



Chamber-by-chamber alignments in 1_5_4

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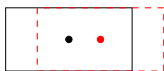
10 September, 2007



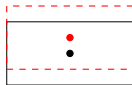
Preparing event samples

- ▶ I never heard back about the official 1_5_4 \rightarrow AlCaRecoMu, so I filtered them myself
- ▶ `/castor/cern.ch/user/p/pivarski/AlCaRecoMu/ideal`
35 good, 13 bad
- ▶ `/castor/cern.ch/user/p/pivarski/AlCaRecoMu/miscal`
26 good, 13 bad
(that's an inefficiency)
- ▶ This project used the good `ideal` sample to search for optimum sets of alignment parameters
- ▶ Unknown number of events/tracks/hits, but very likely overkill
- ▶ Starting point is *after* disk-by-disk alignments

Theory: x, y, ϕ_z are 1st-order; ϕ_x, ϕ_y are 2nd-order to y, x ; and $z \dots$



x : offset in r_x



y : offset in r_y

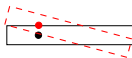


z : sensitive only
through angled
tracks



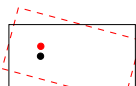
ϕ_x : r_y linear in y

(slope $\propto 1 - \cos \phi_x$)



ϕ_y : r_x linear in x

(slope $\propto 1 - \cos \phi_y$)

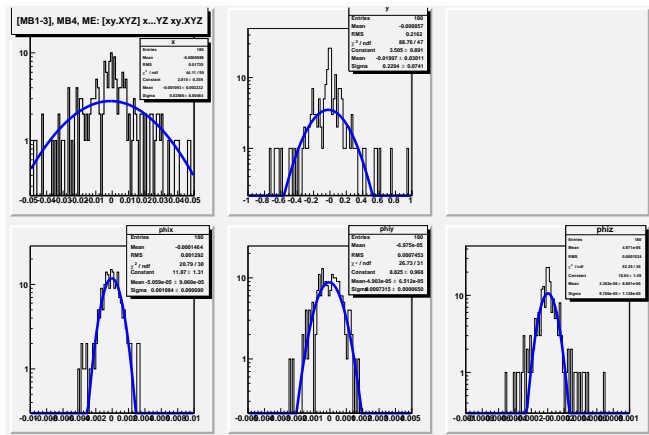


ϕ_z : r_x linear in y
and

r_y linear in x
(slope $\propto \sin \phi_z$)

z is important! (slide 1 of 2)

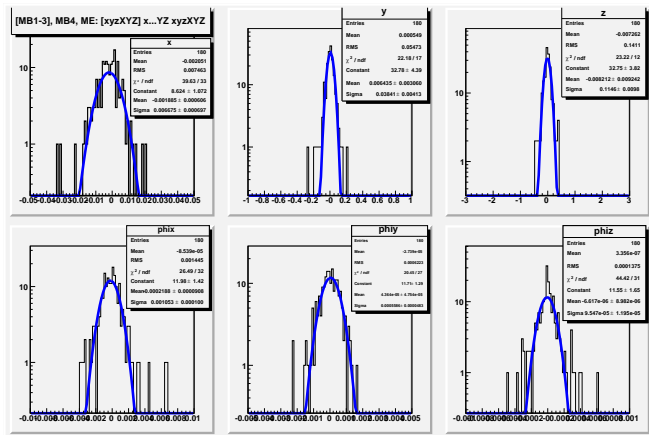
Barrel stations 1–3: z is fixed (and misaligned)



All plots are aligned positions minus correct positions (MC)

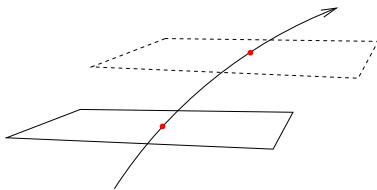
z is important! (slide 2 of 2)

Barrel stations 1–3: z is allowed to float in alignment

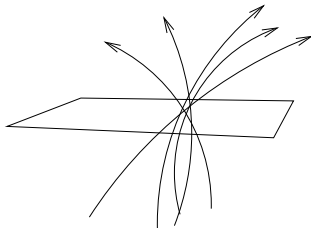


All plots are aligned positions minus correct positions (MC)

Why is that?



Single track:
x-z or y-z position is degenerate
with track intersection point

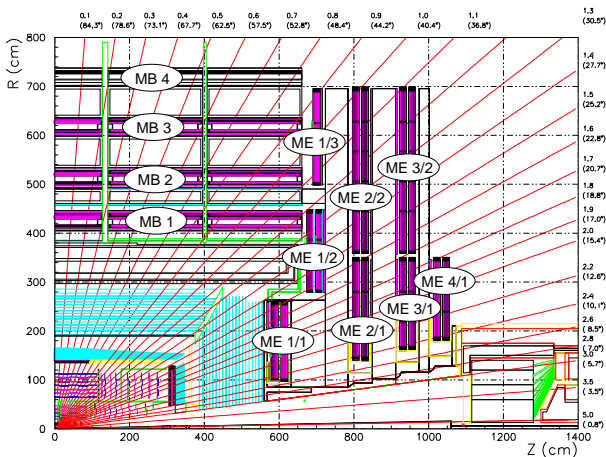


Many tracks:
complementary measurements
can't be degenerate with all of them!

(Also, chambers are not 2-D surfaces but 6–12 layers thick.
However, the above is a more important part of the explanation.)

Important distinction among barrel chambers

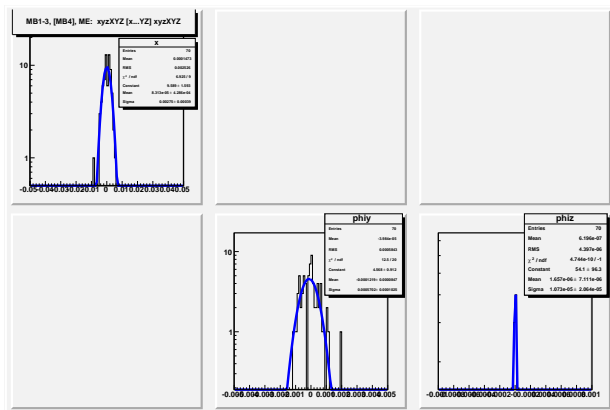
- ▶ Stations 1–3: full x - y measurement (stereo superlayers)
- ▶ Station 4: x only (purely one-dimensional!)



Barrel station 4 (outermost chambers)

Super-precise x and ϕ_z (better intrinsic resolution???)

y , ϕ_x are off-limits (cause divergences through numerical error)



what about z ? hmmm... I didn't try that...



Barrel alignment results

Stations 1–3

x	$67 \mu\text{m}$	1.05 mrad	ϕ_x
y	$384 \mu\text{m}$	0.56 mrad	ϕ_y
z	1.15 mm	0.095 mrad	ϕ_z

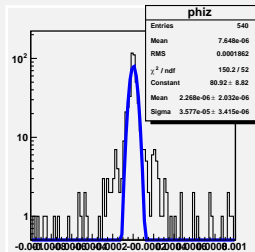
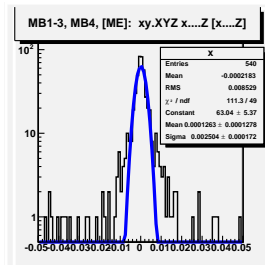
...and very Gaussian!!! Few outliers (see p. ??)!

Station 4

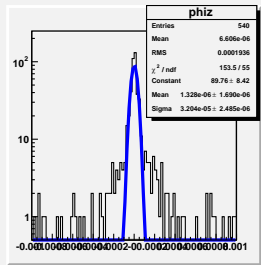
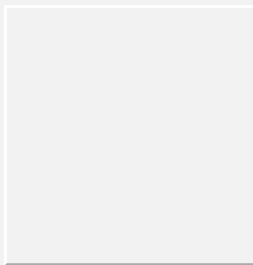
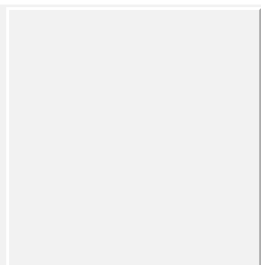
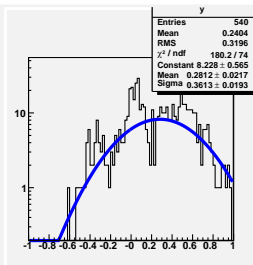
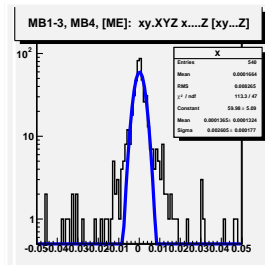
x	$28 \mu\text{m}$	0.57 mrad	ϕ_y
		0.004 mrad	ϕ_z

If ϕ_y is fixed, $x \rightarrow 12 \mu\text{m}$
(unnecessary ultraprecision)

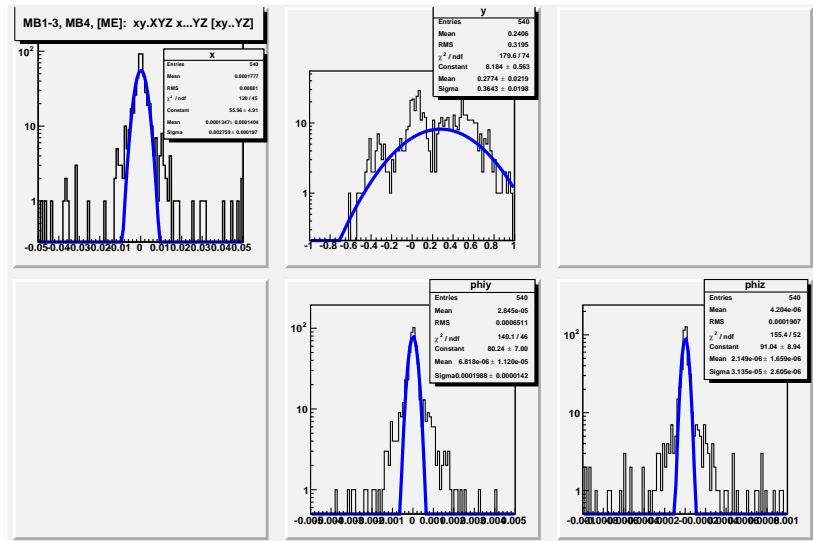
Full evolution of endcap: $x \dots \phi_z$ (1/5)



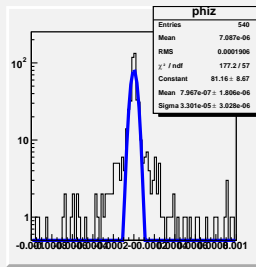
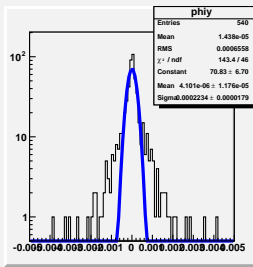
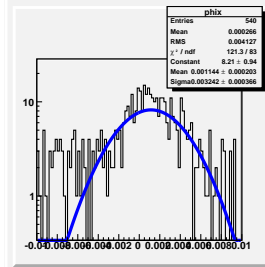
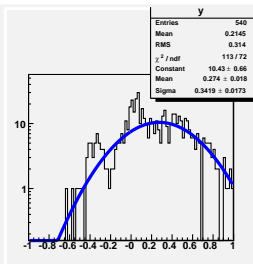
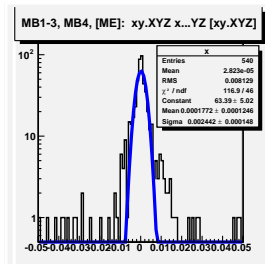
Full evolution of endcap: $xy \dots \phi_z$ (2/5)



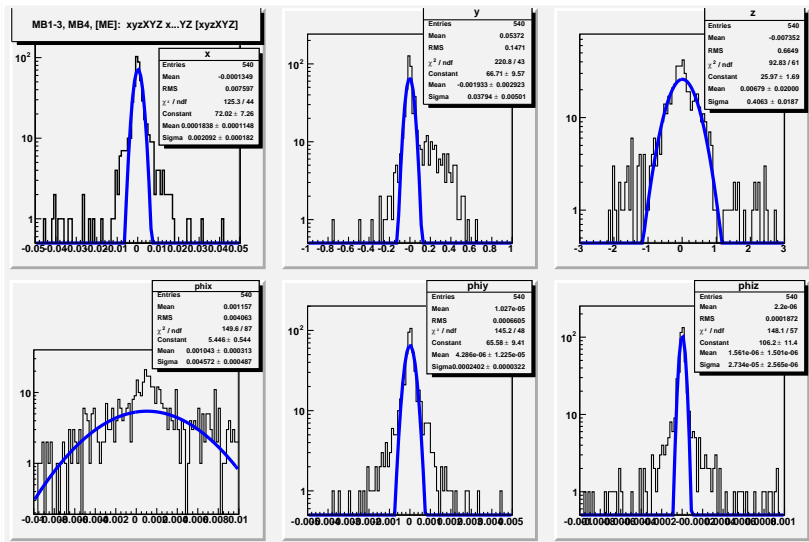
Full evolution of endcap: $xy.. \phi_y \phi_z$ (3/5)



Full evolution of endcap: $xy.\phi_x\phi_y\phi_z$ (4/5)

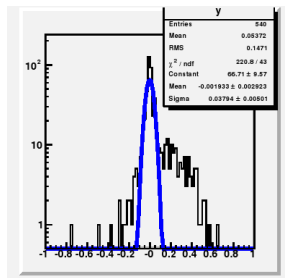


Full evolution of endcap: $xyz\phi_x\phi_y\phi_z$ (5/5)



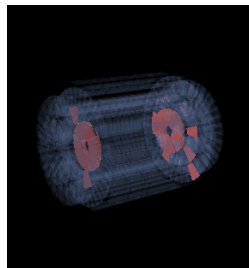
Wow! What's going on?

Allowing z to float helps y enormously, though there's a strange asymmetric secondary distribution.

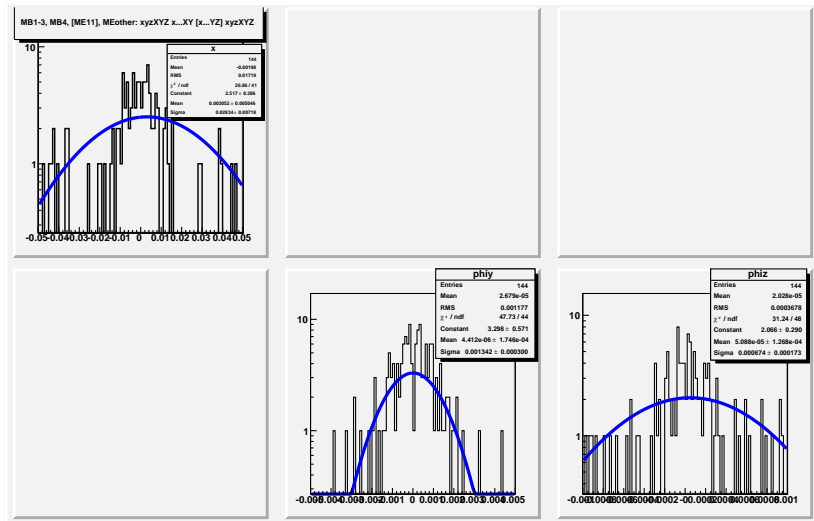


I asked our spiffy analysis tool which chambers have $y_{\text{misalign}} > 2$ mm

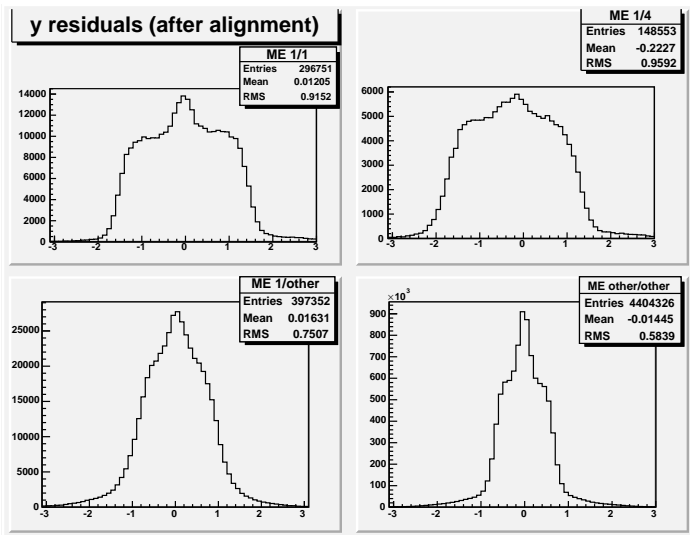
They're (almost) all in ME1/1!



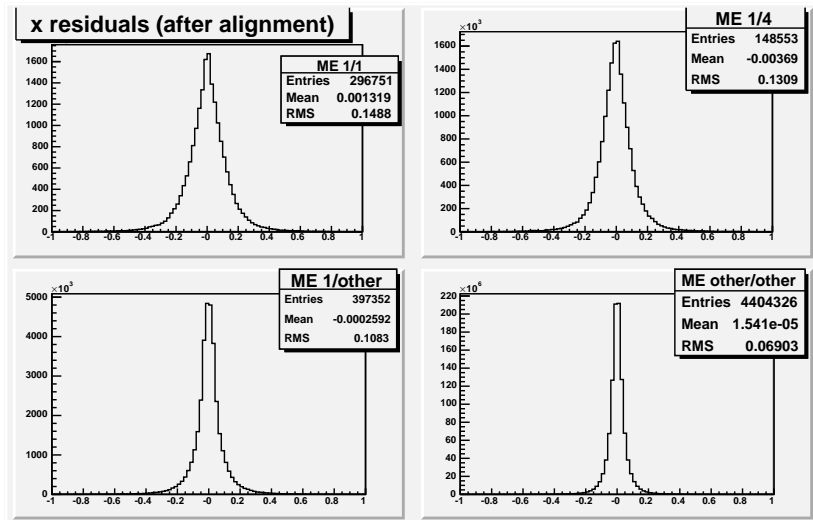
Is ME1/1 one-dimensional? NO. (I didn't think so.)



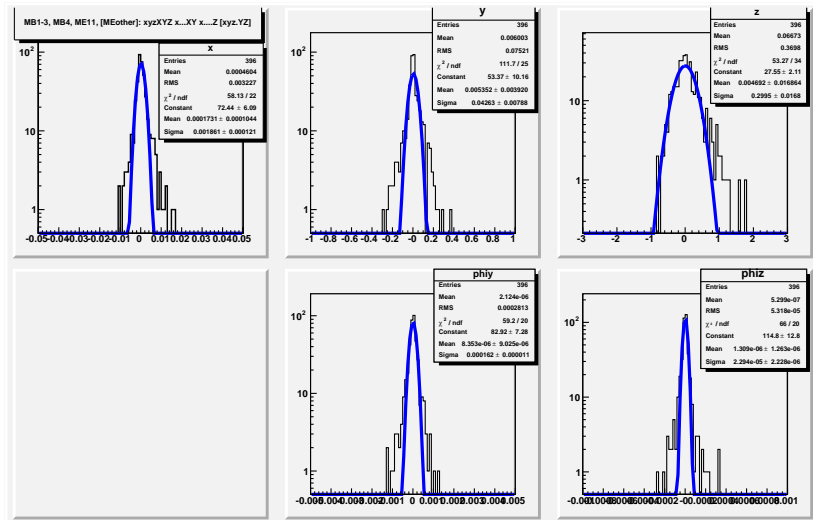
The y residual distributions are a *little* asymmetric...



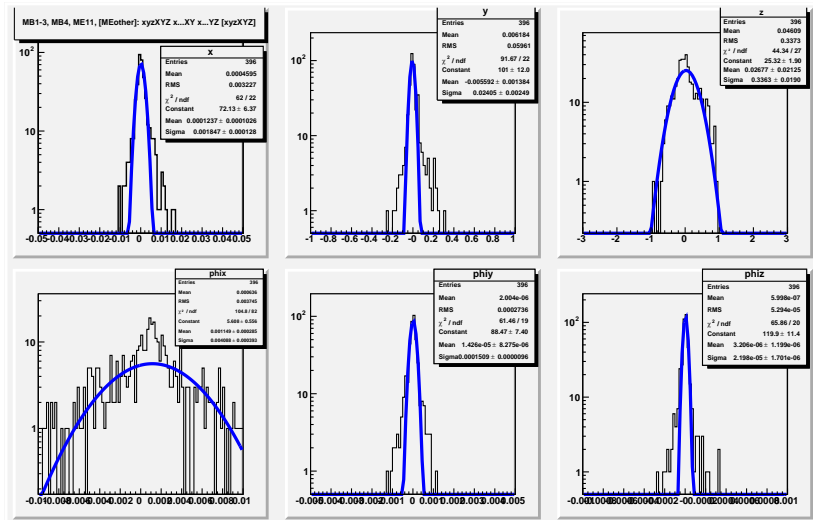
The x residual distributions, for completeness



Endcap without ME1/1: $xyz.\phi_y\phi_z$



Endcap without ME1/1: $xyz\phi_x\phi_y\phi_z$





Endcap without ME1/1 results

Resolution is nearly Gaussian— the long tails are gone

	fitted core	standard deviation
x	$19\ \mu\text{m}$	$32\ \mu\text{m}$
y	$240\ \mu\text{m}$	$596\ \mu\text{m}$
z	$3.0\ \text{mm}$	$3.7\ \text{mm}$
ϕ_x	$4.1\ \text{mrad}$	$3.7\ \text{mrad}$
ϕ_y	$0.16\ \text{mrad}$	$0.28\ \text{mrad}$
ϕ_z	$0.03\ \text{mrad}$	$0.05\ \text{mrad}$

After alignment ϕ_x is worse than before. However, excluding ϕ_x from the fit broadens y resolution to $240\ \mu\text{m}$ core, $596\ \mu\text{m}$ stdev. Tie breaker: momentum resolution. Coming soon.

And these include internal layer-by-layer misalignments (100's of μm , as measured by Karoly)!



Summary, conclusions, and questions

- ▶ With high-statistics, no miscalibration, no tracker misalignment: we see beautiful resolution in all but ME1/1
- ▶ Presumably we can get ME1/1 right by applying some physical insight (worked for MB4), but I think I'm lacking knowledge of the system



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- ▶ Presumably we can get ME1/1 right by applying some physical insight (worked for MB4), but I think I'm lacking knowledge of the system
- ▶ For instance, “ME1/1” and “ME1/4” (in software) describe two parts of some kind of “double-chamber” system. How does that work exactly?
- ▶ Alignment software allows “ME1/1” and “ME1/4” to float independently, which is probably wrong. Is it disastrously wrong?



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- ▶ For instance, “ME1/1” and “ME1/4” (in software) describe two parts of some kind of “double-chamber” system. How does that work exactly?
- ▶ Alignment software allows “ME1/1” and “ME1/4” to float independently, which is probably wrong. Is it disastrously wrong?
- ▶ ME1/1 y distribution has the same asymmetry as the rest of the endcap did when z was misaligned and not allowed to float. . .