

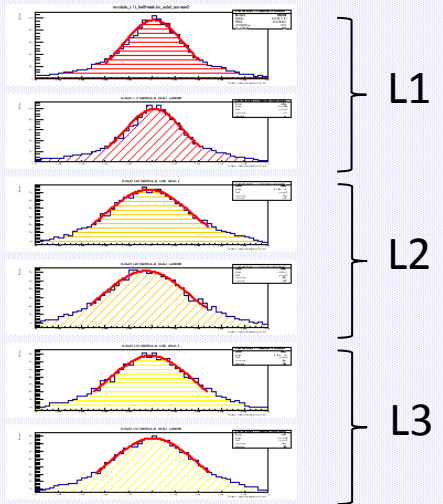
Test of alignment pass0 2016 data

- Geometry: v4-4-fieldmap
- Check on 17 file stubs (~50000 events each)
- Randomly chosen files
 - 7636 (0, 10, 100)
 - 7800 (0, 10, 100)
 - 7983 (10, 100)
 - 8028 (0, 10, 100)
 - 8064 (0, 10, 20)
 - 8087 (0, 10, 100)
- Check consistency of residuals throughout the file sequence and compared to an MC sample with nominal geometry (max. expected systematic error)
- For now: u residuals after GBL, comparison of mean values and sigmas
- To come: kinks (φ and λ), u res vs u profiles, ...

u residuals after GBL

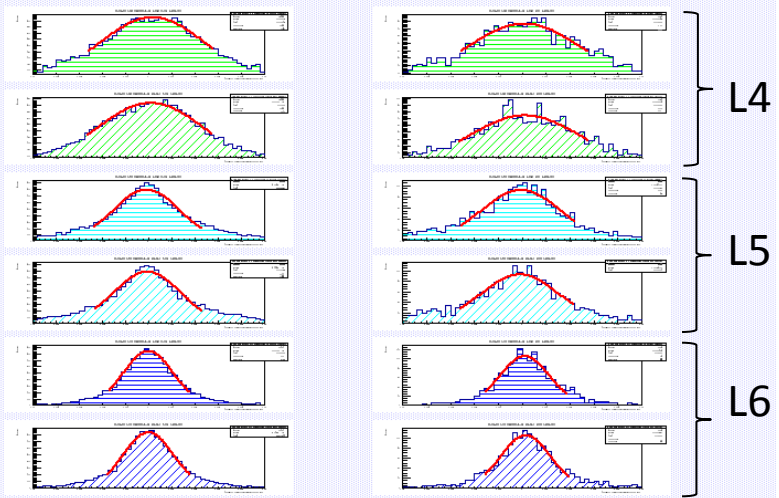
TOP

axial
stereo



hole

slot

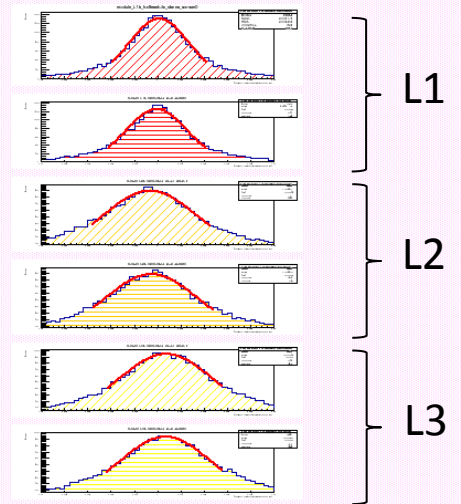


hole

slot

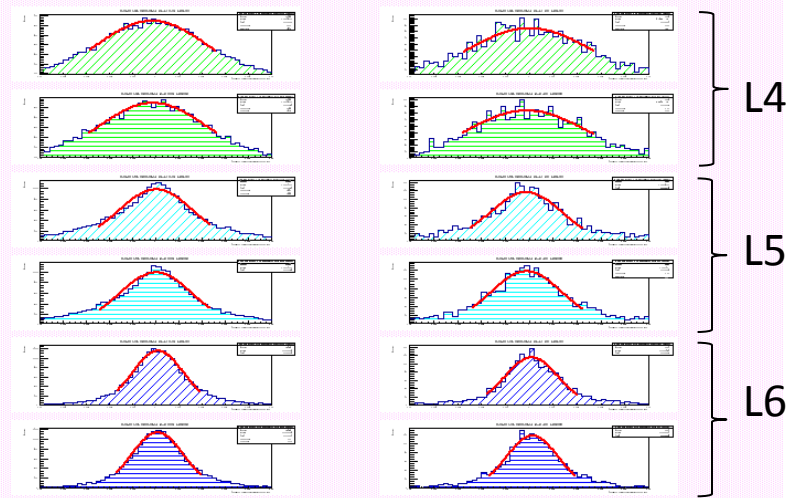
BOTTOM

axial
stereo



hole

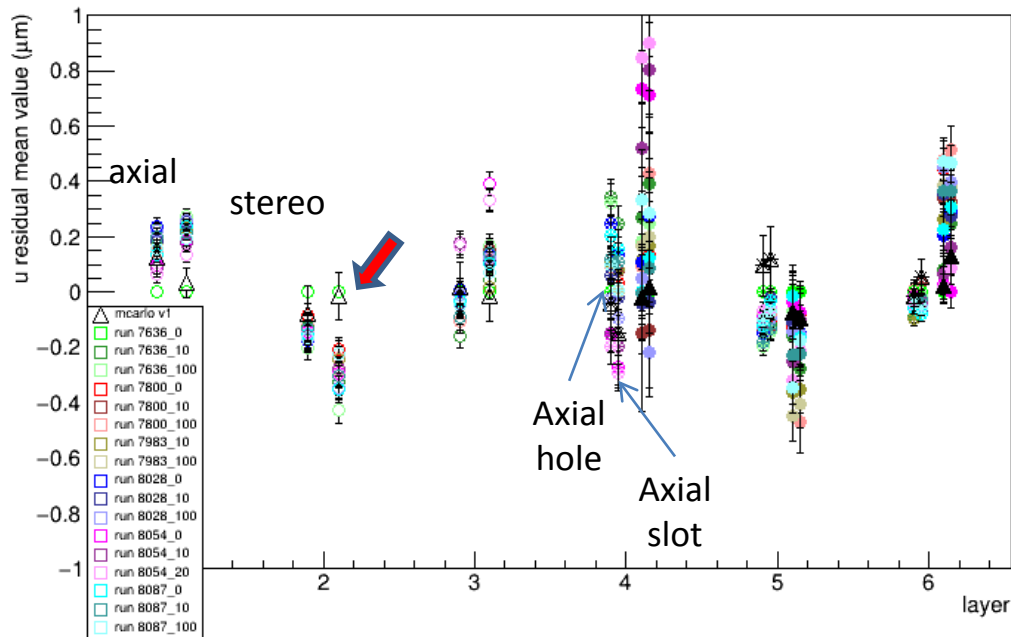
slot



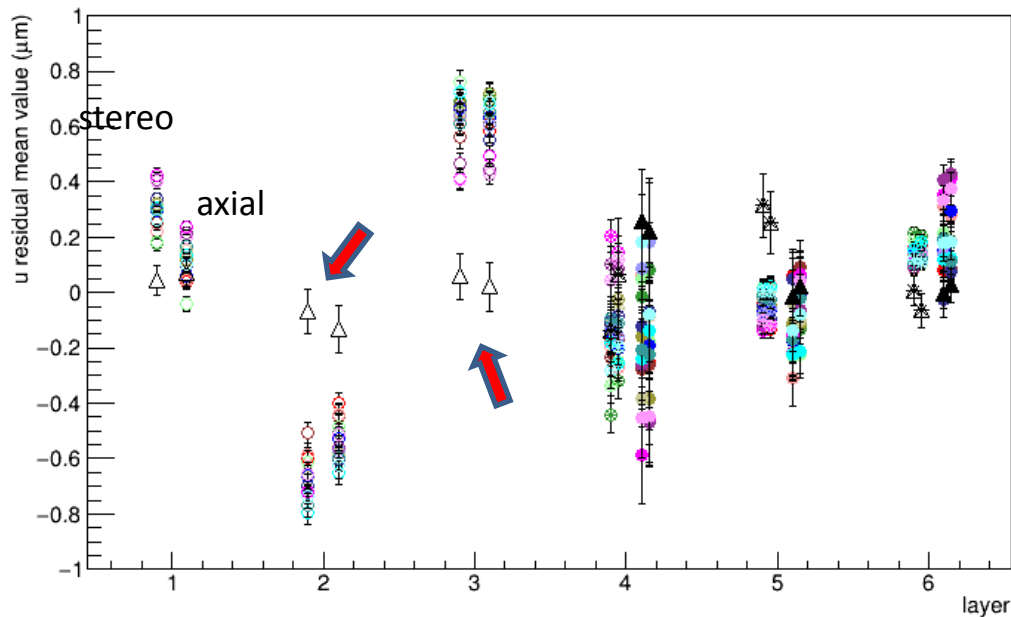
hole

slot

top residuals, mean value (μm)

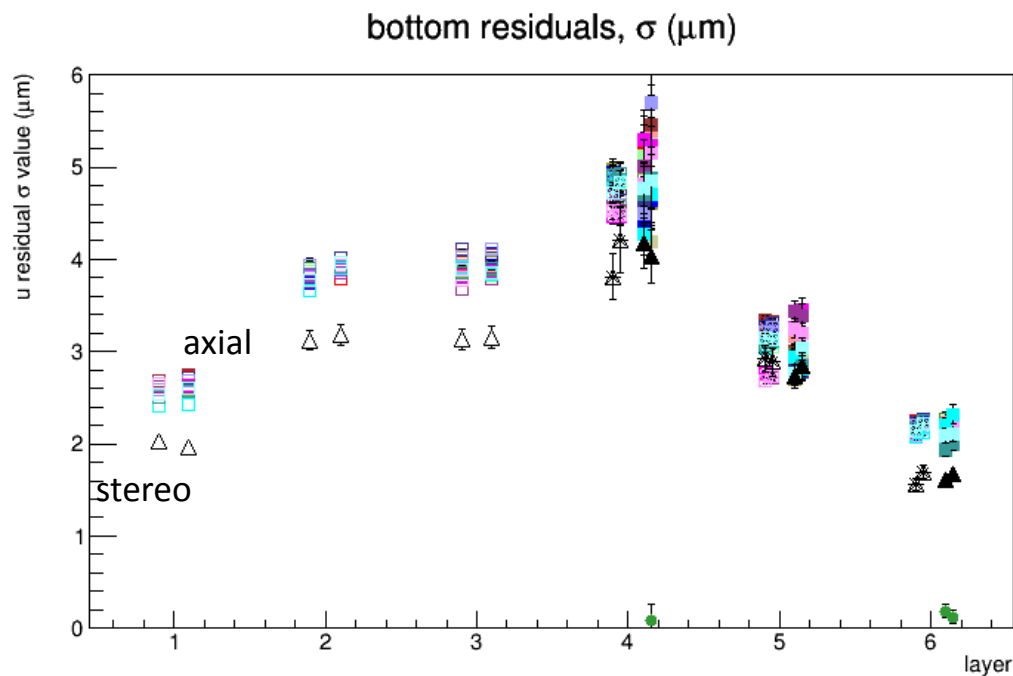
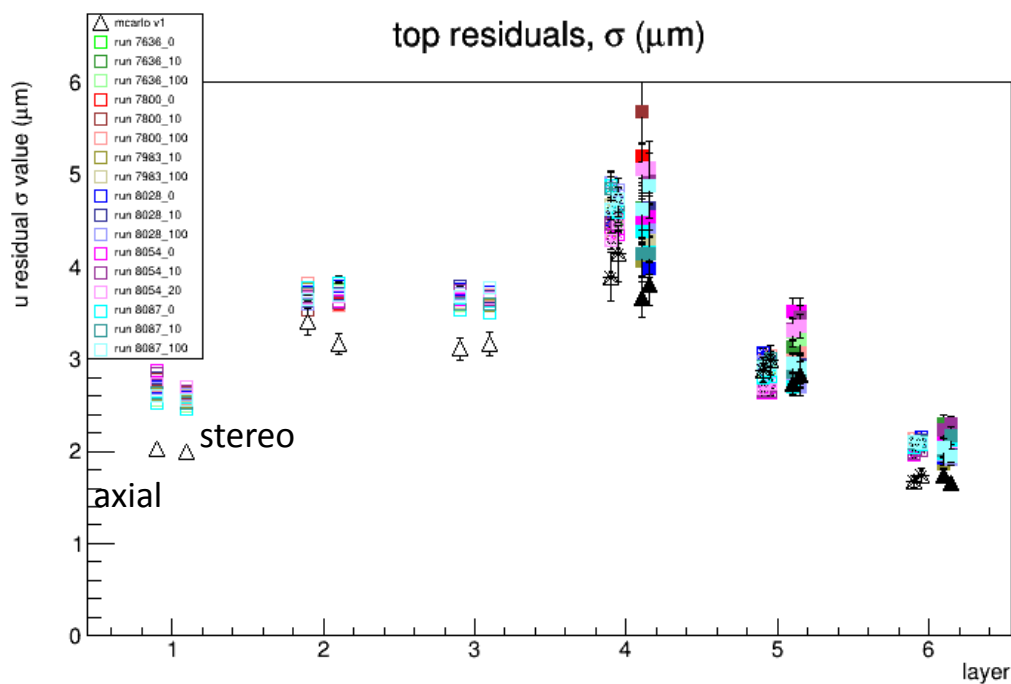


bottom residuals, mean value (μm)



Top&Bottom u residuals after GBL: mean values

- Distributions of mean values from gaussian fit of the u residual spectra
- Errors are the errors from the fit
- TOP: mean values around the reference MC values except for
 - Sensor 2 stereo, $\sim 0.3 \mu\text{m}$
- STEREO
 - Sensor 2 axial+stereo, $\sim 0.6-0.7 \mu\text{m}$
 - Sensor 3 axial+stereo, $\sim 0.6 \mu\text{m}$
(Probably correlated)
- Alignment can be improved but these offsets are within the sigma of the distributions



Top&Bottom u residuals after GBL: sigmas

- Distributions of sigmas from gaussian fit of the u residual spectra
- Errors are the errors from the fit
- Lower limit: sigma of MC distributions (with nominal geometry, v1)
 - Systematic error: sigmas of MC distributions: between 2 and 4 μm
- Maximum sigmas: below 6 μm
- The alignment with 4.4-fieldmap geometry looks acceptable