ProtoDUNE DP
Pandora reconstruction updates

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DRA meeting - 06/05/2020

Pandora reconstruction for DP

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- Pandora used by many LArTPC experiments, including ProtoDUNE SP and DUNE FD
- Complete collection of detectors with DP
- Reconstruction already setup and working for ProtoDUNE DP!
- A small number of algorithms needs to be re-implemented for DP

Pandora reconstruction for DP (2)

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- DP reconstruction is an ongoing Pandora team development

- **Contact persons:** Maria Brigida Brunetti maria.brunetti@warwick.ac.uk
  Etienne Chardonnet chardonn@apc.in2p3.fr
  (or get in touch with anyone from Pandora group!)

- Ongoing items & TODO list organised through DP Pandora Slack channel and https://github.com/PandoraPFA/LArContent/projects/1

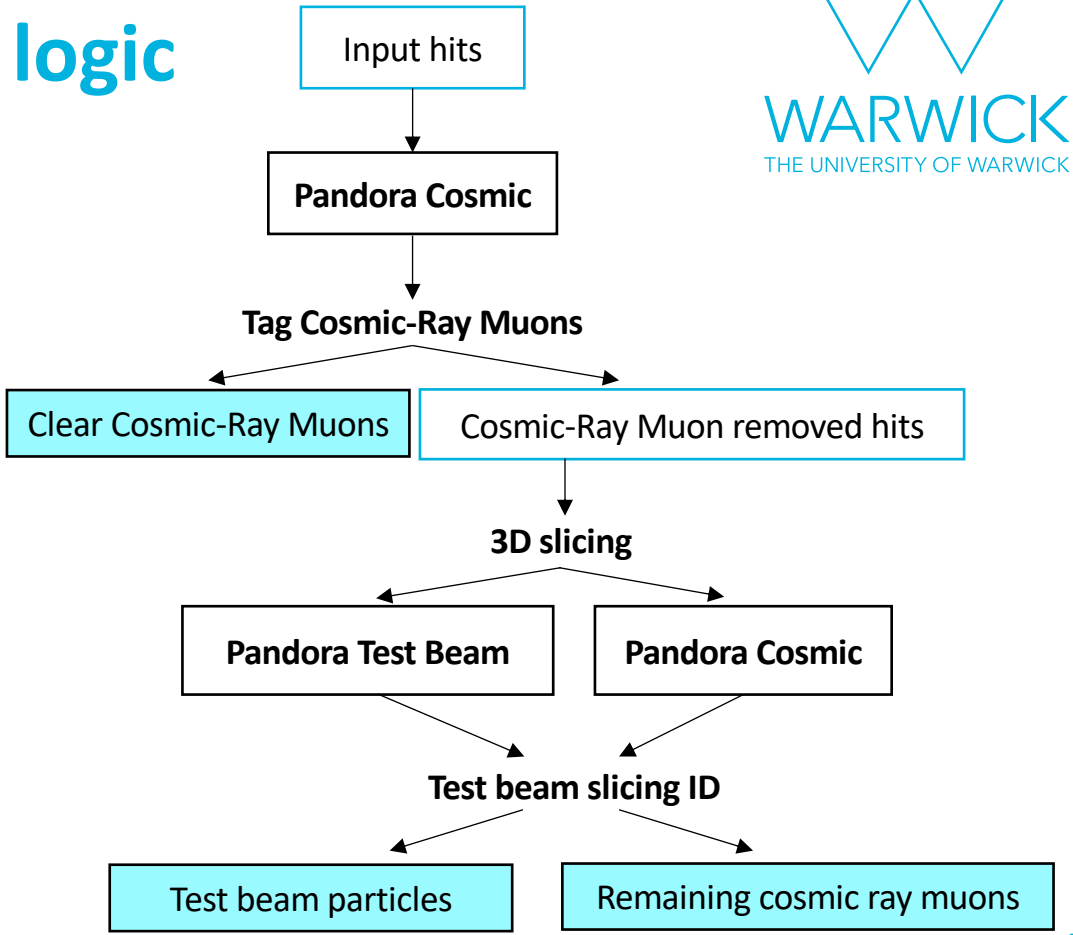
Outline

- Pandora Reconstruction logic
- Adapting Pandora to Dual Phase: a roadmap
- Overview of ongoing work
- Summary and next steps

Reconstruction full logic

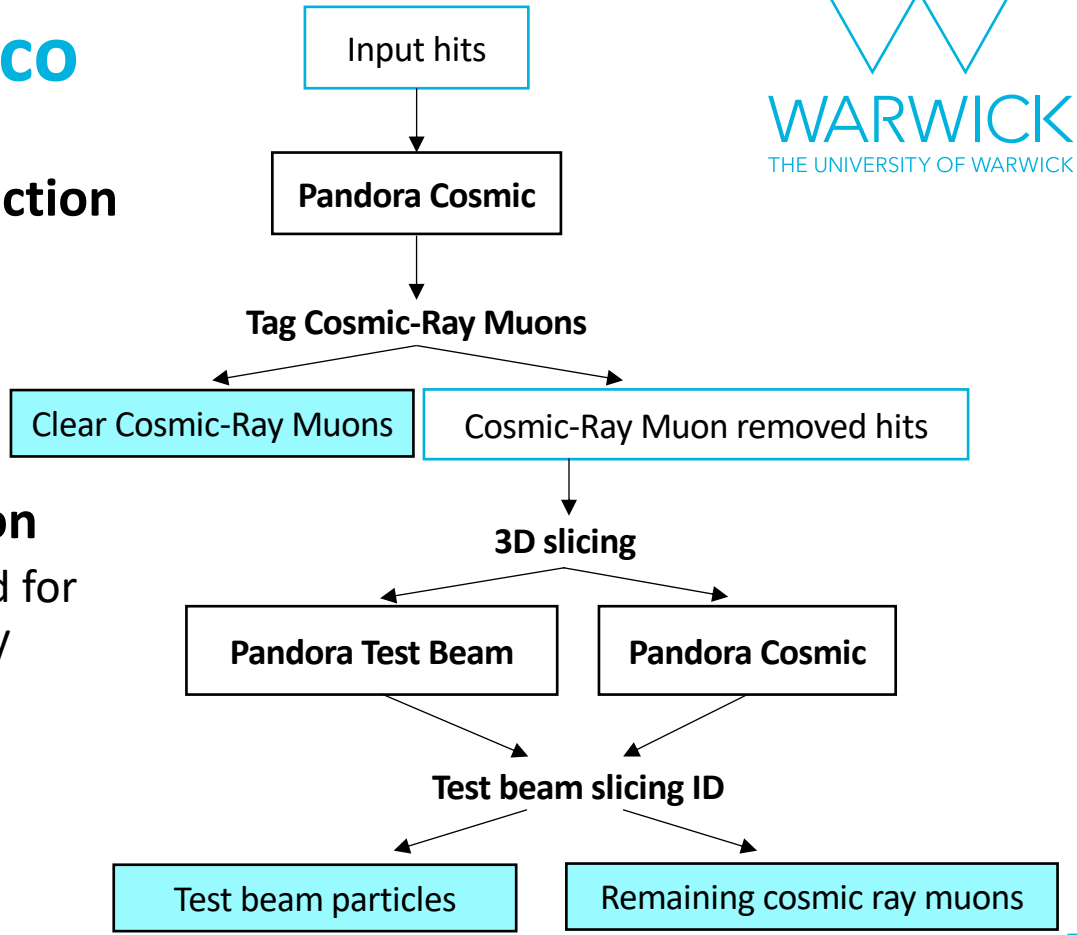
- Consolidated reconstruction runs two algorithm chains:

  Cosmic and **Test Beam**



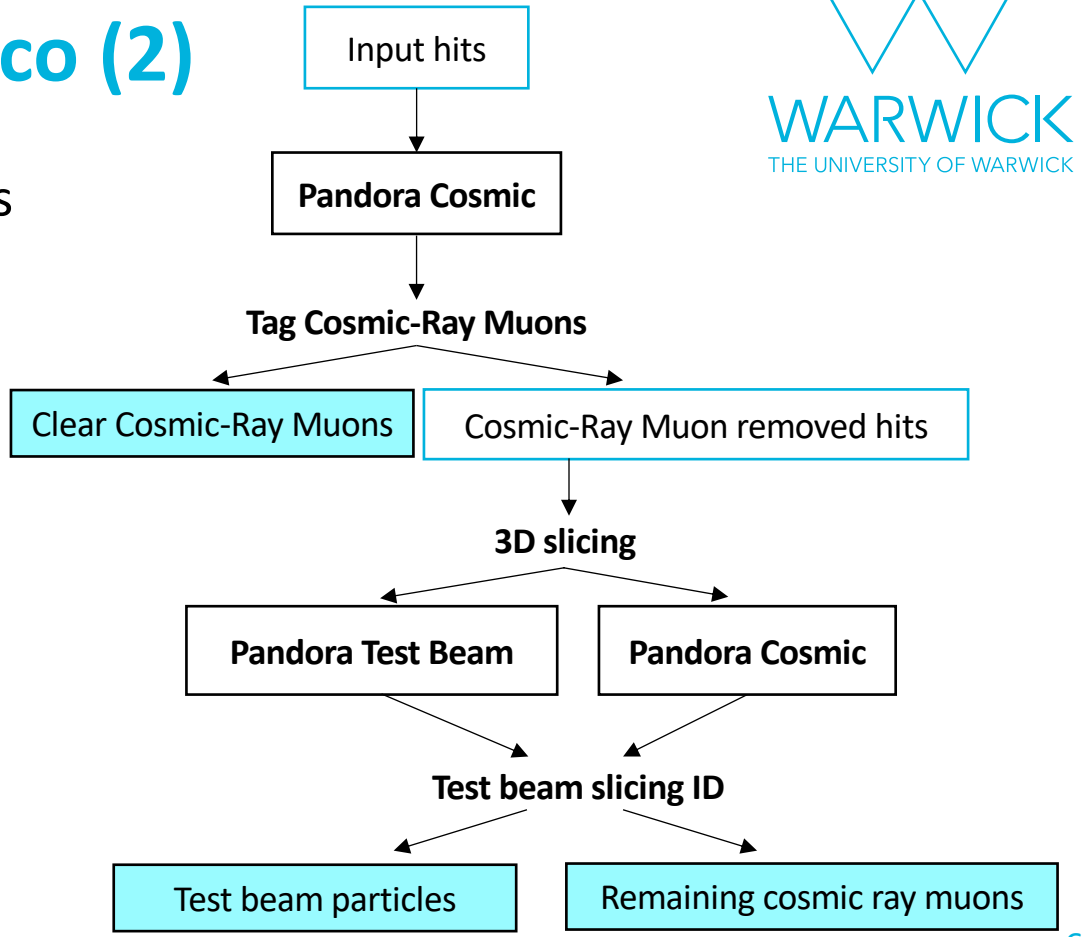
Roadmap for DP reco

- **Cosmic-ray muon reconstruction**
  - 2D reco audit
  - 2D → 3D matching adapted for 2-view readout
- **Beam particle reconstruction**
  - Algorithm changes motivated for the cosmic reco, as necessary



Roadmap for DP reco (2)

- Train machine learning steps
  - Vertex ID
  - Slice ID
- Train the classification of output tracks and showers in output hierarchies
- Sample creation
  - Cosmics
  - Beam particles
  - Cosmics + beam particles



Ongoing work

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- 2D pattern recognition assessment/adaptation (ongoing)
  (M. B. Brunetti, I. Mawby)
- Setup framework for two-view 2D → 3D matching ✓
  (J. Marshall)
- 2D → 3D matching with calorimetry (ongoing)
  (E. Chardonnet, D. Brailsford)

Hit width cluster merging algorithm

(I. Mawby)

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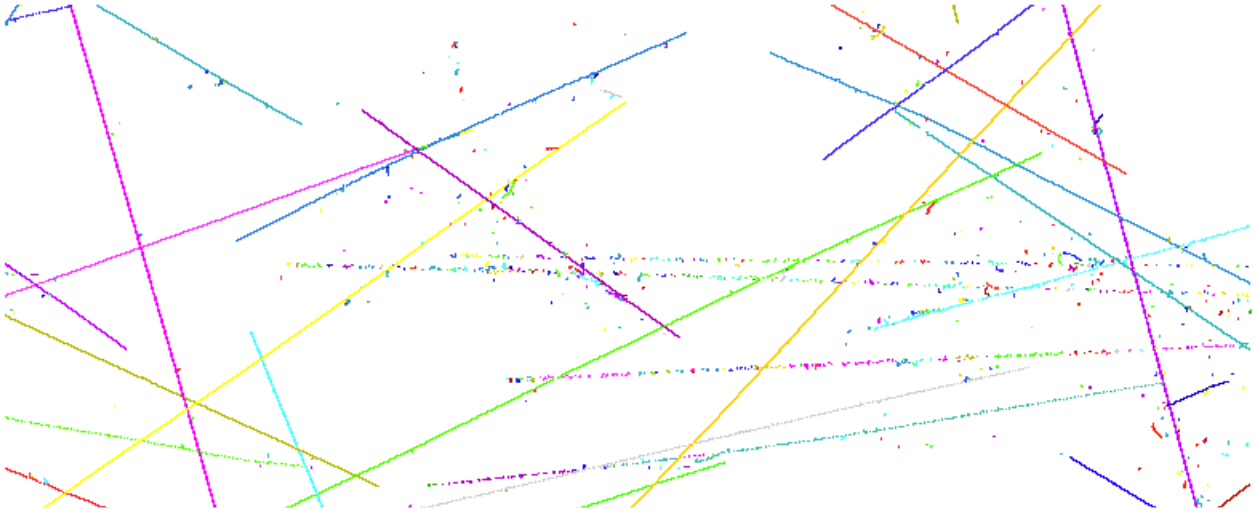
- Tracks parallel to drift direction are *sparse* → low completeness



Hit width cluster merging algorithm (2)

(I. Mawby)

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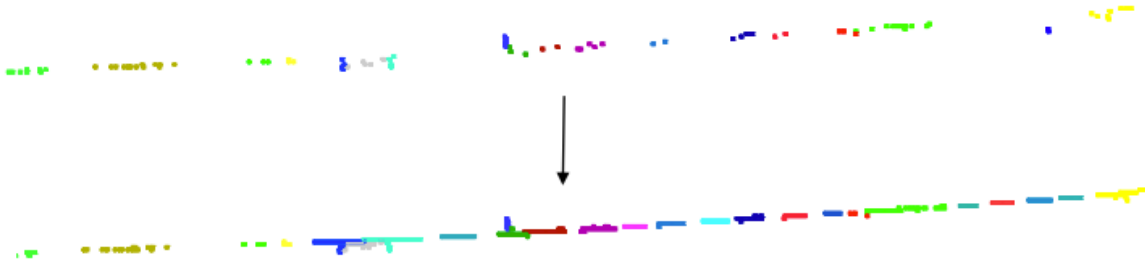
- Option to turn hit widths on in pandoramodules_dune.fcl



Hit widths off

Hit widths on

- Need to write new algorithms that use them

Hit width cluster merging algorithm (3)

(I. Mawby)

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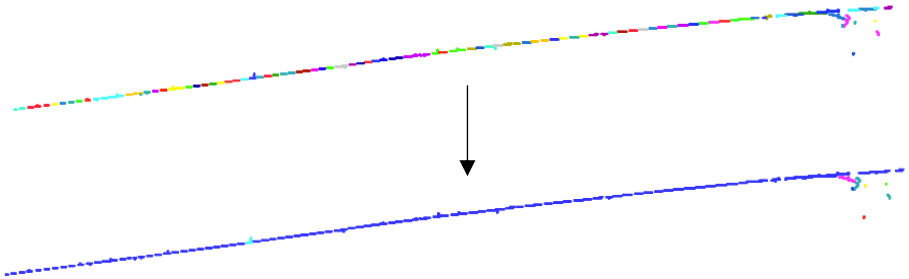
- HitWidthClusterMergingAlgorithm increases completeness
  - Walk along clusters
  - Merging decision based on coordinates of extrema and cluster direction

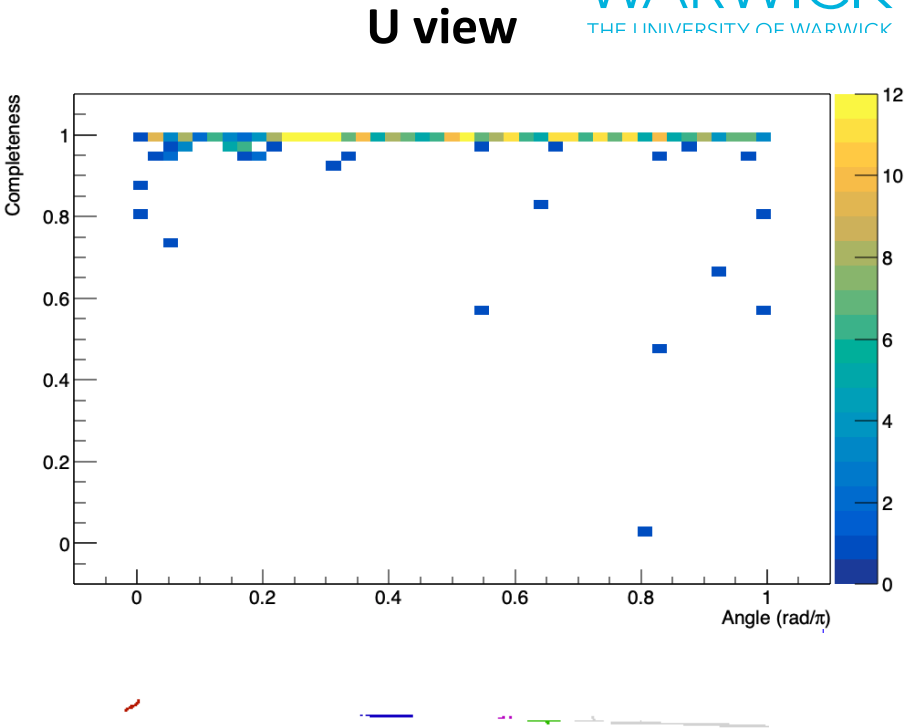


Hit Widths Cluster Merging Algorithm on

- Ready to be merged in LArSoft (will be enabled by default for DP)

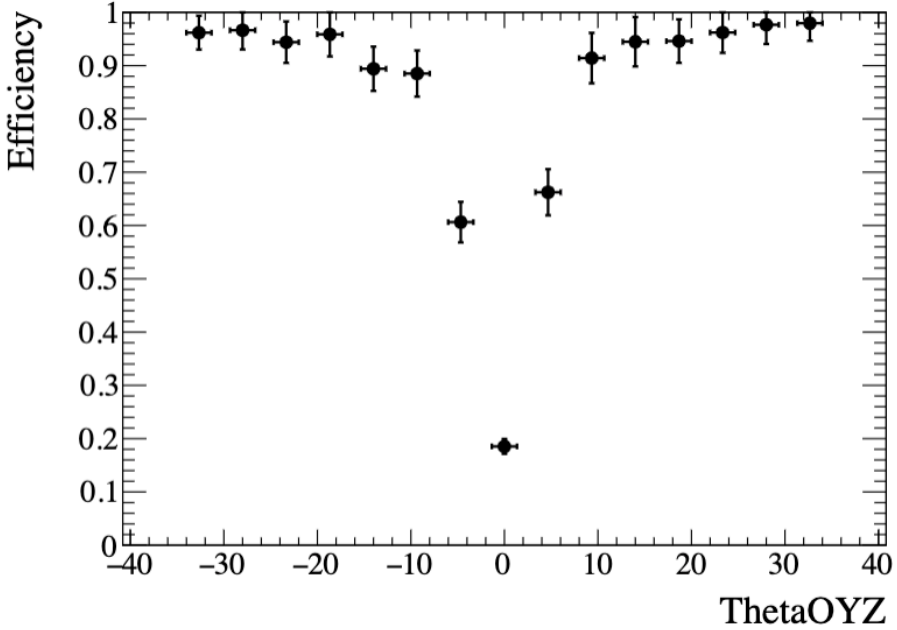
Single muon completeness (2D)

- Single muons in ProtoDUNE DP
- Momentum 10 GeV
- Uniform ThetaXZ distribution, ThetaYZ=0
- Hit width cluster merging algorithm enabled at end of 2D reco
- Increases overall completeness: **~97% → ~99% (U view)**
- **~54% → ~60% (V view, parallel to particles)**

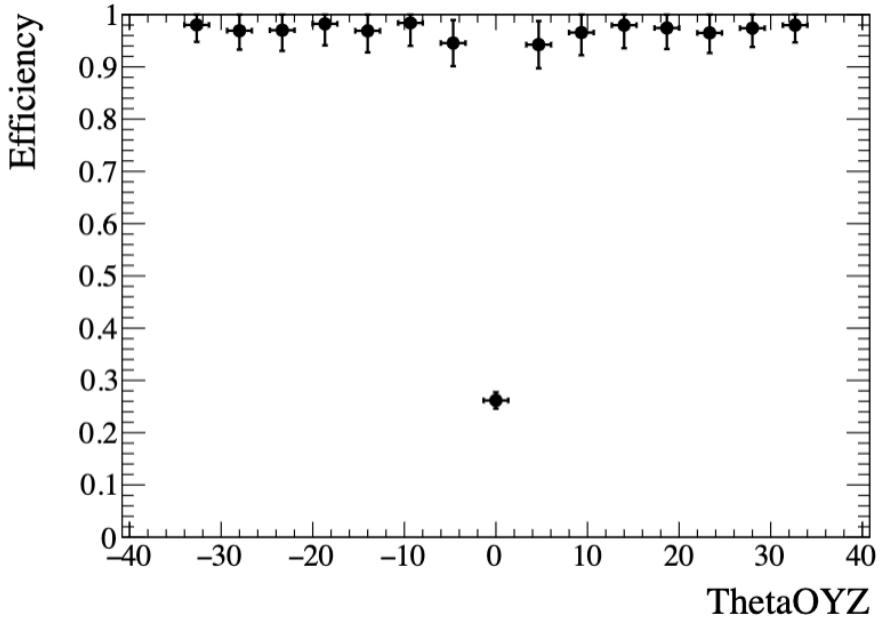


Single muon efficiency (3D)

(E. Chardonnet)



Hit With Cluster Merging Algorithm ON



2D → 3D matching (E. Chardonnet, D. Brailsford)

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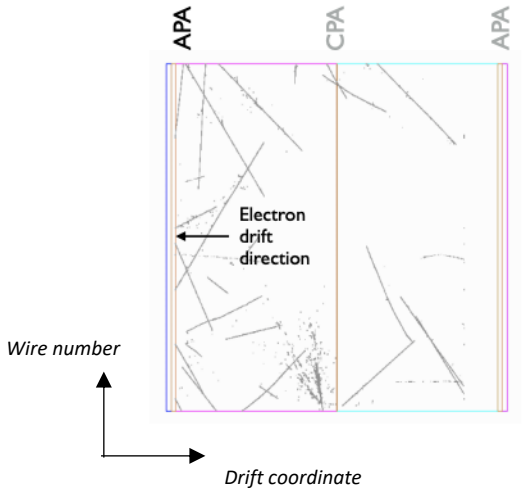
- **Follows 2D pattern recognition** performed in available views
- **Aim:** match 2D clusters across views to create 3D particles

Starting point: ProtoDUNE SP



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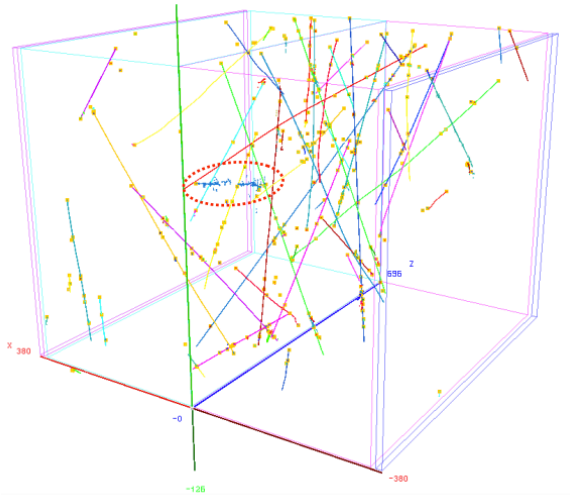

2D → 3D matching with three views

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- Only two non-parallel views required for inferring position in 3D
- However, redundant information necessary to correctly identify matches!

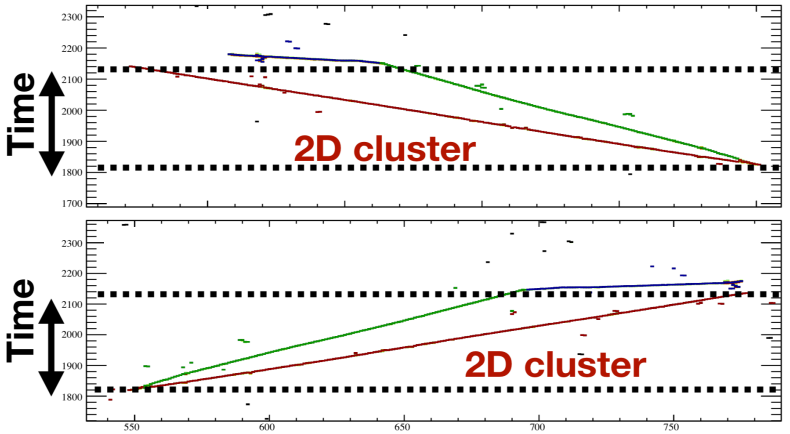
- Several 2D → 3D matching algorithms in Pandora

- Main algorithm requires three views:
  - Two views used to predict cluster position in third view
  - Inferred position compared to real position in third view

- New solution required for two-view detectors such as ProtoDUNE DP
- A strong possibility: **use of calorimetric information** (all new)

Procedure

1. Find all cluster pairs across two views
   (in the example: RR, RG, GR, GG)
2. Identify region of overlap
   (dotted region)



Two-particle development example

Resampled fractional charge profiles

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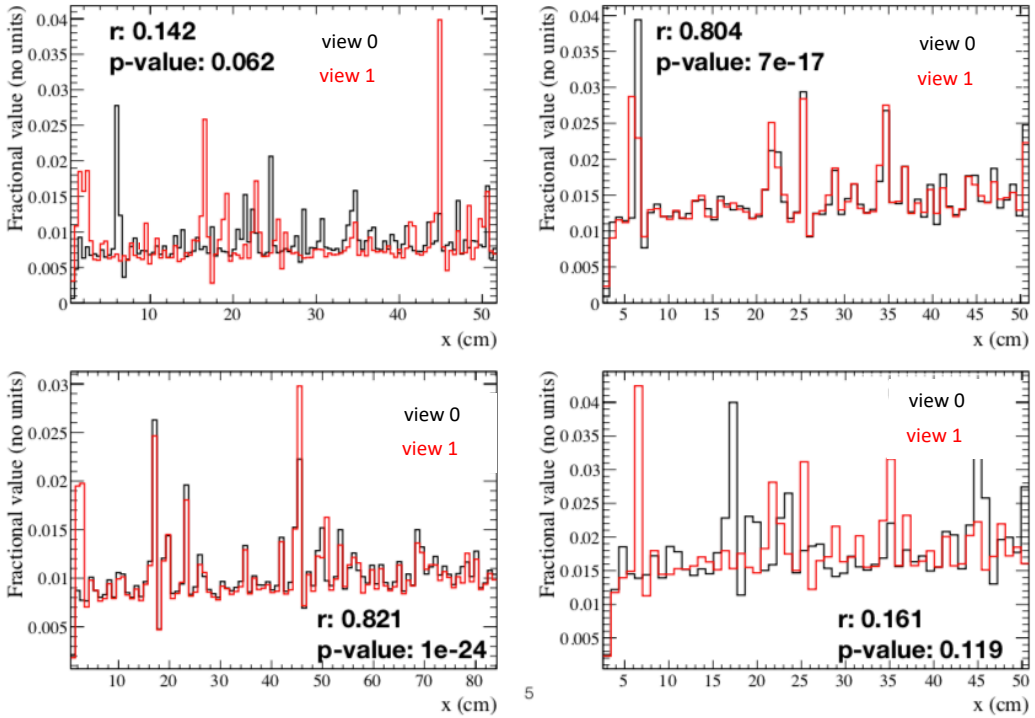
3. Build fractional charge profiles
   (downsampled and equally binned)
4. Calculate correlation coefficient r and p-value

Correct matches:

high r, low p-value

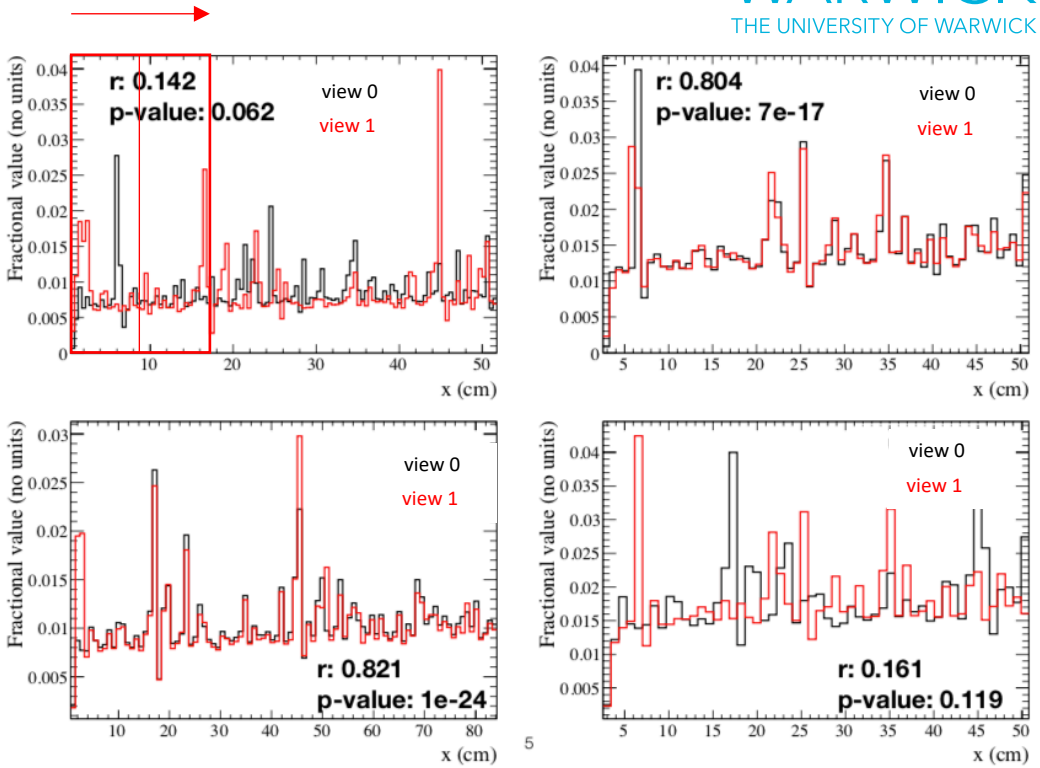


ProtoDUNE DP di-muon sample originating from common point

Sliding window scores

Starting from profiles, can also study local correlation:

1. Slide window across fractional charge profile
2. **Matching score**: 1 – p-value
3. Record score from center of window



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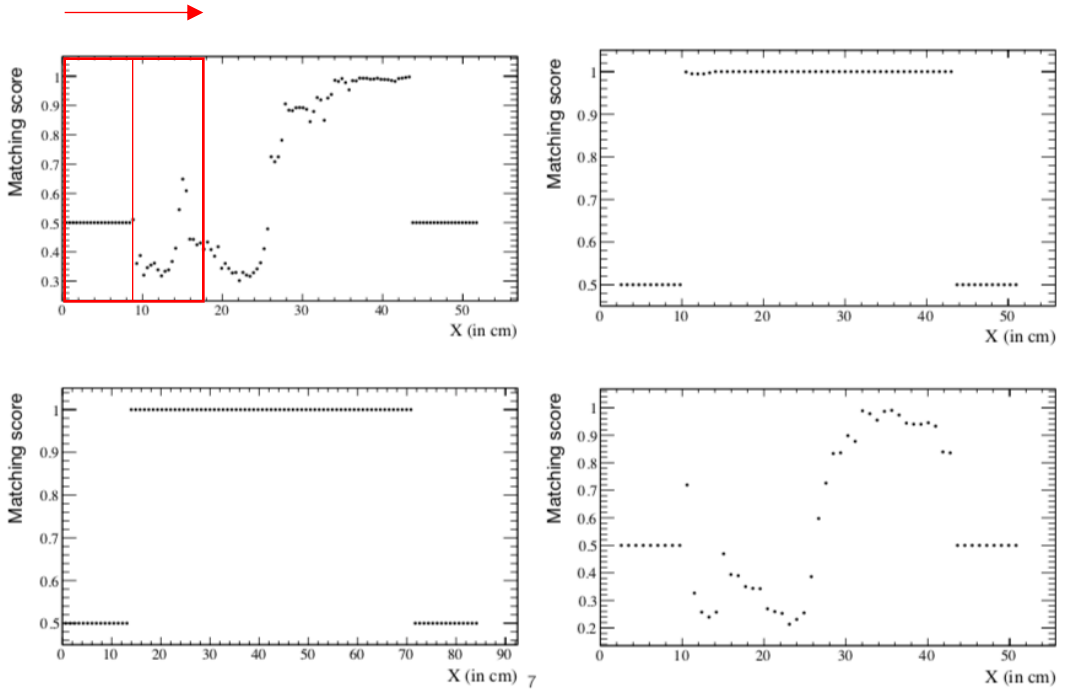


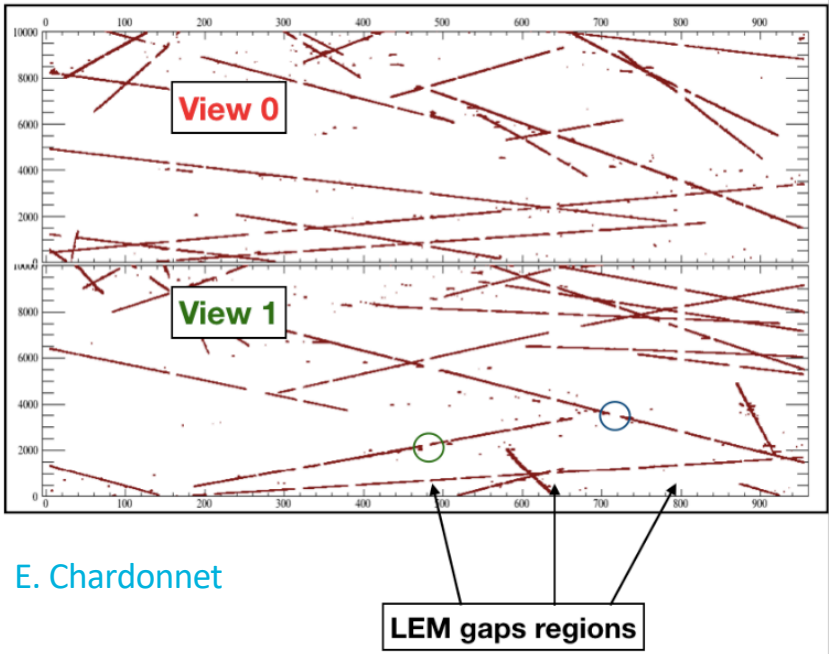
Correct matches:

Matching score flat at 1

ProtoDUNE DP di-muon sample originating from common point

2D → 3D matching next steps

- Three tools being developed for cluster **matching**, **merging** and **splitting**
- Charge information can be also used to match clusters across the LEM gaps, in addition to other variables



E. Chardonnet

Summary

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- Clear roadmap for DP reconstruction
- 2D pattern recognition works well for DP
- Recent improvement thanks to Hit Width Cluster Merging Algorithm
- Further adaptations and new algorithms being explored
- 2D →3D matching being adapted for Dual Phase technology including calorimetric information
- Good separation is achieved with current checks
- Next steps identified. Expect updates soon!

Pandora Liaisons

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Experiment/detector	Liaisons
DUNE FD single phase	Dom Brailsford, Andy Chappell
ProtoDUNE single phase	Leigh Whitehead, Steve Dennis
DUNE dual phase (ProtoDUNE graduating to FD)	Maria Brigida Brunetti, Etienne Chardonnet
MicroBooNE	Andy Smith, Alex Moor
SBN	Dom Brailsford, Ed Tyley, Yun-Tse Tsai

Please, do get in touch about any comment or concern!

Spares

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Statistical parenthesis

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- For uncorrelated bi-variate normal distribution pairs, correlation coefficient follows Student t-distribution:

$$t = r\sqrt{\frac{n-2}{1-r^2}}$$

- For large samples, can hold for non-gaussian variables
- p-value: right-tail integral of t-distribution

- Is this assumption good?

Statistical parenthesis (2)

- Toy study performed with 10000 fake fractional charge profiles
- Two matching and one non-matching profile simulated:
  - Profile 1 = Landau n.1 + gaussian smearing n.1
  - Profile 2 = Landau n.1 + gaussian smearing n.2
  - Profile 3 = Landau n.2
- p-value is not flat **(A)** → not statistically robust
- Alternative p-value calculation:

  permutation test – yields flat p-value **(B)**