Matching MINOS to PEANUT Tracks

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Step 1 : MINOS Track pre-selection :

For the time period where we have PEANUT data, I select all MINOS Near Detector runs and write out all tracks witch have a track vertex (starting point in MINOS planes 1, 2 or 3.

For these tracks I write out the following parameters. Each MINOS sub-run is a one hour duration. My processing generates a ".dat" file with the tracks for each sub run.

MINOS Track Parameters :

1. minos spill time (UTC seconds from 1970; GMT)
2. spill time corrected to PEANUT time (minos time – 54000 seconds)
3. track begin plane (1, 2, 3)
4. track theta x
5. track theta y
6. track x-vertex (meters)
7. track y-vertex (meters)
8. track chi-square p.d.f.
9. track pass flag (1 = pass = good fit_
10. track containment (1 = yes -> momentum from range is OK)
11. track momentum (absolute value because no sign from range)
12. track momentum from range if applicable
13. track momentum from curvature (includes sign)

Step 2: Match PEANUT tracks to MINOS spills

Using the Nagoya file **3dtrks.dat** as input, I select PEANUT spills containing ntrk == 1.

I read through all of my MINOS track files and match the time stamp of the PEANUT track with a MINOS spill. This is very efficient (exact number to come later). We only miss on the rare times when the MINOS Near Detecotr

may be taking a pedestal or calibration run, or shut down to replace some electronics.

Step 3 : Match PEANUT tracks to MINOS tracks (by angle)

Once the matched spill is found, the parameters of all MINOS tracks in that spill (which typically are 3 – 6 per spill) are stored in arrays. I then loop over the track angles to select the track which matches most closely in angle. Once the best match is found I write out the following parameters to the file **matched_tracks.dat**.
This file (text format) is posted on my web page :
http://home.fnal.gov/~rameika/peanut/data.

The parameters in this file are the following :

1) spill number (in a single MINOS file : not very relevant)
2) index of the matched track in the MINOS spill
3) matched minos time
4) peanut time
5) theta-x of peanut track
6) theta-y of peanut track
7) peanut x (at downstream fiber plane) in cm
8) peanut y (at downstream fiber plane) in cm
9) x-projection of peanut track to first plane of minos (cm)
10) y- projection of peanut track to first plane of minos (cm)
11) theta-x of best matched minos track
12) theta-y of best matched minos track
13) delta-x peanut to minos track
14) delta-y peanut to minos track
15) x-vertex of the matched minos track (cm; in minos coordinates)
16) y-vertex of the matched minos track (cm; in minos coordinates)
17) # x hits on peanut track
18) # y hits on peanut track
19) starting x plane of peanut track
20) starting y plane of peanut track
21) track pass flag for minos track
22) chi2/dof for minos track
23) # planes in the minos track
24) momentum of the minos track
25) momentum from range (if stopping in detector) of minos track
26) momentum from curvature of minos track

Step 4 : Analysis of “matched” tracks

Figures refer to the figures that can be found in http://home.fnal.gov/~rameika/peanut/analysis/peanut_figs.ps. There is one figure per page.

Figure 1 shows the x-y coordinates of the “best” matched track in the MINOS spill to the PEANUT track. Hence, you can see that for most of the tracks they are lined up with the PEANUT track. The ones giving us the outline of MINOS are actually bad matches. Perhaps these are because the PEANUT track is not very well reconstructed, or is at a very large angle and does not in fact enter the MINOS detector. In this case the “match” is more or less random. This plot has been made by subtracting the offset of the center of the NuMI beam to the MINOS detector which has its origin at the center of the magnet coil hole. These offsets are Y = 13.97 cm and X = 148.9 cm. Having done this, it can be seen that the PEANUT detector is setting high and to the east of the NuMI beam center. (Note that the scatter plot is as if you are looking upstream into the beam.)

Figure 2 shows the Y and X coordinates of the PEANUT tracks at the downstream plane of PEANUT (upper plots) and projected to the first plane of MINOS (lower plots, not corrected for the MINOS coordinate offset).

Figure 3 shows the Y and X projections of the tracks from Figure 1.

Figure 4 (upper) shows the track angle of the MINOS tracks from Figure 1.

Figure 4 (lower) shows the track angle of the PEANUT tracks with a cut at 0.6.

Figure 5 (upper) shows Figure 4 (lower) superimposed on Figure 4 (upper).

Figure 5 (lower) shows the difference in angle between the MINOS and PEANUT tracks with no cuts except the PEANUT angle less than 0.6.

Figure 6 shows the X and Y angular resolution for angle matches better than +/- 100 mrad. These cuts retains 82% of the tracks. The angular resolution is about 30 mrad. If we cut on delta theta total we retain 17,852 events (80%).

Figure 7 shows the X and Y residuals for the PEANUT tracks projected to MINOS compared to the position of the MINOS track vertex, for those tracks passing the +/- 100 mrad total delta angle cut. We should probably cut a bit harder, but as a first pass this gives us the PEANUT-MINOS offsets in X and Y, which are 17 cm and 13 cm respectively. We can also see that the RMS of the distributions is just under 4 cm, the width of the MINOS scintillator strips.