Chamber Resolution

Yet another quick note showing some preliminary results on chamber resolution as a function of distance from the wire. The resolution was computed by binning the distance from the wire in 100 μm wide bins. Two methods were used: fitting the residuals in each of these bins to a Gaussian distribution, and computing σ from the FWHM. Figure 1 shows the result after 13 iterations (for each method).

Several points should be noted here:

1. Time zero was not fine tuned. This would be the next step, namely to iterate the tracking to obtain the best time zero for each wire. A note will soon be posted to describe how this will be done.

Inaccuracies in time zero effect the region close to the wire. Since for DME the drift distance as a function of time becomes fairly constant away from the wire, inaccuracies in time zero (of the order of few ns) have little effect on the resolution in the second have of the cell.

2. Multiple scattering has not been accounted for in this calculation. The resolution seen here is therefore worse than the intrinsic chamber resolution. To extract the intrinsic chamber resolution one would have to incorporate MS in the Kalman filter, and then compute the resolution separately for each plane. The resolution in the first few planes will be closer to the intrinsic chamber resolution.

3. The FWHM method is more accurate than a Gaussian fit. Since the residual distributions are not quite Gaussian in shape, the Gaussian fit does not work well, and typically falls short of the peak of the residuals distribution, thereby resulting in a higher σ than reflected by the width of the residual distributions. A shortcoming, however, of the FWHM method is that it does not account for possible long tails (or a wide distribution at the base), although such long tails are mostly due to other factors (calibrations, bad hits, etc.) than due to the intrinsic chamber resolution.

4. Finally, this data was computed from straight through π runs at 120 Mev/c. One would also like to compute the resolution at other angles. Possible inaccuracies in foil positions will show at high angles as a deterioration in the resolution in the bins close to the cell edges.

Don't forget the keyword "preliminary results"!!

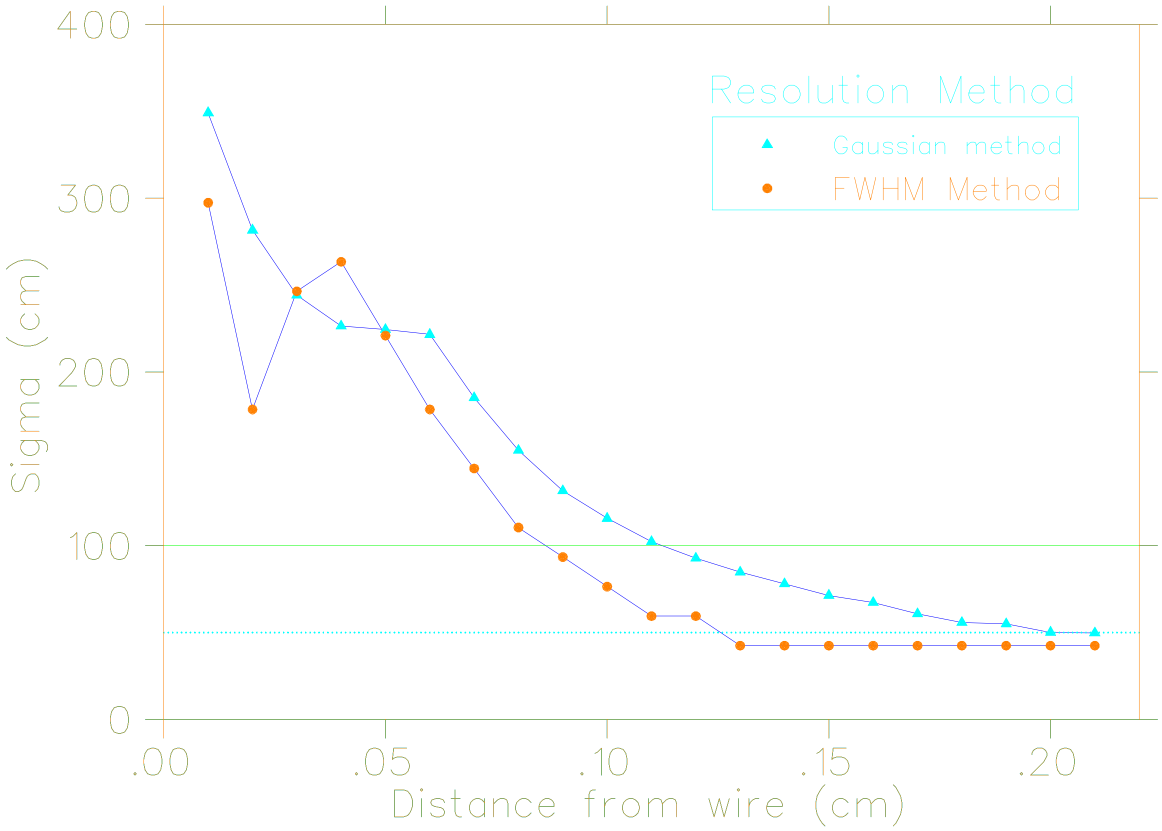

Figure 1: Chamber resolution as determined from run 1790.