 mrad (unbelievable)
  - by process of elimination, it is not a misalignment
- Note that the slope is *the same for all chambers*
  - conclusion: it is a deformation of the chambers themselves, chambers are too narrow by 5 mm along the x dimension (or too wide— I've made sign mistakes before)
  - it is the largest remaining effect in the width of the DT residuals distribution