Consequences of Positive Ion Distortions

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Detector Physics Working Group

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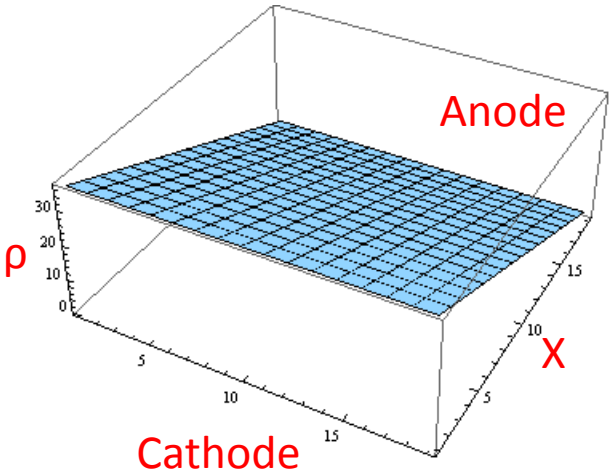
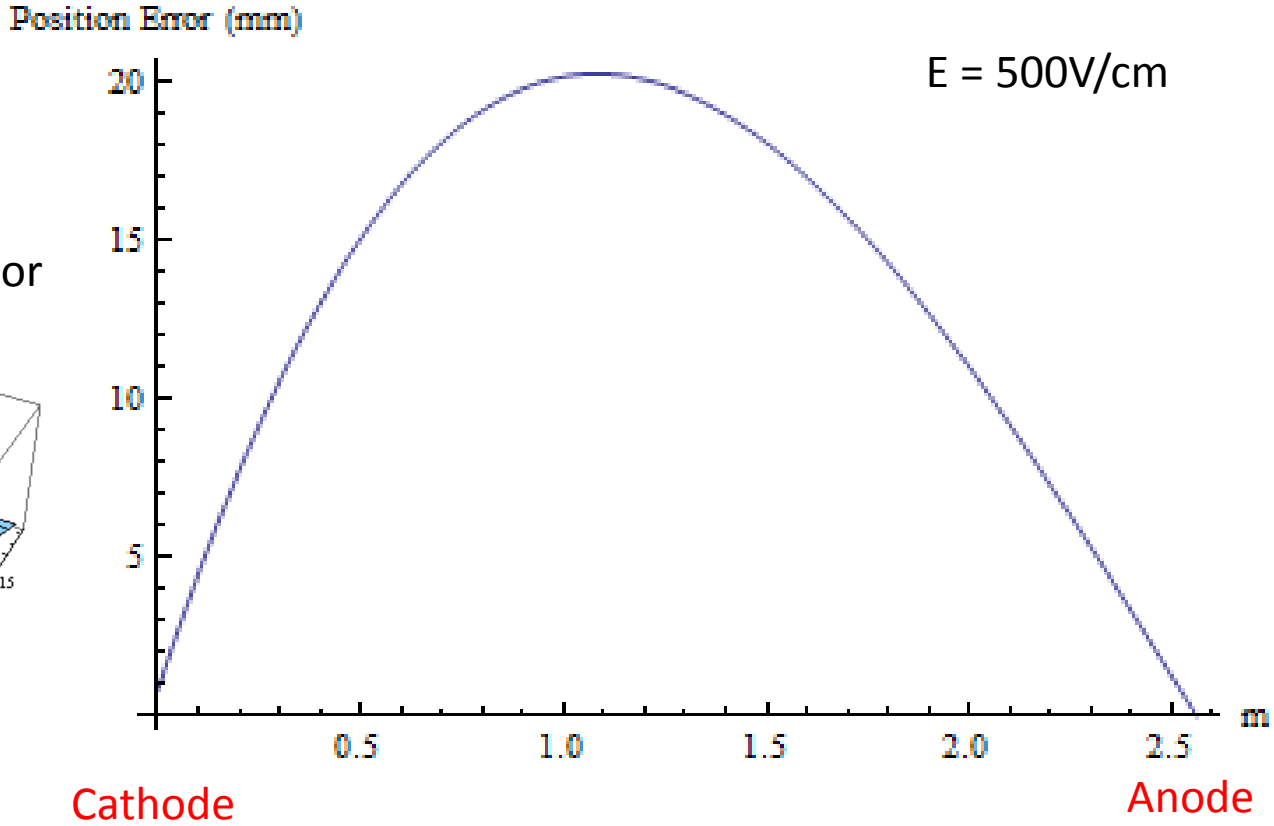
Size of Distortions Time

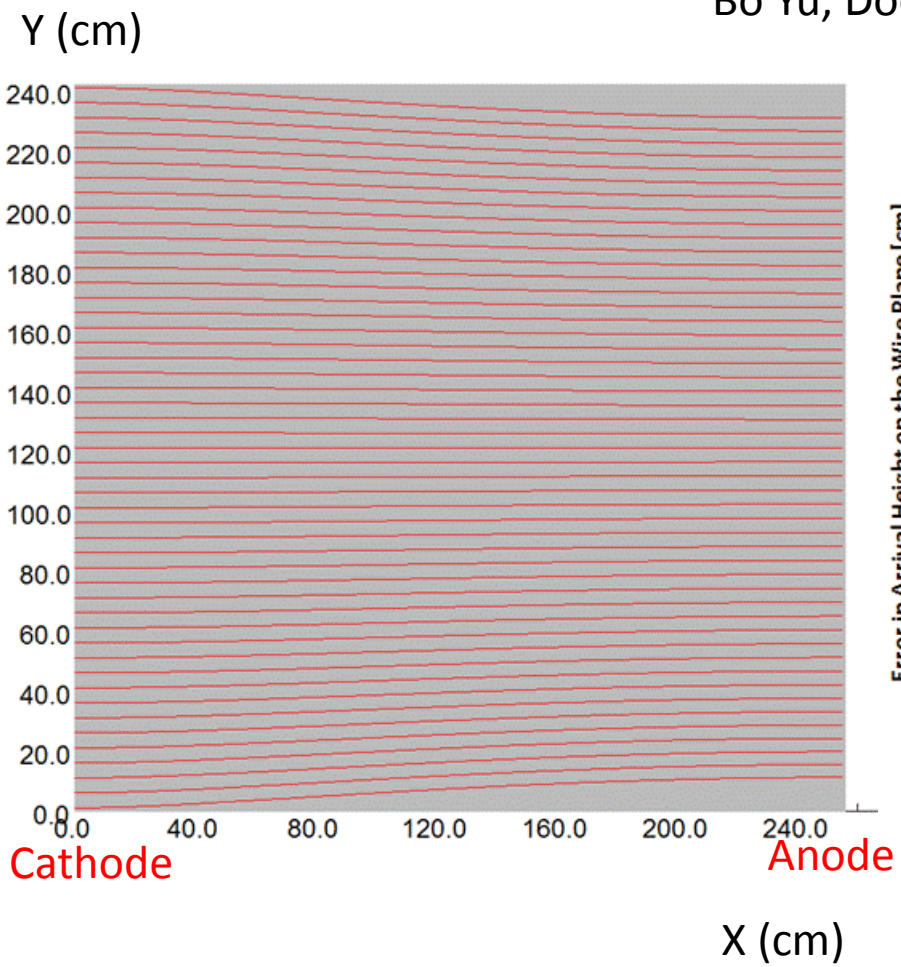
Positive Ions across Detector

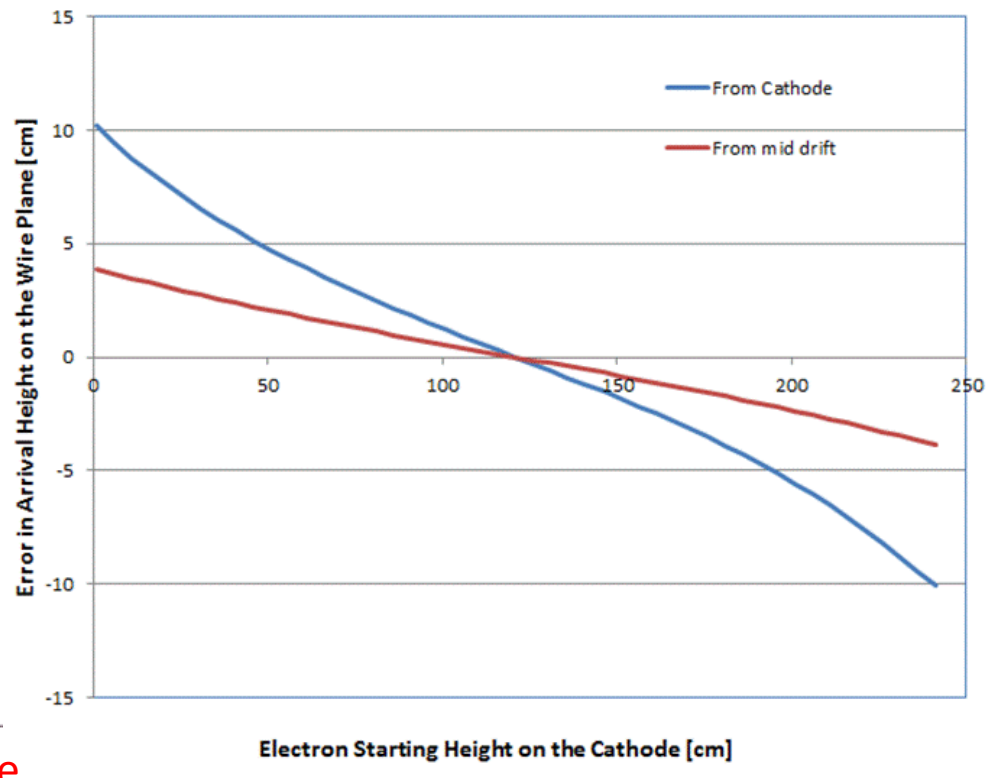




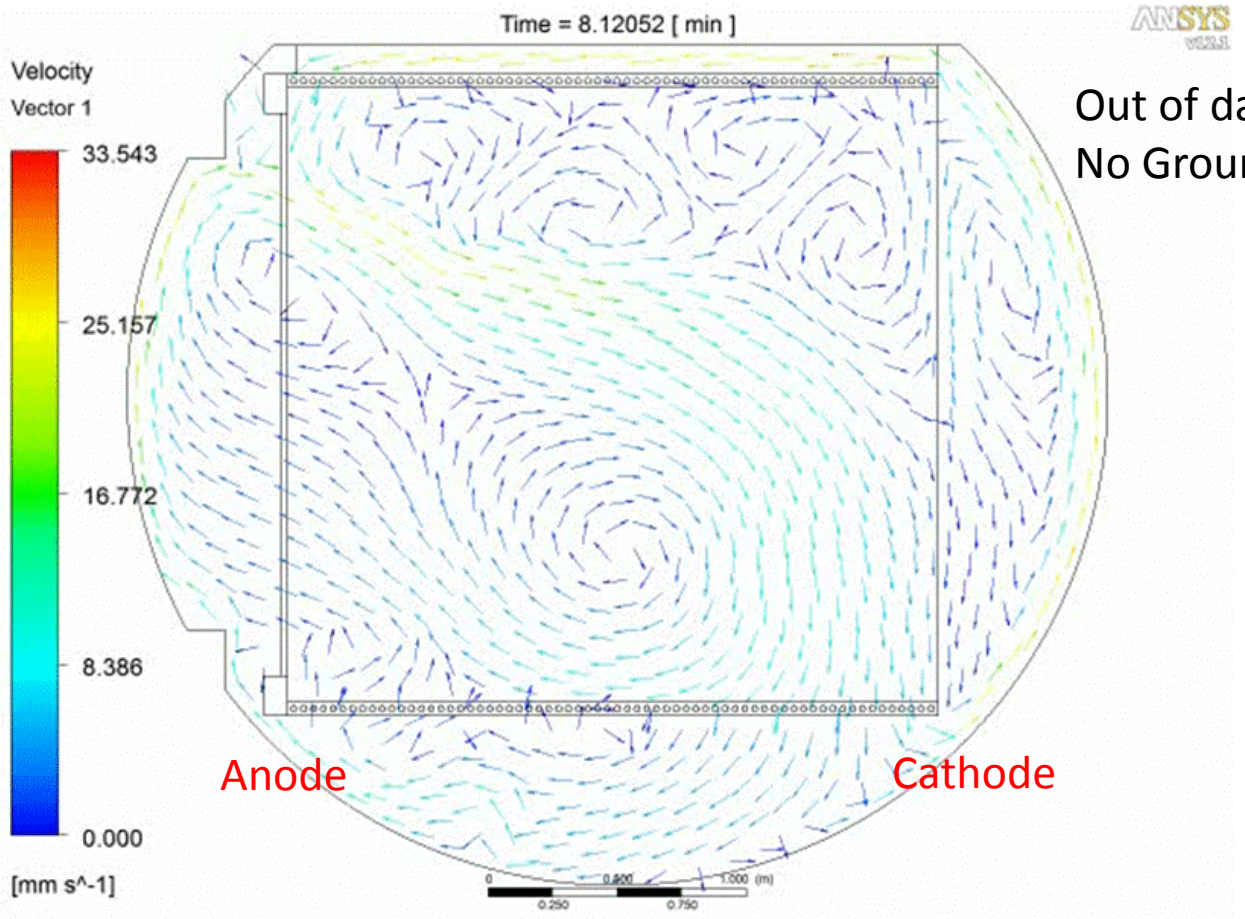
Size of Distortions Space

Bo Yu, DocDB #1377





Added complication – LAr movement



Out of date:
No Ground Plane Above

Erik Voirin - Fermilab MicroBooNe Buoyancy Driven Flow Analysis 23

Positive Ion Distortion Implementation

Will discussed implementation at tomorrow's simulation meeting

- Field map/argon drift distortions give a 1 to 1 mapping from electron production position to y-z plane and drift time coordinates.
- Diffusion and turbulence break the 1 to 1 mapping.
- LArSoft uses 1 to 1 mapping + diffusion to determine wire and time

Will have three options (fcl parameter selectable) in simulations:

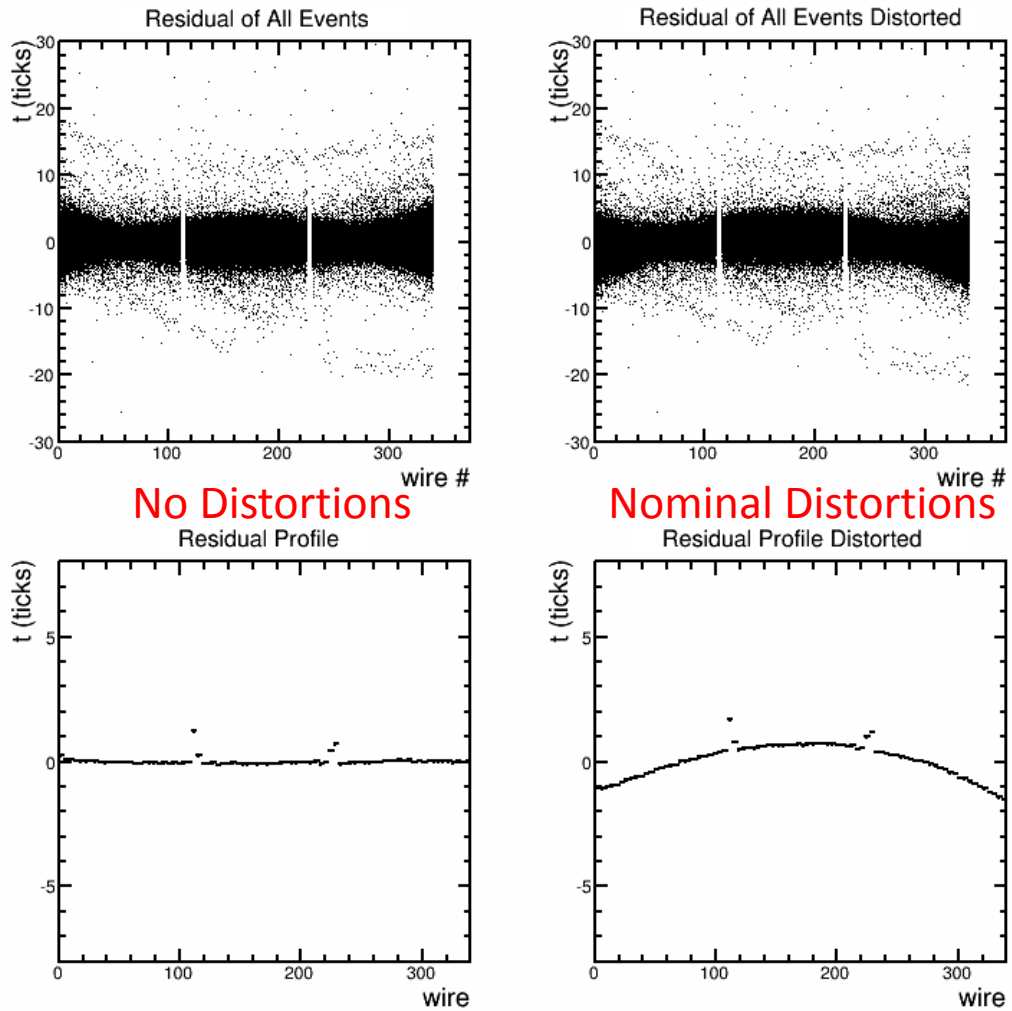
1. No positive ion distortions (what we have now)
2. Only time distortions
   a) Analytic calculation of distortion
   b) May take too long (a long in calculation of voxel drift time)
3. Mapping matrix of distortions
   a) May be 1D, 2D, or 3D distortions
   b) Might take up too much memory (might have to increase grid size)
   c) Could include argon flow

Can we measure distortions with muons?

Micah Groh –
LBNE DocDB #9454, #9587 –
time distortions in 35T prototype

E = 500 V/cm
P_μ = 6 GeV/c

Best line fits
Tick = .5 μsec ≈ 4 mm



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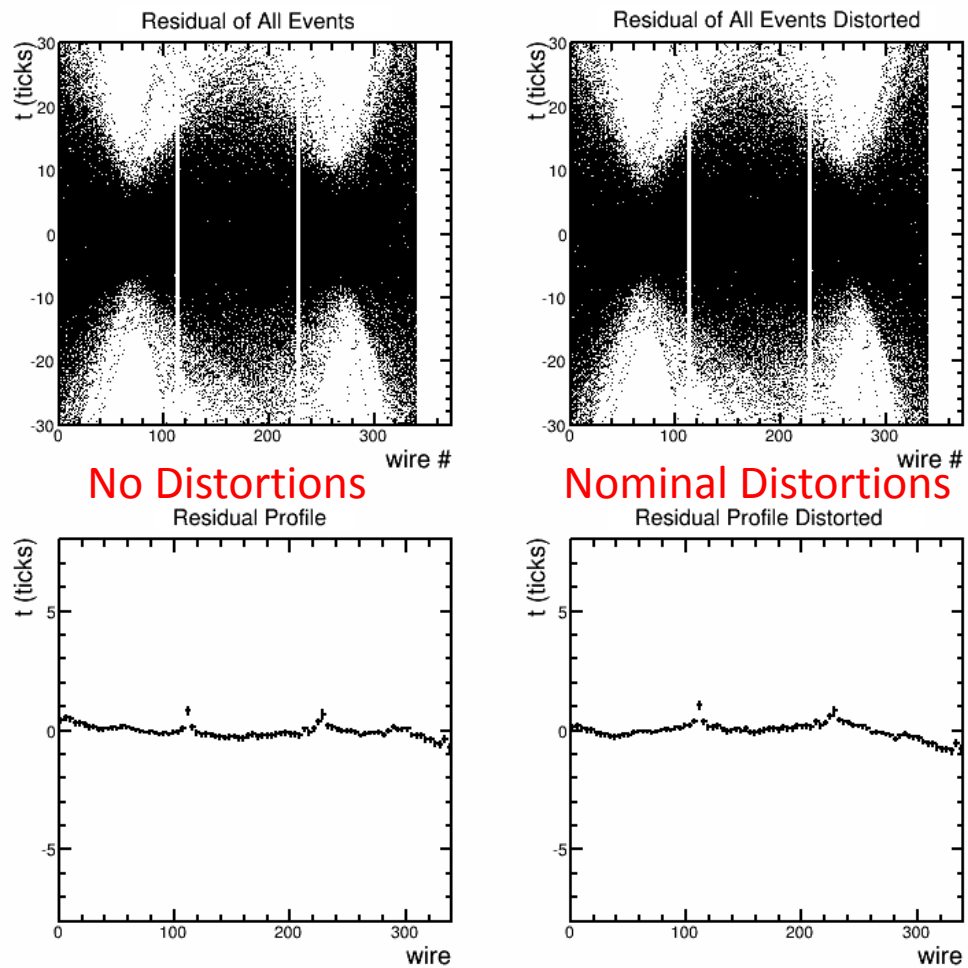

Can we measure distortions with laser?

Muon Problems:

- Don't have nominal track
- Multiple scattering

Laser Problems:

- Areas of drift volume not covered

Muon Advantages:

- Covers entire detector uniformly

Laser Advantages:

- Nominal positions known (with possibly single offset parameters)
- No multiple scattering
- Front/back comparison might tell us about Ar drift effects

Unfolding

3D inverse mapping:

- Requires reconstructed 3D space points (time, wire-y, wire-z)
- Does not effect plane-to-plane matching
- Mapping may be time dependent due to argon flow
- Mapping needs to be certified by in situ measurements

Time only unfolding:

- No analytic inverse but can be done numerically
- Can be done independent of y-z position, but may not be good near edges
- Need to study if this helps resolution/reconstruction etc.

All unfolding needs t(start) from PMTs.